

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
27 November 2003 (27.11.2003)

PCT

(10) International Publication Number
WO 03/097810 A2

(51) International Patent Classification⁷: C12N

Trebol Street, San Diego, CA 92126 (US). FARWELL, Robert [US/US]; 4415 Terreno Court, San Diego, CA 92124 (US). CHATMAN, Kelly [US/US]; P.O. Box 429, Solana Beach, CA 92075 (US).

(21) International Application Number: PCT/US03/15712

(22) International Filing Date: 15 May 2003 (15.05.2003)

(74) Agent: EINHORN, Gregory, P.; Fish & Richardson P.C., 4350 La Jolla Village Drive, Suite 500, San Diego, CA 92122 (US).

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
10/146,772 15 May 2002 (15.05.2002) US
10/241,742 9 September 2002 (09.09.2002) US

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

US 10/241,742 (CIP)
Filed on 9 September 2002 (09.09.2002)
US 10/146,772 (CIP)
Filed on 15 May 2002 (15.05.2002)

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

(71) Applicant (*for all designated States except US*): DIVERSA CORPORATION [US/US]; 4955 Directors Place, San Diego, CA 92121 (US).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): DESANTIS, Grace [CA/US]; 3520 Lebon Drive, Apt. 5223, San Diego, CA 92121 (US). SHORT, Jay, M. [US/US]; 681 Paseo Delicias, Box 7214, Rancho Santa Fe, CA 92067 (US). BURK, Mark [US/US]; 12634 Intermezzo Way, San Diego, CA 92130 (US). WONG, Kevin [US/US]; 11304

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: NITRILASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AND USING THEM

(57) Abstract: The invention relates to nitrilases and to nucleic acids encoding the nitrilases. In addition methods of designing new nitrilases and method of use thereof are also provided. The nitrilases have increased activity and stability at increased pH and temperature.



WO 03/097810 A2

NITRILASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AND USING THEM

CROSS-REFERENCES TO RELATED APPLICATIONS

[0001] This application claims the benefit of priority to U.S. Patent Application Serial
5 No. (USSN) 10/241,742, filed September 9, 2002, and USSN 10/146,772, filed May 15,
2002, which claims the benefit of priority to USSN 60/351,336, filed January 22, 2002,
USSN 60/309, 006, filed July 30, 2001, and USSN 60/300,189, filed June 21, 2001; and is a
continuation-in-part of USSN 09/751,299, filed December 28, 2000, which claims the benefit
of priority to each of USSN 60/254,414, filed December 7, 2000, and USSN 60/173,609,
10 filed December 29, 1999. These applications are hereby incorporated by reference into the
subject application in their entireties for all purposes.

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FIELD OF THE INVENTION

[0003] The invention relates generally to the field of molecular biology, biochemistry and
20 chemistry, and particularly to enzymatic proteins having nitrilase activity. The invention also
relates to polynucleotides encoding the enzymes, and to uses of such polynucleotides and
enzymes.

BACKGROUND OF THE INVENTION

[0004] There are naturally occurring enzymes which have great potential for use in
25 industrial chemical processes for the conversion of nitriles to a wide range of useful products
and intermediates. Such enzymes include nitrilases which are capable of converting nitriles
directly to carboxylic acids. Nitrilase enzymes are found in a wide range of mesophilic
micro-organisms, including species of *Bacillus*, *Nocardia*, *Bacteridium*, *Rhodococcus*,

micro-organisms, including species of *Bacillus*, *Nocardia*, *Bacteridium*, *Rhodococcus*, *Micrococcus*, *Brevibacterium*, *Alcaligenes*, *Acinetobacter*, *Corynebacterium*, *Fusarium* and *Klebsiella*. Additionally, there are thermophilic nitrilases which exist in bacteria.

[0005] There are two major routes from a nitrile to an analogous acid: (1) a nitrilase
5 catalyzes the direct hydrolysis of a nitrile to a carboxylic acid with the concomitant release of ammonia; or (2) a nitrile hydratase adds a molecule of water across the carbon-nitrogen bonding system to give the corresponding amide, which can then act as a substrate for an amidase enzyme which hydrolyzes the carbon-nitrogen bond to give the carboxylic acid product with the concomitant release of ammonia. The nitrilase enzyme therefore provides
10 the more direct route to the acid.

[0006] A nitrile group offers many advantages in devising synthetic routes in that it is often easily introduced into a molecular structure and can be carried through many processes as a masked acid or amide group. This is only of use, however, if the nitrile can be unmasked at the relevant step in the synthesis. Cyanide represents a widely applicable C₁-synthon
15 (cyanide is one of the few water-stable carbanions) which can be employed for the synthesis of a carbon framework. However, further transformations of the nitrile thus obtained are impeded due to the harsh reaction conditions required for its hydrolysis using normal chemical synthesis procedures. The use of enzymes to catalyze the reactions of nitriles is attractive because nitrilase enzymes are able to effect reactions with fewer environmentally
20 hazardous reagents and by-products than in many traditional chemical methods. Indeed, the chemoselective biocatalytic hydrolysis of nitriles represents a valuable alternative because it occurs at ambient temperature and near physiological pH.

[0007] The importance of asymmetric organic synthesis in drug design and discovery has fueled the search for new synthetic methods and chiral precursors which can be utilized in
25 developing complex molecules of biological interest. One important class of chiral molecules is the α -substituted carboxylic acids, which include the α -amino acids. These molecules have long been recognized as important chiral precursors to a wide variety of complex biologically active molecules, and a great deal of research effort has been dedicated to the development of methods for the synthesis of enantiomerically pure α -amino acids and
30 chiral medicines.

[0008] Of particular use to synthetic chemists who make chiral medicines would be an enzyme system which is useful under non-sterile conditions, which is useful in non-biological laboratories, which is available in a form convenient for storage and use; which has broad

substrate specificity, which acts on poorly water soluble substrates; which has predictable product structure; which provides a choice of acid or amide product; and which is capable of chiral differentiation. Accordingly, there is a need for efficient, inexpensive, high-yield synthetic methods for producing enantiomerically pure α -substituted carboxylic acids, such as, for example, α -amino acids and α -hydroxy acids.

[0009] In addition, often, the discovery or evolution of an enzyme to perform a particular transformation can be aided by the availability of a convenient high throughput screening or selection process. While a surrogate substrate may be used when an effective ultra high throughput (UHTP) screen is not available, it may be desirable to screen directly for an enzyme that performs specifically the desired transformation. The challenges of designing a UHTP screen is evident when, for example, the discovery or evolution program is aimed at uncovering a stereoselective transformation to generate only one stereoisomer or enantiomer. In this case, there is a paucity of high throughput screening methods available. While, the most straightforward method is to use chiral liquid or gas phase separation to separate the two enantiomers in question, often this approach does not afford the very high throughput capacity that is required. By using mass spectroscopy (MS) techniques, very high throughput screens are possible. However, when applied in a conventional manner, MS does not afford information on chirality or enantioselectivity.

[00010] Another approach is to chemically derivatize the enantiomeric mixture with a single enantiomer compound, thus generating a diastereomeric mixture of compounds that can be characterized by separation on an achiral stationary phase. Again, this is a cumbersome approach and does not lend itself well to high throughput screening.

[00011] Throughout this application, various publications are referenced by author and date. The disclosures of these publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art as known to those skilled therein as of the date of the invention described and claimed herein.

SUMMARY OF THE INVENTION

[00012] The present invention is directed to an isolated or recombinant nucleic acid comprising nucleotides having a sequence at least about 50% identical to SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177,

179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, or variants thereof, wherein the nucleic acid encodes a polypeptide having a nitrilase activity. In alternative aspects of the invention, the nucleic acid comprises nucleotides having a sequence at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete identity (100% identical) to the SEQ ID NO: or variants thereof. Exemplary variants may include, for example, the following variations of SEQ ID NO:195, 205, 207, 209, OR 237, having one or more mutations: at positions 163-165 AAA, AAG, GGT, GGC, GGA, GGG, CAA, or CAG; at positions 178-180 GAA or GAG; at positions 331-333 TCT, TCC, TCA, TCG, AGT, or AGC; at positions 568-570 CAT, CAC, TCT, TCC, TCA, TCG, AGT, AGC, ACT, ACC, ACA, TCA, TAT, TAC, ATG or ACG; at positions 571-573 TTA, TTG, CTT, CTC, CTA, CTG, GTT, GTC, GTA, GTG, ATG, ACT, ACC, ACA, GAT, GAC, GGT, GGC, GGA, GGG, GAA, GAG, TAT, TAC, or ACG; at positions 595-597 GAA, GAG, TTA, TTG, CTT, CTC, CTA, or CTG; at positions 664-666 TTA, TTG, CTT, CTC, CTA, or CTG; or any combination thereof. In one aspect of the invention, the variants encode a polypeptide having improved or diminished enantioselectivity, for example, in the conversion of a 3-hydroxyglutarylnitrile (HGN) to (R)-4-Cyano-3-hydroxybutyrate, than the polypeptide encoded by the SEQ ID NO.

[00013] In one aspect of the invention, the nucleic acid comprises nucleotides having a sequence substantially identical to the SEQ ID NO: or variants thereof. In another aspect, the invention provides for an isolated or recombinant nucleic acid comprising consecutive nucleotides having a sequence at least 79 % identical to SEQ ID NO: 33, wherein the nucleic acid encodes a polypeptide having nitrilase activity. The invention provides for a fragment of the nucleic acid, wherein the fragment encodes a polypeptide having nitrilase activity. The invention also provides for an isolated or recombinant nucleic acid complementary to any of the nucleic acids. The invention also provides for an isolated or recombinant nucleic acid

that hybridizes to any one of the nucleic acids under stringent conditions. In one aspect, the stringent conditions comprise at least 50% formamide, and about 37°C to about 42°C.

[00014] The invention provides for a nucleic acid probe comprising from about 15 nucleotides to about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 150, 200, 250, 300, 350, 400, 450, 500 or more nucleotides, wherein at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more consecutive nucleotides are at least 50% complementary to a nucleic acid target region within a nucleic acid sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, variants thereof, or their complements. In one aspect, the nucleic acid probe comprises consecutive nucleotides which are at least 55% complementary to the nucleic acid target region. In one aspect, the invention provides for a nucleic acid probe, wherein the consecutive nucleotides are at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more or 100% complementary to the nucleic acid target region. In another aspect, the nucleic acid consists essentially of from about 20 to about 50 nucleotides. In other aspects, the nucleic acid can be at least about 20, 25, 30, 35, 40, 45, 50, 75, 100, 150 nucleotides in length.

[00015] The invention provides for a nucleic acid vector capable of replication in a host cell, wherein the vector comprises the nucleic acid of the invention. The invention also provides for a host cell comprising the nucleic acid. The invention also provides for a host organism comprising the host cell. In one aspect, the host organism comprises a gram negative bacterium, a gram positive bacterium or a eukaryotic organism. In another aspect, the gram negative bacterium comprises *Escherichia coli*, or *Pseudomonas fluorescens*. In a

further aspect, the gram positive bacterium comprises *Streptomyces diversa*, *Lactobacillus gasseri*, *Lactococcus lactis*, *Lactococcus cremoris*, or *Bacillus subtilis*. In a further aspect, the eukaryotic organism comprises *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Pichia pastoris*, *Kluyveromyces lactis*, *Hansenula polymorpha*, or *Aspergillus niger*.

5 [00016] The invention provides for an isolated or recombinant nucleic acid encoding a polypeptide comprising amino acids having a sequence at least 50% identical to SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 10 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 15 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, or variants thereof, wherein the polypeptide has nitrilase activity. In one aspect, the polypeptide comprises amino acids having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 20 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more or 100% identity to the SEQ ID NO: or variants thereof. Exemplary variants may include, for example, the following variations of SEQ ID NO:196, 206, 208, 210 or 238, having one or more mutations: at residue 55 lysine, glycine, or glutamine; at residue 60 glutamic acid; at residue 25 111 serine, at residue 190, serine, histidine, tyrosine or threonine; at residue 191, leucine, valine, methionine, aspartic acid, glycine, glutamic acid, tyrosine or threonine; at residue 199 glutamic acid or leucine; at residue 222 leucine; or any combination thereof.

[00017] The invention also provides for an isolated or recombinant nucleic acid encoding a polypeptide comprising at least 10 consecutive amino acids having a sequence identical to a 10 portion of an amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154,

156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190,
192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226,
228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262,
264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298,
5 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334,
336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370,
372, 374, 376, 378, 380, 382, 384, 386, or variants thereof.

[00018] An isolated or recombinant polypeptide comprising amino acids having a
sequence at least about 50% identical to SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24,
10 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74,
76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116,
118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152,
154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188,
190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224,
15 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260,
262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296,
298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332,
334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368,
370, 372, 374, 376, 378, 380, 382, 384, 386, or variants thereof, wherein the polypeptide has
20 nitrilase activity. In one aspect of the invention, the polypeptide comprises amino acids
having a sequence at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%,
60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%,
76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%,
92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more or 100% identical to the SEQ ID NO:
25 or variants thereof.

[00019] The invention provides an isolated or recombinant nucleic acid comprising
nucleotides having a sequence as set forth in any one of the following SEQ ID NOS:1, 3, 5, 7,
9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59,
61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105,
30 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141,
143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177,
179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213,
215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249,

251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, and variants thereof

5 (hereinafter referred to as "Group A nucleic acids"). The invention is also directed to nucleic acids having specified minimum percentages of sequence identity to any of the Group A nucleic acids sequences.

[00020] In another aspect, the invention provides an isolated (purified) or recombinant polypeptide comprising amino acid residues having a sequence as set forth in any one of the
10 following SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200,
15 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380,
20 382, 384, 386, and variants thereof, (hereinafter referred to as "Group B amino acid sequences"). The invention is also directed to purified polypeptides having specified minimum percentages of sequence identity to any of the Group B amino acid sequences.

[00021] The invention provides for a fragment of the polypeptide which is at least 50 amino acids in length, and wherein the fragment has nitrilase activity. Furthermore, the
25 invention provides for a peptidomimetic of the polypeptide or a fragment thereof having nitrilase activity. The invention provides for a codon-optimized polypeptide or a fragment thereof, having nitrilase activity, wherein the codon usage is optimized for a particular organism or cell. Narum et al. *Infect. Immun.* 2001 Dec, 69(12):7250-3 describes codon-optimization in the mouse system. Outchkourov et al. *Protein Expr. Purif.* 2002 Feb;
30 24(1):18-24 describes codon-optimization in the yeast system. Feng et al. *Biochemistry* 2000 Dec 19, 39(50):15399-409 describes codon-optimization in *E. coli*. Humphreys et al. *Protein Expr. Purif.* 2000 Nov, 20(2):252-64 describes how codon usage affects secretion in *E. coli*.

[00022] In one aspect, the organism or cell comprises a gram negative bacterium, a gram positive bacterium or a eukaryotic organism. In another aspect of the invention, the gram negative bacterium comprises *Escherichia coli*, or *Pseudomonas fluorescens*. In another aspect of the invention, the gram positive bacterium comprise *Streptomyces diversa*,
5 *Lactobacillus gasseri*, *Lactococcus lactis*, *Lactococcus cremoris*, or *Bacillus subtilis*. In another aspect of the invention, the eukaryotic organism comprises *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Pichia pastoris*, *Kluyveromyces lactis*, *Hansenula polymorpha*, or *Aspergillus niger*.

[00023] In another aspect, the invention provides for a purified antibody that specifically
10 binds to the polypeptide of the invention or a fragment thereof, having nitrilase activity. In one aspect, the invention provides for a fragment of the antibody that specifically binds to a polypeptide having nitrilase activity.

[00024] The invention provides for an enzyme preparation which comprises at least one of the polypeptides of the invention, wherein the preparation is liquid or dry. The enzyme
15 preparation includes a buffer, cofactor, or second or additional protein. In one aspect the preparation is affixed to a solid support. In one aspect of the invention, the solid support can be a gel, a resin, a polymer, a ceramic, a glass, a microelectrode and any combination thereof. In another aspect, the preparation can be encapsulated in a gel or a bead.

[00025] The invention further provides for a composition which comprises at least one
20 nucleic acid of the invention which comprises at least one polypeptide of the invention or a fragment thereof, or a peptidomimetic thereof, having nitrilase activity, or any combination thereof.

[00026] The invention provides for a method for hydrolyzing a nitrile to a carboxylic acid comprising contacting the molecule with at least one polypeptide of the invention or a
25 fragment thereof, or a peptidomimetic thereof, having nitrilase activity, under conditions suitable for nitrilase activity. In one aspect, the conditions comprise aqueous conditions. In another aspect, the conditions comprise a pH of about 8.0 and/or a temperature from about 37° C to about 45° C.

[00027] The invention provides for a method for hydrolyzing a cyanohydrin moiety or an
30 aminonitrile moiety of a molecule, the method comprising contacting the molecule with at least one polypeptide of the invention, or a fragment thereof, or a peptidomimetic thereof, having nitrilase activity, under conditions suitable for nitrilase activity.

[00028] The invention provides for a method for making a chiral α -hydroxy acid molecule, a chiral amino acid molecule, a chiral β -hydroxy acid molecule, or a chiral gamma-hydroxy acid molecule, the method comprising admixing a molecule having a cyanohydrin moiety or an aminonitrile moiety with at least one polypeptide having an amino acid sequence at least 50% identical to any one of the Group B amino acid sequences or a fragment thereof, or a peptidomimetic thereof, having enantio-selective nitrilase activity. In one aspect, the chiral molecule is an (*R*)-enantiomer. In another aspect, the chiral molecule is an (*S*)-enantiomer. In one aspect of the invention, one particular enzyme can have R-specificity for one particular substrate and the same enzyme can have S-specificity for a different particular substrate.

[00029] The invention also provides for a method for making a composition or an intermediate thereof, the method comprising admixing a precursor of the composition or intermediate, wherein the precursor comprises a cyanohydrin moiety or an aminonitrile moiety, with at least one polypeptide of the invention or a fragment or peptidomimetic thereof having nitrilase activity, hydrolyzing the cyanohydrin or the aminonitrile moiety in the precursor thereby making the composition or the intermediate thereof. In one aspect, the composition or intermediate thereof comprises (*S*)-2-amino-4-phenyl butanoic acid. In a further aspect, the composition or intermediate thereof comprises an L-amino acid. In a further aspect, the composition comprises a food additive or a pharmaceutical drug.

[00030] The invention provides for a method for making an (*R*)-ethyl 4-cyano-3-hydroxybutyric acid, the method comprising contacting a hydroxyglutaryl nitrile with at least one polypeptide having an amino acid sequence of the Group B amino acid sequences, or a fragment or peptidomimetic thereof having nitrilase activity that selectively produces an (*R*)-enantiomer, so as to make (*R*)-ethyl 4-cyano-3-hydroxybutyric acid. In one aspect, the *ee* is at least 95% or at least 99%. In another aspect, the hydroxyglutaryl nitrile comprises 1,3-dicyano-2-hydroxy-propane or 3-hydroxyglutaronitrile. In a further aspect, the polypeptide has an amino acid sequence of any one of the Group B amino acid sequences, or a fragment or peptidomimetic thereof having nitrilase activity.

[00031] The invention also provides a method for making an (*S*)-ethyl 4-cyano-3-hydroxybutyric acid, the method comprising contacting a hydroxyglutaryl nitrile with at least one polypeptide having an amino acid sequence of the Group B amino acid sequences, or a fragment or peptidomimetic thereof having nitrilase activity that selectively produces an (*S*)-enantiomer, so as to make (*S*)-ethyl 4-cyano-3-hydroxybutyric acid.

[00032] The invention provides a method for making an (*R*)-mandelic acid, the method comprising admixing a mandelonitrile with at least one polypeptide having an amino acid sequence of any one of the Group B amino acid sequences or any fragment or peptidomimetic thereof having appropriate nitrilase activity. In one aspect, the (*R*)-mandelic acid comprises (*R*)-2-chloromandelic acid. In another aspect, the (*R*)-mandelic acid comprises an aromatic ring substitution in the *ortho*-, *meta*-, or *para*- positions; a 1-naphthyl derivative of (*R*)-mandelic acid, a pyridyl derivative of (*R*)-mandelic acid or a thienyl derivative of (*R*)-mandelic acid or a combination thereof.

[00033] The invention provides a method for making an (*S*)-mandelic acid, the method comprising admixing a mandelonitrile with at least one polypeptide having an amino acid sequence of Group B sequences or any fragment or peptidomimetic thereof having nitrilase activity. In one aspect, the (*S*)-mandelic acid comprises (*S*)-methyl benzyl cyanide and the mandelonitrile comprises (*S*)-methoxy-benzyl cyanide. In one aspect, the (*S*)-mandelic acid comprises an aromatic ring substitution in the *ortho*-, *meta*-, or *para*- positions; a 1-naphthyl derivative of (*S*)-mandelic acid, a pyridyl derivative of (*S*)-mandelic acid or a thienyl derivative of (*S*)-mandelic acid or a combination thereof.

[00034] The invention also provides a method for making an (*S*)-phenyl lactic acid derivative or an (*R*)-phenyllactic acid derivative, the method comprising admixing a phenyllactonitrile with at least one polypeptide selected from the group of the Group B amino acid sequences or any active fragment or peptidomimetic thereof that selectively produces an (*S*)-enantiomer or an (*R*)-enantiomer, thereby producing an (*S*)-phenyl lactic acid derivative or an (*R*)-phenyl lactic acid derivative.

[00035] The invention provides for a method for making the polypeptide of the invention or a fragment thereof, the method comprising (a) introducing a nucleic acid encoding the polypeptide into a host cell under conditions that permit production of the polypeptide by the host cell, and (b) recovering the polypeptide so produced.

[00036] The invention provides for a method for generating a nucleic acid variant encoding a polypeptide having nitrilase activity, wherein the variant has an altered biological activity from that which naturally occurs, the method comprising (a) modifying the nucleic acid by (i) substituting one or more nucleotides for a different nucleotide, wherein the nucleotide comprises a natural or non-natural nucleotide; (ii) deleting one or more nucleotides, (iii) adding one or more nucleotides, or (iv) any combination thereof. In one aspect, the non-natural nucleotide comprises inosine. In another aspect, the method further

comprises assaying the polypeptides encoded by the modified nucleic acids for altered nitrilase activity, thereby identifying the modified nucleic acid(s) encoding a polypeptide having altered nitrilase activity. In one aspect, the modifications of step (a) are made by PCR, error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis, ligase chain reaction, *in vitro* mutagenesis, ligase chain reaction, oligonucleotide synthesis, any DNA-generating technique and any combination thereof. In another aspect, the method further comprises at least one repetition of the modification step (a).

[00037] The invention further provides a method for making a polynucleotide from two or more nucleic acids, the method comprising: (a) identifying regions of identity and regions of diversity between two or more nucleic acids, wherein at least one of the nucleic acids comprises a nucleic acid of the invention; (b) providing a set of oligonucleotides which correspond in sequence to at least two of the two or more nucleic acids; and, (c) extending the oligonucleotides with a polymerase, thereby making the polynucleotide.

[00038] The invention further provides a screening assay for identifying a nitrilase, the assay comprising: (a) providing a plurality of nucleic acids or polypeptides comprising at least one of the nucleic acids of the invention, or at least one of the polypeptides of the invention; (b) obtaining polypeptide candidates to be tested for nitrilase activity from the plurality; (c) testing the candidates for nitrilase activity; and (d) identifying those polypeptide candidates which are nitrilases. In one aspect, the method further comprises modifying at least one of the nucleic acids or polypeptides prior to testing the candidates for nitrilase activity. In another aspect, the testing of step (c) further comprises testing for improved expression of the polypeptide in a host cell or host organism. In a further aspect, the testing of step (c) further comprises testing for nitrilase activity within a pH range from about pH 3 to about pH 12. In a further aspect, the testing of step (c) further comprises testing for nitrilase activity within a pH range from about pH 5 to about pH 10. In another aspect, the testing of step (c) further comprises testing for nitrilase activity within a temperature range from about 4 °C to about 80 °C. In another aspect, the testing of step (c) further comprises testing for nitrilase activity within a temperature range from about 4 °C to about 55 °C. In another aspect, the testing of step (c) further comprises testing for nitrilase activity which results in an enantioselective

reaction product. In another aspect, the testing of step (c) further testing for nitrilase activity which results in a regio-selective reaction product.

[00039] The invention provides for use of the nucleic acids of the invention, or a fragment or peptidomimetic thereof having nitrilase activity, in a process designed to optimize one
5 aspect of the gene or one aspect of the polypeptide encoded by the gene. In one aspect, the process comprises introducing modifications into the nucleotide sequence of the nucleic acid. In another aspect, the modifications are introduced by PCR, error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo
0 mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis, ligase chain reaction, *in vitro* mutagenesis, ligase chain reaction, oligonucleotide synthesis, any other DNA-generating technique or any combination thereof. In a further aspect, the process is repeated.

[00040] The invention provides for use of the polypeptide of the invention, or a fragment
5 or peptidomimetic thereof having nitrilase activity, in an industrial process. In one aspect, the process is for production of a pharmaceutical composition, the process is for production of a chemical, the process is for production of a food additive, the process is catalyzing the breakdown of waste, or the process is production of a drug intermediate. In a further aspect, the process comprises use of the polypeptide to hydrolyze a hydroxyglutaryl nitrile substrate.
0 In a further aspect, the process is for production of LIPITOR™. In another aspect, the polypeptide used comprises a polypeptide having consecutive amino acids of the sequence SEQ ID NO:44, 196, 208, 210, or 238 or a fragment thereof having nitrilase activity. In another aspect, the process is production of a detergent. In another aspect, the process is production of a food product.

[00041] The invention provides for use of a nucleic acid of the invention, or a fragment
5 thereof encoding a polypeptide having nitrilase activity, in the preparation of a transgenic organism.

[00042] The invention provides for a kit comprising (a) the nucleic acid of the inventions, or a fragment thereof encoding a polypeptide having nitrilase activity, or (b) the polypeptide
0 of the invention, or a fragment or a peptidomimetic thereof having nitrilase activity, or a combination thereof; and (c) a buffer.

[00043] The invention provides for a method for modifying a molecule comprising: (a) mixing a polypeptide of the invention or a fragment or peptidomimetic thereof having

nitrilase activity, with a starting molecule to produce a reaction mixture; (b) reacting the starting molecule with the polypeptide to produce the modified molecule.

[00044] The invention provides for a method for identifying a modified compound comprising: (a) admixing a polypeptide of the invention, or a fragment or peptidomimetic thereof having nitrilase activity, with a starting compound to produce a reaction mixture and thereafter a library of modified starting compounds; (b) testing the library to determine whether a modified starting compound is present within the library which exhibits a desired activity; (c) identifying the modified compound exhibiting the desired activity.

[00045] The invention provides a screening assay for enantioselective transformation comprising: (a) providing a molecule having two prochiral or enantiotopic moieties; (b) labeling at least one prochiral or enantiotopic moiety of the molecule; (b) modifying at least one of the two moieties by a selective catalyst; and (c) detecting results by mass spectroscopy. The screening assay can be used to determine or monitor the % enantiomeric excess (ee) or determine the % diastomeric excess (de). An exemplary label useful in the assay is a heavier isotope or a lighter isotope. The selective catalyst useful in the assay can be an enzyme. The screening assay may be performed with both moieties labeled. The screening assay may be performed in both directions, *i.e.*, from the reactants to the products as well as from the products to the reactants.

[00046] The invention provides for a computer readable medium having stored thereon a nucleic acid of the invention, e.g., a nucleic acid comprising at least one nucleotide sequence selected from the group consisting of: SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, and variants thereof, and/or at least one amino acid sequence selected from the group consisting of: SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70,

72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 5 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, and variants thereof.

10 **[00047]** The invention provides for a computer system comprising a processor and a data storage device, wherein the data storage device has stored thereon a nucleic acid of the invention, e.g., a nucleic acid comprising at least one nucleotide sequence selected from the group consisting of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 15 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 20 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, and variants thereof, and/or at least one amino acid sequence selected from the group consisting of: SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 25 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 30 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374,

376, 378, 380, 382, 384, 386, and variants thereof. In one aspect, the computer system further comprises a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon. In another aspect, the sequence comparison algorithm comprises a computer program that identifies polymorphisms.

5 [00048] The invention provides for a method for identifying a feature in a sequence which comprises: (a) inputting the sequence into a computer; (b) running a sequence feature identification program on the computer so as to identify a feature within the sequence; and (c) identifying the feature in the sequence, wherein the sequence comprises a nucleic acid of the invention, e.g., a nucleic acid comprising at least one of SEQ ID NOS:1-386, its variants, or
10 any combination thereof.

[00049] The invention provides for an assay for identifying a functional fragment of a polypeptide which comprises: (a) obtaining a fragment of at least one polypeptide of the invention; (b) contacting at least one fragment from step (a) with a substrate having a cyanohydrin moiety or an aminonitrile moiety under reaction conditions suitable for nitrilase
15 activity; (c) measuring the amount of reaction product produced by each at least one fragment from step (b); and (d) identifying the at least one fragment which is capable of producing a nitrilase reaction product; thereby identifying a functional fragment of the polypeptide. In one aspect, the fragment of step (a) is obtained by synthesizing the fragment. In another aspect, the fragment of step (a) is obtained by fragmenting the polypeptides.

20 [00050] The invention provides for an assay for identifying a functional variant of a polypeptide which comprises: (a) obtaining at least one variant of at least one polypeptide of the invention; (b) contacting at least one variant from step (a) with a substrate having a cyanohydrin moiety or an aminonitrile moiety under reaction conditions suitable for nitrilase activity; (c) measuring the amount of reaction product produced by each at least one variant
25 from step (b); and (d) identifying the at least one variant which is capable of producing a nitrilase reaction product; thereby identifying a functional variant of the polypeptide.

BRIEF DESCRIPTION OF THE DRAWINGS

[00051] Figure 1 shows chemical reaction schemes wherein stereoselective nitrilases hydrolyze a cyanohydrin or an aminonitrile to produce a chiral α -hydroxy acid or α -amino
30 acid.

[00052] Figure 2 illustrates an OPA based cyanide detection assay used for identifying the presence of nitrilase activity.

[00053] Figure 3 is an illustration of a spectroscopic system for the detection and quantification of α -hydroxy acids based on stereoselective lactate dehydrogenases.

[00054] Figure 4 is an illustration of a spectroscopic system for the detection and quantification of α -amino acids based on stereoselective amino acid oxidase.

5 [00055] Figure 5 is a flow diagram illustrating the steps of a nitrilase screening method.

[00056] Figures 6A-6E are chromatograms characteristic of the substrate and product combination for D-phenylglycine showing a blank sample (Fig. 6A), an enzymatic reaction sample (Fig. 6B); a negative control consisting of cell lysate in buffer (Fig. 6C); a chiral analysis of phenylglycine (Fig. 6D); and coelution of the nitrile peak with the D-enantiomer
10 (Fig. 6E).

[00057] Figures 7A-7E illustrate chromatograms which are characteristic of substrate and product combinations for (R)-2-chloromandelic acid. Fig. 7A shows only 2-chloromandelonitrile in buffer; Fig. 7B shows a chloromandelic acid standard. The chromatogram in Fig. 7C shows the appearance of product and the reduction of substrate
15 peaks.

[00058] Figures 8A-8B illustrate chromatograms characteristic of substrate and product combinations for (S)-phenyllactic acid.

[00059] Figures 9A-9B illustrate chromatograms characteristic of substrate and product combinations for L-2-methylphenylglycine.

20 [00060] Figures 10A-10C illustrate chromatograms characteristic of substrate and product combinations for L-*tert*-leucine.

[00061] Figures 11A-11C illustrate chromatograms characteristic of substrate and product combinations for (S)-2-amino-6-hydroxy hexanoic acid.

[00062] Figures 12A-12D illustrate chromatograms characteristic of substrate and product
25 combinations for 4-methyl-D-leucine and 4-methyl-L-leucine.

[00063] Figures 13A-13B illustrate chromatograms characteristic of substrate and product combinations for (S)-cyclohexylmandelic acid.

[00064] Figures 14A-14B illustrate two exemplary standard curves for quantitation in connection with the screening assay of the invention.

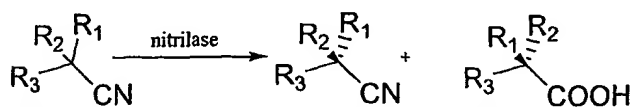
30 [00065] Figure 15 illustrates selected compounds that can be produced from a nitrilase-catalyzed reaction using an enzyme and/or a method of the invention.

[00066] Figure 16 illustrates selected compounds that can be produced from a nitrilase-catalyzed reaction using an enzyme and/or a method of the invention.

[00067] Figure 17 illustrates an exemplary nitrilase reaction of the invention.

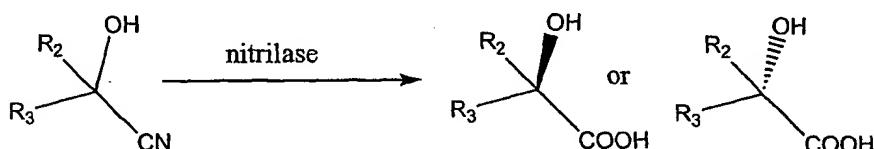
DETAILED DESCRIPTION OF THE INVENTION

[00068] The present invention relates to nitrilases, nucleic acids encoding nitrilases, and uses therefor. As used herein, the term "nitrilase" encompasses any polypeptide having any nitrilase activity, for example, the ability to hydrolyze nitriles into their corresponding carboxylic acids and ammonia. Nitrilases have commercial utility as biocatalysts for use in the synthesis of enantioselective aromatic and aliphatic amino acids or hydroxy acids.

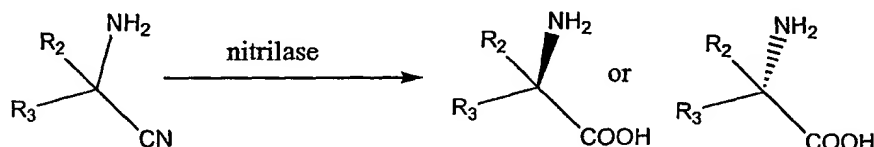


[00069] Nitrilase chemistry is as follows:

10 [00070] A nitrilase reaction for the preparation of hydroxy acids is as follows:



[00071] A nitrilase reaction for the preparation of amino acids is as follows:



15 [00072] In addition, in each of the foregoing hydrolysis reactions, two water molecules are consumed and one ammonia molecule is released.

[00073] There are several different types of assays which can be performed to test for the presence of nitrilase activity in a sample or to test whether a particular polypeptide exhibits nitrilase activity. For example, assays can detect the presence or absence of products or by-products from a chemical reaction catalyzed by a nitrilase. For example, the presence of nitrilase activity can be detected by the production of α -hydroxy acids or α -amino acids from, respectively, cyanohydrins or aminonitriles, and the level of nitrilase activity can be

20

quantified by measuring the relative quantities of the reaction products produced. Figure 1 shows chemical reaction schemes using stereoselective nitrilases to create chiral α -hydroxy acids or α -amino acids in high yield. The starting material is an aldehyde or an imine which is produced from an aldehyde by reaction with ammonia. Reaction of the aldehyde or imine with hydrogen cyanide results in the production of enantiomeric mixtures of the corresponding cyanohydrins and aminonitriles. A stereoselective nitrilase can then be used to stereoselectively convert one enantiomer into the corresponding α -hydroxy acid or α -amino acid. Figure 3 illustrates schematically the stereoselective nitrilase-dependent production and spectrophotometric detection of α -hydroxy acids based on lactate dehydrogenase conversion of the α -hydroxy acids to the corresponding α -keto acids and concomitant oxidation-reduction of a detectable dye. Figure 4 illustrates schematically the stereoselective nitrilase-dependent production and spectrophotometric detection of α -amino acids based on amino acid oxidase conversion of the α -amino acids to the corresponding α -keto acids and concomitant oxidation-reduction of a detectable dye.

[00074] Nitrilases contemplated for use in the practice of the present invention include those which stereoselectively hydrolyze nitriles or cyanohydrins into their corresponding acids and ammonia. In one aspect, nitrilases of the invention can stereoselectively hydrolyze nitriles or cyanohydrins into their corresponding acids and ammonia. Nitrilases include, for example, nitrilases of the invention, e.g., those set forth in the Group B amino acid sequences. Some nitrilases which stereoselectively hydrolyze their substrates are set forth in the Tables hereinbelow.

[00075] The nitrilases of the invention share the following additional characteristics: (1) full-length amino acid sequences from about 333 amino acids to about 366 amino acids, (2) aggregation and activity as homo-multimers of about 2 subunits to about 16 subunits, (3) presence of a catalytic triad of the consecutive amino acids Glu-Lys-Cys, (4) pH optima from about pH 5 to about pH 9, and (5) temperature optima from about 0°C to about 100°C, or from about 40°C to about 50°C.

Consensus Sequences Among New Nitrilases

[00076] The nitrilases disclosed herein were studied using bioinformatics and sequence comparison programs and the following consensus information was collected. Three regions of conserved motifs were identified within the nitrilase polypeptides. These correspond to the catalytic triad (E-K-C) present in nitrilase enzymes. (H. Pace and C. Brenner (Jan. 15,

2001) "The Nitrilase Superfamily: classification, structure and function" *Genome Biology*
Vol. 2, No. 1, pp 1-9.)

[00077] The abbreviations used herein are conventional one letter codes for the amino acids: A, alanine; B, asparagine or aspartic acid; C, cysteine; D aspartic acid; E, glutamate, glutamic acid; F, phenylalanine; G, glycine; H histidine; I isoleucine; K, lysine; L, leucine; M, methionine; N, asparagine; P, proline; Q, glutamine; R, arginine; S, serine; T, threonine; V, valine; W, tryptophan; Y, tyrosine; Z, glutamine or glutamic acid. See L. Stryer, *Biochemistry*, 1988, W. H. Freeman and Company, New York.

[00078] The computer sequence comparisons made among the nitrilase polypeptide sequences of the invention resulted in the identification of these motifs within each amino acid sequence:

F	P	<u>E</u>	t	<i>f</i>	r	<u>R</u>	<u>K</u>	L	.	P	T	L	.	<u>C</u>	W	<u>E</u>	h	.	.	P
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[00079] The following residues (those that are underlined) are completely conserved among all of the identified nitrilases: the third amino acid in the first motif or region (E, glutamate); the second residue in the second motif (R, arginine); the third residue in the second motif (K, lysine); the third residue in the third motif (C, cysteine); and the fifth residue in the third motif (E, glutamate).

[00080] In the boxes, upper case letters indicate 90% or greater consensus among the nitrilases of the invention, while lower case letters indicate 50% or greater consensus. An italicized letter indicates 30% or greater consensus among the nitrilases of the invention. A dot in a box indicates a residue which is not conserved.

[00081] The sequences of nitrilases in the nitrilase branch of the nitrilase superfamily were described as having a catalytic triad in the Pace and Brenner article (*Genome Biology*, 2001, Vol. 2, No. 1, pp. 1-9). However, the catalytic triad regions of the nitrilases of this invention differ from those previously identified in the Pace and Brenner reference in the following ways:

[00082] Differences in the first motif: The F in the first box of the first motif is conserved in 90% of the nitrilases of the invention, rather than in only 50% of those previously identified. The fourth residue of the first motif is a "t", threonine in the nitrilases of this invention, and it is found at 50% or greater consensus. However, that residue was identified by Pace and Brenner as "a" (alanine). The last residue of the first motif was

identified as "f" (phenylalanine) and was indicated to occur at 50% or greater consensus. However, the nitrilases of this invention only show "f" (phenylalanine occurring at 30% consensus.

5 [00083] Differences in the second motif: There is an "r" (arginine) in the first box of the second motif of the nitrilases of this invention. However, the Pace and Brenner consensus shows an "h" (histidine) in that position. The "R" (arginine) in the second box is completely conserved in the nitrilases of the present invention, however that residue only appears at 90% consensus in the Pace and Brenner reference. The "L" (leucine) in the fourth box of the second motif is conserved in 90% or more of the nitrilases of this invention.

10 However, the Pace and Brenner nitrilases only showed conservation of that residue in 50% of the sequences. Similarly, the "P" (proline) at the sixth box of the second motif is conserved in 90% or more of the nitrilases of this invention. However, the Pace and Brenner nitrilases only showed conservation of that residue in 50% of the sequences.

[00084] Differences in the third motif: The "L" in the first box is conserved at 90% or greater in the nitrilases of the invention. However, the Pace and Brenner reference only shows that residue appearing 50% of the time. Finally, the sixth box in the third motif in the nitrilases of the invention show a histidine 50% of the time or more. However, the Pace and Brenner reference indicates that that position shows an asparagine ("n") 50% of the time.

[00085] The invention provides for an isolated polypeptide having nitrilase activity which

20 polypeptide comprises three regions, wherein the first region comprises five amino acids and wherein the first amino acid of the first region is F and the fourth amino acid of the first region is T. The invention also provides for an isolated polypeptide having nitrilase activity which polypeptide comprises three regions, wherein the second region comprises seven amino acids and wherein the first amino acid of the second region is R, wherein the second

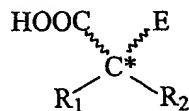
25 amino acid of the second region is R, and wherein the sixth amino acid of the second region is P. The invention also provides for an isolated polypeptide having nitrilase activity which polypeptide comprises three regions, wherein the third region comprises nine amino acids and wherein the first amino acid of the third region is L and the sixth amino acid of the third region is H.

30 [00086] The invention also provides for an isolated polypeptide having nitrilase activity which polypeptide comprises three consensus subsequences, wherein the first consensus subsequence is FPETF, wherein the second consensus subsequence is RRKLXPT, and wherein the third consensus subsequence is LXCWEHXXP.

[00087] The invention also provides for an isolated polypeptide having nitrilase activity which polypeptide comprises three consensus subsequences, wherein the first consensus subsequence is FPXXX, wherein the second consensus subsequence is XRKLXPT, and wherein the third consensus subsequence is LXCWEXXXP.

5

[00088] In accordance with the present invention, methods are provided for producing enantiomerically pure α -substituted carboxylic acids. The enantiomerically pure α -substituted carboxylic acids produced by the methods of the present invention have the following structure:



10

wherein:

$\text{R}_1 \neq \text{R}_2$ and R_1 and R_2 are otherwise independently -H, substituted or unsubstituted alkyl, alkenyl, alkynyl, aryl, heteroaryl, cycloalkyl, or heterocyclic, wherein said substituents are lower alkyl, hydroxy, alkoxy, amino, mercapto, cycloalkyl, heterocyclic, aryl, heteroaryl, aryloxy, or halogen or optionally R_1 and R_2 are directly or indirectly covalently joined to form a functional cyclic moiety, and E is $-\text{N}(\text{R}_x)_2$ or $-\text{OH}$, wherein each R_x is independently -H or lower alkyl.

15

[00089] As used herein, the term "alkyl" refers to straight or branched chain or cyclic hydrocarbon groups of from 1 to 24 carbon atoms, including methyl, ethyl, n-propyl, isopropyl, n-butyl, isobutyl, tert-butyl, n-pentyl, n-hexyl, and the like. The term "lower alkyl" refers to monovalent straight or branched chain or cyclic radicals of from one to about six carbon atoms.

20

[00090] As used herein, "alkenyl" refers to straight or branched chain or cyclic hydrocarbon groups having one or more carbon-carbon double bonds, and having in the range of about 2 to about 24 carbon atoms.

25

[00091] As used herein, "alkynyl" refers to straight or branched chain or cyclic hydrocarbon groups having at least one carbon-carbon triple bond, and having in the range of about 2 to about 24 carbon atoms.

[00092] As used herein, "cycloalkyl" refers to cyclic hydrocarbon groups containing in the range of about 3 to about 14 carbon atoms.

30

[00093] As used herein, "heterocyclic" refers to cyclic groups containing one or more heteroatoms (*e.g.*, N, O, S, P, Se, B, etc.) as part of the ring structure, and having in the range of about 3 to about 14 carbon atoms.

5 [00094] As used herein, "aryl" refers to aromatic groups (*i.e.*, cyclic groups with conjugated double-bond systems) having in the range of about 6 to about 14 carbon atoms.

[00095] As used herein with respect to a chemical group or moiety, the term "substituted" refers to such a group or moiety further bearing one or more non-hydrogen substituents. Examples of such substituents include, without limitation, oxy (*e.g.*, in a ketone, aldehyde, ether, or ester), hydroxy, alkoxy (of a lower alkyl group), amino, thio, mercapto (of a lower
10 alkyl group), cycloalkyl, substituted cycloalkyl, heterocyclic, substituted heterocyclic, aryl, substituted aryl, heteroaryl, substituted heteroaryl, aryloxy, substituted aryloxy, halogen, trifluoromethyl, cyano, nitro, nitron, amino, amido, -C(O)H, acyl, oxyacyl, carboxyl, carbamate, sulfonyl, sulfonamide, sulfuryl, and the like.

[00096] In preferred aspects, the enantiomerically pure α -substituted carboxylic acid
15 produced by the methods of the present invention is an α -amino acid or α -hydroxy acid. In some aspects, the enantiomerically pure α -amino acid is D-phenylalanine, D-phenylglycine, L-methylphenylglycine, L-*tert*-leucine, D-alanine, or D-hydroxynorleucine ((*S*)-2-amino-6-hydroxy hexanoic acid), R-pantolactone, 2-chloromandelic acid, or (*S*)- or (*R*)-mandelic acid and the enantiomerically pure α -hydroxy acid is (*S*)-cyclohexylmandelic acid. As used
20 herein, a "small molecule" encompasses any molecule having a molecular weight from at least 25 Daltons.

[00097] The term "about" is used herein to mean approximately, roughly, around, or in the region of. When the term "about" is used in conjunction with a numerical range, it modifies that range by extending the boundaries above and below the numerical values set forth. In
25 general, the term "about" is used herein to modify a numerical value above and below the stated value by a variance of 20 percent up or down (higher or lower).

[00098] As used herein, the word "or" means any one member of a particular list and also includes any combination of members of that list.

[00099] The phrase "nucleic acid" as used herein refers to a naturally occurring or
30 synthetic oligonucleotide or polynucleotide, whether DNA or RNA or DNA-RNA hybrid, single-stranded or double-stranded, sense or antisense, which is capable of hybridization to a complementary nucleic acid by Watson-Crick base-pairing. Nucleic acids of the invention can also include nucleotide analogs (*e.g.*, BrdU), and non-phosphodiester internucleoside

linkages (*e.g.*, peptide nucleic acid (PNA) or thiodiester linkages). In particular, nucleic acids can include, without limitation, DNA, RNA, cDNA, gDNA, ssDNA or dsDNA or any combination thereof. In some aspects, a "nucleic acid" of the invention includes, for example, a nucleic acid encoding a polypeptide as set forth in the Group B amino acid sequences, and variants thereof. The phrase "a nucleic acid sequence" as used herein refers to a consecutive list of abbreviations, letters, characters or words, which represent nucleotides. In one aspect, a nucleic acid can be a "probe" which is a relatively short nucleic acid, usually less than 100 nucleotides in length. Often a nucleic acid probe is from about 50 nucleotides in length to about 10 nucleotides in length. A "target region" of a nucleic acid is a portion of a nucleic acid that is identified to be of interest.

[000100] A "coding region" of a nucleic acid is the portion of the nucleic acid which is transcribed and translated in a sequence-specific manner to produce into a particular polypeptide or protein when placed under the control of appropriate regulatory sequences. The coding region is said to encode such a polypeptide or protein.

[000101] The term "gene" refers to a coding region operably joined to appropriate regulatory sequences capable of regulating the expression of the polypeptide in some manner. A gene includes untranslated regulatory regions of DNA (*e.g.*, promoters, enhancers, repressors, etc.) preceding (upstream) and following (downstream) the coding region (open reading frame, ORF) as well as, where applicable, intervening sequences (*i.e.*, introns) between individual coding regions (*i.e.*, exons).

[000102] "Polypeptide" as used herein refers to any peptide, oligopeptide, polypeptide, gene product, expression product, or protein. A polypeptide is comprised of consecutive amino acids. The term "polypeptide" encompasses naturally occurring or synthetic molecules.

[000103] In addition, as used herein, the term "polypeptide" refers to amino acids joined to each other by peptide bonds or modified peptide bonds, *e.g.*, peptide isosteres, and may contain modified amino acids other than the 20 gene-encoded amino acids. The polypeptides can be modified by either natural processes, such as post-translational processing, or by chemical modification techniques which are well known in the art. Modifications can occur anywhere in the polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification can be present in the same or varying degrees at several sites in a given polypeptide. Also a given polypeptide can have many types of modifications. Modifications include, without

limitation, acetylation, acylation, ADP-ribosylation, amidation, covalent cross-linking or cyclization, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of a phosphatidylinositol, disulfide bond formation,

5 demethylation, formation of cysteine or pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pergylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, and transfer-RNA mediated addition of amino acids to protein such as arginylation. (See *Proteins – Structure and Molecular Properties* 2nd Ed., T.E. Creighton,
10 W.H. Freeman and Company, New York (1993); *Posttranslational Covalent Modification of Proteins*, B.C. Johnson, Ed., Academic Press, New York, pp. 1-12 (1983)).

[000104] As used herein, the term "amino acid sequence" refers to a list of abbreviations, letters, characters or words representing amino acid residues.

[000105] As used herein, the term "isolated" means that a material has been removed from
15 its original environment. For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides can be part of a vector and/or such polynucleotides or polypeptides could be part of a composition, and would be isolated in that such a vector or composition is not part
20 of its original environment.

[000106] As used herein with respect to nucleic acids, the term "recombinant" means that the nucleic acid is covalently joined and adjacent to a nucleic acid to which it is not adjacent in its natural environment. Additionally, as used herein with respect to a particular nucleic acid in a population of nucleic acids, the term "enriched" means that the nucleic acid
25 represents 5% or more of the number of nucleic acids in the population of molecules. Typically, the enriched nucleic acids represent 15% or more of the number of nucleic acids in the population of molecules. More typically, the enriched nucleic acids represent 50%, 90% or more of the number of nucleic acids in the population molecules.

[000107] "Recombinant" polypeptides or proteins refer to polypeptides or proteins
30 produced by recombinant DNA techniques, *i.e.*, produced from cells transformed by an exogenous recombinant DNA construct encoding the desired polypeptide or protein. "Synthetic" polypeptides or proteins are those prepared by chemical synthesis (*e.g.*, solid-phase peptide synthesis). Chemical peptide synthesis is well known in the art (see, *e.g.*,

Merrifield (1963), *Am. Chem. Soc.* 85:2149-2154; Geysen et al. (1984), *Proc. Natl. Acad. Sci., USA* 81:3998) and synthesis kits and automated peptide synthesizer are commercially available (e.g., Cambridge Research Biochemicals, Cleveland, United Kingdom; Model 431A synthesizer from Applied Biosystems, Inc., Foster City, CA). Such equipment provides ready access to the peptides of the invention, either by direct synthesis or by synthesis of a series of fragments that can be coupled using other known techniques.

[000108] As used herein with respect to pairs of nucleic acid or amino acid sequences, "identity" refers to the extent to which the two sequences are invariant at positions within the sequence which can be aligned. The percent identity between two given sequences can be calculated using an algorithm such as BLAST (Altschul et al. (1990), *J. Mol. Biol.* 215:403-410). See www.ncbi.nlm.nih.gov/Education/BLASTinfo. When using the BLAST algorithm for sequences no longer than 250 nucleotides or about 80 amino acids ("short queries"), the search parameters can be as follows: the filter is off, the scoring matrix is PAM30, the word size is 3 or 2, the E value is 1000 or more, and the gap costs are 11, 1. For sequences longer than 250 nucleotides or 80 amino acid residues, the default search parameters can be used. The BLAST website provides advice for special circumstances which is to be followed in such circumstances.

[000109] As used herein, "homology" has the same meaning as "identity" in the context of nucleotide sequences. However, with respect to amino acid sequences, "homology" includes the percentage of identical and conservative amino acid substitutions. Percentages of homology can be calculated according to the algorithms of Smith and Waterman (1981), *Adv. Appl. Math.* 2:482.

[000110] As used herein in the context of two or more nucleic acid sequences, two sequences are "substantially identical" when they have at least 99.5% nucleotide identity, when compared and aligned for maximum correspondence, as measured using the known sequence comparison algorithms described above. In addition, for purposes of determining whether sequences are substantially identical, synonymous codons in a coding region may be treated as identical to account for the degeneracy of the genetic code. Typically, the region for determination of substantial identity must span at least about 20 residues, and most commonly the sequences are substantially identical over at least about 25-200 residues.

[000111] As used herein in the context of two or more amino acid sequences, two sequences are "substantially identical" when they have at least 99.5% identity, when compared and aligned for maximum correspondence, as measured using the known sequence

comparison algorithms described above. In addition, for purposes of determining whether sequences are substantially identical, conservative amino acid substitutions may be treated as identical if the polypeptide substantially retains its biological function.

[000112] "Hybridization" refers to the process by which a nucleic acid strand joins with a complementary strand through hydrogen bonding at complementary bases. Hybridization assays can be sensitive and selective so that a particular sequence of interest can be identified even in samples in which it is present at low concentrations. Stringent conditions are defined by concentrations of salt or formamide in the prehybridization and hybridization solutions, or by the hybridization temperature, and are well known in the art. Stringency can be increased by reducing the concentration of salt, increasing the concentration of formamide, or raising the hybridization temperature. In particular, as used herein, "stringent hybridization conditions" include 42°C in 50% formamide, 5X SSPE, 0.3% SDS, and 200 ng/ml sheared and denatured salmon sperm DNA, and equivalents thereof. Variations on the above ranges and conditions are well known in the art.

[000113] The term "variant" refers to polynucleotides or polypeptides of the invention modified at one or more nucleotides or amino acid residues (respectively) and wherein the encoded polypeptide or polypeptide retains nitrilase activity. Variants can be produced by any number of means including, for example, error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site-saturated mutagenesis or any combination thereof.

[000114] Methods of making peptidomimetics based upon a known sequence is described, for example, in U.S. Patent Nos. 5,631,280; 5,612,895; and 5,579,250. Use of peptidomimetics can involve the incorporation of a non-amino acid residue with non-amide linkages at a given position. One aspect of the present invention is a peptidomimetic wherein the compound has a bond, a peptide backbone or an amino acid component replaced with a suitable mimic. Examples of unnatural amino acids which may be suitable amino acid mimics include β -alanine, L- α -amino butyric acid, L- γ -amino butyric acid, L- α -amino isobutyric acid, L- ϵ -amino caproic acid, 7-amino heptanoic acid, L-aspartic acid, L-glutamic acid, N- ϵ -Boc-N- α -CBZ-L-lysine, N- ϵ -Boc-N- α -Fmoc-L-lysine, L-methionine sulfone, L-norleucine, L-norvaline, N- α -Boc-N- δ CBZ-L-ornithine, N- δ -Boc-N- α -CBZ-L-ornithine, Boc-p-nitro-L-phenylalanine, Boc-hydroxyproline, Boc-L-thioprolin.

[000115] As used herein, "small molecule" encompasses a molecule having a molecular weight from about 20 daltons to about 1.5 kilodaltons.

[000116] The molecular biological techniques, such as subcloning, were performed using routine methods which would be well known to one of skill in the art. (Sambrook, J.

- 5 Fritsch, EF, Maniatis, T. (1989) Molecular Cloning: A Laboratory Manual (2nd ed.), Cold Spring Harbor Laboratory Press, Plainview NY.).

Computer Systems

- [000117] In one aspect of the invention, any nucleic acid sequence and/or polypeptide sequence of the invention can be stored, recorded, and manipulated on any medium which
10 can be read and accessed by a computer. As used herein, the words "recorded" and "stored" refer to a process for storing information on a computer medium. Another aspect of the invention is a computer readable medium having recorded thereon at least 2, 5, 10, 15 or 20 nucleic acid sequences as set forth in SEQ ID NOS: 1-386, and sequences substantially identical thereto. In a further aspect, another aspect is the comparison among and between
15 nucleic acid sequences or polypeptide sequences of the invention and the comparison between sequences of the invention and other sequences by a computer. Computer readable media include magnetically readable media, optically readable media, electronically readable media and magnetic/optical media. For example, the computer readable media may be a hard disk, a floppy disk, a magnetic tape, CD-ROM, Digital Versatile Disk (DVD), Random
20 Access Memory (RAM), or Read Only Memory (ROM) as well as other types of other media known to those skilled in the art.

- [000118] Aspects of the invention include systems (*e.g.*, internet based systems), particularly computer systems which store and manipulate the sequence information described herein. As used herein, "a computer system" refers to the hardware components,
25 software components, and data storage components used to analyze a sequence (either nucleic acid or polypeptide) as set forth in at least any one of SEQ ID NOS: 1-386 and sequences substantially identical thereto. The computer system typically includes a processor for processing, accessing and manipulating the sequence data. The processor can be any well-known type of central processing unit, such as, for example, the Pentium III from Intel
30 Corporation, or similar processor from Sun, Motorola, Compaq, AMD or International Business Machines.

[000119] Typically the computer system is a general purpose system that comprises the processor and one or more internal data storage components for storing data, and one or more data retrieving devices for retrieving the data stored on the data storage components.

5 [000120] In one particular aspect, the computer system includes a processor connected to a bus which is connected to a main memory (preferably implemented as RAM) and one or more internal data storage devices, such as a hard drive and/or other computer readable media having data recorded thereon. In some aspects, the computer system further includes one or more data retrieving device for reading the data stored on the internal data storage devices.

10 [000121] The data retrieving device may represent, for example, a floppy disk drive, a compact disk drive, a magnetic tape drive, or a modem capable of connection to a remote data storage system (*e.g.*, via the internet) etc. In some aspects, the internal data storage device is a removable computer readable medium such as a floppy disk, a compact disk, a magnetic tape, etc. containing control logic and/or data recorded thereon. The computer system may advantageously include or be programmed by appropriate software for reading
15 the control logic and/or the data from the data storage component once inserted in the data retrieving device.

[000122] The computer system includes a display which is used to display output to a computer user. It should also be noted that the computer system can be linked to other computer systems in a network or wide area network to provide centralized access to the
20 computer system. In some aspects, the computer system may further comprise a sequence comparison algorithm. A "sequence comparison algorithm" refers to one or more programs which are implemented (locally or remotely) on the computer system to compare a nucleotide sequence with other nucleotide sequences and/or compounds stored within a data storage means.

25 Uses of Nitrilases

[000123] Nitrilases have been identified as key enzymes for the production of chiral α -hydroxy acids, which are valuable intermediates in the fine chemicals industry, and as pharmaceutical intermediates. The nitrilase enzymes of the invention are useful to catalyze the stereoselective hydrolysis of cyanohydrins and aminonitriles, producing chiral α -
30 hydroxy- and α -amino acids, respectively.

[000124] Stereoselective enzymes provide a key advantage over chemical resolution methods as they do not require harsh conditions and are more environmentally compatible. The use of nitrilases is of particular interest for the production of chiral amino acids and α -hydroxy acids. Using a stereoselective nitrilase, dynamic resolution conditions can be established, due to the racemisation of the substrate under aqueous conditions. Thus 100% theoretical yields are achievable.

[000125] This invention is directed to the nitrilases which have been discovered and isolated from naturally occurring sources. This invention is also directed to evolving novel genes and gene pathways from diverse and extreme environmental sources. In an effort to develop the most extensive assortment of enzymes available, DNA was extracted directly from samples that have been collected from varying habitats around the globe. From these efforts, the largest collection of environmental genetic libraries in the world was developed. Through extensive high-throughput screening of these libraries, 192 new sequence-unique nitrilase enzymes have been discovered to date. Previous to this invention, fewer than 20 microbial-derived nitrilases had been reported in the literature and public databases.

[000126] Biocatalysts, such as nitrilases, play an important role in catalyzing metabolic reactions in living organisms. In addition, biocatalysts have found applications in the chemical industry, where they can perform many different reactions. Some examples of the advantages of the use of nitrilases is that they provide: high enantio-, chemo- and regio-selectivity; they function under mild reaction conditions; they provide direct access to products – with minimal protection; they have high catalytic efficiencies; they produce reduced waste compared with the chemical alternatives; they are easily immobilized as enzymes or cells; they are recoverable, recyclable and are capable of being manipulated via molecular biological techniques; they can be regenerated in whole cell processes; they are tolerant to organic solvents; and importantly, they can be evolved or optimized. Optimized nitrilases are presented herein as working examples of the invention.

[000127] Nitrilases catalyze the hydrolysis of nitrile moieties generating the corresponding carboxylic acid. Conventional chemical hydrolysis of nitriles requires strong acid or base and high temperature. However, one advantage of the invention is that nitrilases are provided which perform this reaction under mild conditions. Wide ranges of nitrile substrates can be transformed by nitrilases with high enantio-, chemo- and regio- selectivity.



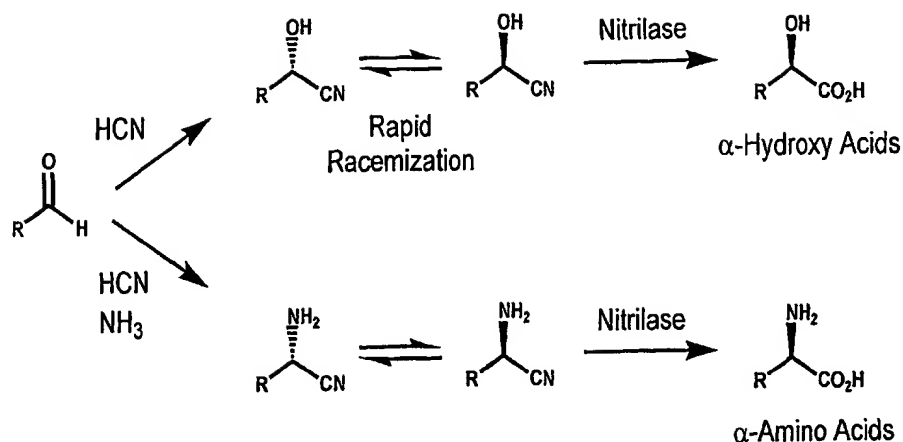
Table 1 - Some characteristics of Nitrilases of the Invention

<u>Previously Discovered Nitrilases</u>		<u>New Nitrilases</u>
Limitations	New Features	Benefits
< 20 reported	>180 newly discovered	Access to a wider substrate range
Homologous	Unique nitrilases, many with little homology to previously known nitrilases	
Narrow substrate Activity spectrum	Broad substrate activity spectrum	
Very few shown to be enantioselective	Enantioselective; both enantiomers accessible	Product with high enantiomeric excess and minimal waste production
Limited stability profile	Stable in a variety of conditions	Potential use in a wide range of process conditions
Inconsistent supply	Consistent supply	Reliable source of product
Not applicable	Amenable to optimization	Good source material leads to better product

5

[000128] Dynamic Kinetic Resolution: The use of the nitrilases allows discrimination between two rapidly equilibrating enantiomers to give a single product in 100% theoretical yield. Nitrilases are utilized for dynamic resolution of key cyanohydrins and aminonitriles to produce enantiomerically pure α -carboxylic and α -amino acids. Newly discovered nitrilases disclosed herein yield products with >95% enantiomeric excess (*ee*) with and >95% yield. The nitrilases perform this transformation efficiently under mild conditions in aqueous solution or in the presence of organic solvent.

10



[000129] These products shown above also include the opposite enantiomers, although they are not shown. In one aspect, the invention provides an isolated nucleic acid having a sequence as set forth in any one of the Group A nucleic acid sequences, having a sequence substantially identical thereto, or having a sequence complementary thereto.

[000130] In another aspect, the invention provides an isolated nucleic acid including at least 20 consecutive nucleotides identical to a portion of a nucleotide sequence as set forth in the Group A nucleic acid sequences, having a sequence substantially identical thereto, or having a sequence complementary thereto.

[000131] In another aspect, the invention provides an isolated nucleic acid encoding a polypeptide having a sequence as set forth in the Group B amino acid sequences, or having a sequence substantially identical thereto.

[000132] In another aspect, the invention provides an isolated nucleic acid encoding a polypeptide having at least 10 consecutive amino acids identical to a portion of a sequence as set forth in the Group B amino acid sequences, or having a sequence substantially identical thereto.

[000133] In yet another aspect, the invention provides a substantially purified polypeptide comprising consecutive amino acid residues having a sequence as set forth in the Group B amino acid sequences, or having a sequence substantially identical thereto.

[000134] In another aspect, the invention provides an isolated antibody that specifically binds to a polypeptide of the invention. The invention also provides for a fragment of the antibody which retains the ability to specifically bind the polypeptide.

5 [000135] In another aspect, the invention provides a method of producing a polypeptide having a sequence as set forth in the Group B amino acid sequences, and sequences substantially identical thereto. The method includes introducing a nucleic acid encoding the polypeptide into a host cell, wherein the nucleic acid is operably joined to a promoter, and culturing the host cell under conditions that allow expression of the nucleic acid.

10 [000136] In another aspect, the invention provides a method of producing a polypeptide having at least 10 consecutive amino acids from a sequence as set forth in the Group B amino acid sequences, and sequences substantially identical thereto. The method includes introducing a nucleic acid encoding the polypeptide into a host cell, wherein the nucleic acid is operably joined to a promoter, and culturing the host cell under conditions that allow expression of the nucleic acid, thereby producing the polypeptide.

15 [000137] In another aspect, the invention provides a method of generating a variant of a nitrilase, including choosing a nucleic acid sequence as set forth in the Group A nucleic acid sequences, and changing one or more nucleotides in the sequence to another nucleotide, deleting one or more nucleotides in the sequence, or adding one or more nucleotides to the sequence.

20 [000138] In another aspect, the invention provides assays for identifying functional variants of the Group B amino acid sequences that retain the enzymatic function of the polypeptides of the Group B amino acid sequences. The assays include contacting a polypeptide comprising consecutive amino acid residues having a sequence identical to a sequence of the Group B amino acid sequences or a portion thereof, having a sequence substantially identical
25 to a sequence of the Group B amino acid sequences or a portion thereof, or having a sequence which is a variant of a sequence of the Group B amino acid sequences that retains nitrilase activity, with a substrate molecule under conditions which allow the polypeptide to function, and detecting either a decrease in the level of substrate or an increase in the level of a specific reaction product of the reaction between the polypeptide and the substrate, thereby
30 identifying a functional variant of such sequences.

Modification of Polypeptides of the Invention

[000139] Enzymes are highly selective catalysts. Their hallmark is the ability to catalyze reactions with exquisite stereo-selectivity, regio-selectivity, and chemo-selectivity that is unparalleled in conventional synthetic chemistry. Moreover, enzymes are remarkably versatile. They can be tailored to function in organic solvents, operate at extreme pHs (for example, acidic or basic conditions) extreme temperatures (for example, high temperatures and low temperatures), extreme salinity levels (for example, high salinity and low salinity), and catalyze reactions with compounds that can be structurally unrelated to their natural, physiological substrates except for the enzymatic active site.

[000140] The invention provides methods for modifying polypeptides having nitrilase activity or polynucleotides encoding such polypeptides in order to obtain new polypeptides which retain nitrilase activity but which are improved with respect to some desired characteristic. Such improvements can include the ability to function (*i.e.*, exhibit nitrilase activity) in organic solvents, operate at extreme or uncharacteristic pHs, operate at extreme or uncharacteristic temperatures, operate at extreme or uncharacteristic salinity levels, catalyze reactions with different substrates, etc.

[000141] The present invention directed to methods of using nitrilases so as to exploit the unique catalytic properties of these enzymes. Whereas the use of biocatalysts (*i.e.*, purified or crude enzymes) in chemical transformations normally requires the identification of a particular biocatalyst that reacts with a specific starting compound, the present invention uses selected biocatalysts and reaction conditions that are specific for functional groups that are present in many starting compounds. Each biocatalyst is specific for one functional group, or several related functional groups, and can react with many starting compounds containing this functional group.

[000142] Enzymes react at specific sites within a starting compound without affecting the rest of the molecule, a process which is very difficult to achieve using traditional chemical methods. This high degree of specificity provides the means to identify a single active compound within a library of compounds. The library is characterized by the series of biocatalytic reactions used to produce it, a so-called "biosynthetic history." Screening the library for biological activities and tracing the biosynthetic history identifies the specific

reaction sequence producing the active compound. The reaction sequence is repeated and the structure of the synthesized compound determined. This mode of identification, unlike other synthesis and screening approaches, does not require immobilization technologies, and compounds can be synthesized and tested free in solution using virtually any type of screening assay. It is important to note, that the high degree of specificity of enzyme reactions on functional groups allows for the "tracking" of specific enzymatic reactions that make up the biocatalytically produced library. (For further teachings on modification of molecules, including small molecules, see PCT Application No. PCT/US94/09174, herein incorporated by reference in its entirety).

- 10 [000143] In one exemplification, the invention provides for the chimerization of a family of related nitrilase genes and their encoded family of related products. Thus according to this aspect of the invention, the sequences of a plurality of nitrilase nucleic acids (*e.g.*, the Group A nucleic acids) serve as nitrilase "templates" which are aligned using a sequence comparison algorithm such as those described above. One or more demarcation points are then identified
- 15 in the aligned template sequences, which are located at one or more areas of homology. The demarcation points can be used to delineate the boundaries of nucleic acid building blocks, which are used to generate chimeric nitrilases. Thus, the demarcation points identified and selected in the nitrilase template molecules serve as potential chimerization points in the assembly of the chimeric nitrilase molecules.
- 20 [000144] Typically, a useful demarcation point is an area of local identity between at least two progenitor templates, but preferably the demarcation point is an area of identity that is shared by at least half of the templates, at least two thirds of the templates, at least three fourths of the templates, or at nearly all of the templates.

- [000145] The building blocks, which are defined by the demarcation points, can then be
- 25 mixed (either literally, in solution, or theoretically, on paper or in a computer) and reassembled to form chimeric nitrilase genes. In one aspect, the gene reassembly process is performed exhaustively in order to generate an exhaustive library of all possible combinations. In other words, all possible ordered combinations of the nucleic acid building blocks are represented in the set of finalized chimeric nucleic acid molecules. At the same
- 30 time, however, the order of assembly of each building block in the 5' to 3' direction in each combination is designed to reflect the order in the templates, and to reduce the production of unwanted, inoperative products.

[000146] In some aspects, the gene reassembly process is performed systematically, in order to generate a compartmentalized library with compartments that can be screened systematically, *e.g.*, one by one. In other words, the invention provides that, through the selective and judicious use of specific nucleic acid building blocks, coupled with the selective and judicious use of sequentially stepped assembly reactions, an experimental design can be achieved where specific sets of chimeric products are made in each of several reaction vessels. This allows a systematic examination and screening procedure to be performed. Thus, it allows a potentially very large number of chimeric molecules to be examined systematically in smaller groups.

[000147] In some aspects, the synthetic nature of the step in which the building blocks are generated or reassembled allows the design and introduction of sequences of nucleotides (*e.g.*, codons or introns or regulatory sequences) that can later be optionally removed in an *in vitro* process (*e.g.*, by mutagenesis) or in an *in vivo* process (*e.g.*, by utilizing the gene splicing ability of a host organism). The introduction of these nucleotides may be desirable for many reasons, including the potential benefit of creating a useful demarcation point.

[000148] The synthetic gene reassembly method of the invention utilizes a plurality of nucleic acid building blocks, each of which has two ligatable ends. Some examples of the two ligatable ends on each nucleic acid building block includes, but are not limited to, two blunt ends, or one blunt end and one overhang, or two overhangs. In a further, non-limiting example, the overhang can include one base pair, 2 base pairs, 3 base pairs, 4 base pairs or more.

[000149] A double-stranded nucleic acid building block can be of variable size. Preferred sizes for building blocks range from about 1 base pair (bp) (not including any overhangs) to about 100,000 base pairs (not including any overhangs). Other preferred size ranges are also provided, which have lower limits of from about 1 bp to about 10,000 bp (including every integer value in between), and upper limits of from about 2 bp to about 100,000 bp (including every integer value in between).

[000150] According to one aspect, a double-stranded nucleic acid building block is generated by first generating two single stranded nucleic acids and allowing them to anneal to form a double-stranded nucleic acid building block. The two strands of a double-stranded nucleic acid building block may be complementary at every nucleotide apart from any that

form an overhang; thus containing no mismatches, apart from any overhang(s).

Alternatively, the two strands of a double-stranded nucleic acid building block can be complementary at fewer than every nucleotide, apart from any overhang(s). In particular, mismatches between the strands can be used to introduce codon degeneracy using methods
5 such as the site-saturation mutagenesis described herein.

[000151] *In vivo* shuffling of molecules is also useful in providing variants and can be performed utilizing the natural property of cells to recombine multimers. While recombination *in vivo* has provided the major natural route to molecular diversity, genetic recombination remains a relatively complex process that involves (1) the recognition of
10 homologues; (2) strand cleavage, strand invasion, and metabolic steps leading to the production of recombinant chiasma; and finally (3) the resolution of chiasma into discrete recombined molecules. The formation of the chiasma requires the recognition of homologous sequences.

[000152] Thus, the invention includes a method for producing a chimeric or recombinant
15 polynucleotide from at least a first polynucleotide and a second polynucleotide *in vivo*. The invention can be used to produce a recombinant polynucleotide by introducing at least a first polynucleotide and a second polynucleotide which share at least one region of partial sequence homology (*e.g.*, the Group A nucleic acid sequences, and combinations thereof) into a suitable host cell. The regions of partial sequence homology promote processes which
20 result in sequence reorganization producing a recombinant polynucleotide. Such hybrid polynucleotides can result from intermolecular recombination events which promote sequence integration between DNA molecules. In addition, such hybrid polynucleotides can result from intramolecular reductive reassortment processes which utilize repeated sequences to alter a nucleotide sequence within a DNA molecule.

[000153] The invention provides a means for generating recombinant polynucleotides
25 which encode biologically active variant polypeptides (*e.g.*, a nitrilase variant). For example, a polynucleotide may encode a particular enzyme from one microorganism. An enzyme encoded by a first polynucleotide from one organism can, for example, function effectively under a particular environmental condition, *e.g.*, high salinity. An enzyme encoded by a
30 second polynucleotide from a different organism can function effectively under a different environmental condition, such as extremely high temperature. A recombined polynucleotide containing sequences from the first and second original polynucleotides encodes a variant

enzyme which exhibits characteristics of both enzymes encoded by the original polynucleotides. Thus, the enzyme encoded by the recombined polynucleotide can function effectively under environmental conditions shared by each of the enzymes encoded by the first and second polynucleotides, *e.g.*, high salinity and extreme temperatures.

- 5 [000154] A variant polypeptide can exhibit specialized enzyme activity not displayed in the original enzymes. For example, following recombination and/or reductive reassortment of polynucleotides encoding nitrilase activity, the resulting variant polypeptide encoded by a recombined polynucleotide can be screened for specialized nitrilase activity obtained from each of the original enzymes, *i.e.*, the temperature or pH at which the nitrilase functions.
- 10 Sources of the original polynucleotides may be isolated from individual organisms ("isolates"), collections of organisms that have been grown in defined media ("enrichment cultures"), or, uncultivated organisms ("environmental samples"). The use of a culture-independent approach to derive polynucleotides encoding novel bioactivities from environmental samples is most preferable since it allows one to access untapped resources of
- 15 biodiversity. The microorganisms from which the polynucleotide may be prepared include prokaryotic microorganisms, such as *Xanthobacter*, *Eubacteria* and *Archaeobacteria*, and lower eukaryotic microorganisms such as fungi, some algae and protozoa. Polynucleotides may be isolated from environmental samples in which case the nucleic acid may be recovered without culturing of an organism or recovered from one or more cultured organisms. In one
- 20 aspect, such microorganisms may be extremophiles, such as hyperthermophiles, psychrophiles, psychrotrophs, halophiles, barophiles and acidophiles. Polynucleotides encoding enzymes isolated from extremophilic microorganisms are particularly preferred. Such enzymes may function at temperatures above 100°C in terrestrial hot springs and deep sea thermal vents, at temperatures below 0°C in arctic waters, in the saturated salt
- 25 environment of the Dead Sea, at pH values around 0 in coal deposits and geothermal sulfur-rich springs, or at pH values greater than 11 in sewage sludge.

- [000155] Examples of mammalian expression systems that can be employed to express recombinant proteins include the COS-7, C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors comprise an origin of replication, a suitable promoter and
- 30 enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 splice and polyadenylation sites may be

used to provide the required nontranscribed genetic elements. U.S. Patent No. 6,054,267 is hereby incorporated by reference in its entirety.

[000156] Host cells containing the polynucleotides of interest can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying genes. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan. Clones, which are identified as having a desired enzyme activity or other property may then be sequenced to identify the recombinant polynucleotide sequence encoding the enzyme having the desired activity or property.

[000157] In one aspect, the invention provides for the isolated nitrilases as either an isolated nucleic acid or an isolated polypeptide wherein the nucleic acid or the polypeptide was prepared by recovering DNA from a DNA population derived from at least one uncultivated microorganism, and transforming a host with recovered DNA to produce a library of clones which is screened for the specified protein, *e.g.* nitrilase activity. U.S. Patent No. 6,280,926, Short, provides descriptions of such methods and is hereby incorporated by reference in its entirety for all purposes.

[000158] Therefore, in a one aspect, the invention relates to a method for producing a biologically active recombinant nitrilase polypeptide and screening such a polypeptide for desired activity or property by:

- 1) introducing at least a first nitrilase polynucleotide and a second nitrilase polynucleotide, said at least first nitrilase polynucleotide and second nitrilase polynucleotide sharing at least one region of sequence homology, into a suitable host cell;
- 2) growing the host cell under conditions which promote sequence reorganization resulting in a recombinant nitrilase polynucleotide;
- 3) expressing a recombinant nitrilase polypeptide encoded by the recombinant nitrilase polynucleotide;
- 4) screening the recombinant nitrilase polypeptide for the desired activity or property; and
- 5) isolating the recombinant nitrilase polynucleotide encoding the recombinant nitrilase polypeptide.

[000159] Examples of vectors which may be used include viral particles, baculovirus, phage, plasmids, phagemids, cosmids, fosmids, bacterial artificial chromosomes, viral DNA (e.g., vaccinia, adenovirus, fowlpox virus, pseudorabies and derivatives of SV40), P1-based artificial chromosomes, yeast plasmids, yeast artificial chromosomes, and any other vectors specific for the hosts of interest (e.g., *Bacillus*, *Aspergillus* and yeast). Large numbers of suitable vectors are known to those of skill in the art, and are commercially available. Examples of bacterial vectors include pQE vectors (Qiagen, Valencia, CA); pBluescript plasmids, pNH vectors, and lambda-ZAP vectors (Stratagene, La Jolla, CA); and pTRC99a, pKK223-3, pDR540, and pRIT2T vectors (Pharmacia, Peapack, NJ). Examples of eukaryotic vectors include pXT1 and pSG5 vectors (Stratagene, La Jolla, CA); and pSVK3, pBPV, pMSG, and pSVLSV40 vectors (Pharmacia, Peapack, NJ). However, any other plasmid or other vector may be used so long as they are replicable and viable in the host.

[000160] A preferred type of vector for use in the present invention contains an f-factor (or fertility factor) origin of replication. The f-factor in *E. coli* is a plasmid which effects high frequency transfer of itself during conjugation and less frequent transfer of the bacterial chromosome itself. A particularly preferred aspect is to use cloning vectors referred to as "fosmids" or bacterial artificial chromosome (BAC) vectors. These are derived from *E. coli* f-factor which is able to stably integrate large segments of genomic DNA.

[000161] The DNA sequence in the expression vector is operably joined to appropriate expression control sequences, including a promoter, to direct RNA synthesis. Useful bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda P_R, P_L and trp. Useful eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression. Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers.

[000162] In addition, the expression vectors can contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells. Useful selectable markers include dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or tetracycline or ampicillin resistance in *E. coli*.

[000163] The vector may be introduced into the host cells using any of a variety of techniques, including transformation, transfection, transduction, viral infection, gene guns, or Ti-mediated gene transfer. Particular methods include calcium phosphate transfection, DEAE-Dextran mediated transfection, lipofection, or electroporation

5 [000164] Reductive Reassortment - In another aspect, variant nitrilase polynucleotides can be generated by the process of reductive reassortment. Whereas recombination is an "inter-molecular" process which, in bacteria, is generally viewed as a "recA-dependent" phenomenon, the process of "reductive reassortment" occurs by an "intra-molecular", recA-independent process. In this aspect, the invention can rely on the ability of cells to mediate
10 reductive processes to decrease the complexity of quasi-repeated sequences in the cell by deletion. The method involves the generation of constructs containing consecutive repeated or quasi-repeated sequences (original encoding sequences), the insertion of these sequences into an appropriate vector, and the subsequent introduction of the vector into an appropriate host cell. The reassortment of the individual molecular identities occurs by combinatorial
15 processes between the consecutive sequences in the construct possessing regions of homology, or between quasi-repeated units. The reassortment process recombines and/or reduces the complexity and extent of the repeated sequences, and results in the production of novel molecular species. Various treatments may be applied to enhance the rate of reassortment, such as ultra-violet light or DNA damaging chemicals. In addition, host cell
20 lines displaying enhanced levels of "genetic instability" can be used.

[000165] Repeated Sequences - Repeated or "quasi-repeated" sequences play a role in genetic instability. In the present invention, "quasi-repeats" are repeats that are not identical in structure but, rather, represent an array of consecutive sequences which have a high degree of similarity or identity sequences. The reductive reassortment or deletion process in the cell
25 reduces the complexity of the resulting construct by deleting sequences between positions within quasi-repeated sequences. Because the deletion (and potentially insertion) events can occur virtually anywhere within the quasi-repetitive units, these sequences provide a large repertoire of potential variants.

[000166] When the quasi-repeated sequences are all ligated in the same orientation, for
30 instance head-to-tail or vice versa, the endpoints of a deletion are, for the most part, equally likely to occur anywhere within the quasi-repeated sequences. In contrast, when the units are presented head-to-head or tail-to-tail, the inverted quasi-repeated sequences can form a

duplex which delineates the endpoints of the adjacent units and thereby favors deletion of discrete units. Therefore, it is preferable in the present invention that the quasi-repeated sequences are joined in the same orientation because random orientation of quasi-repeated sequences will result in the loss of reassortment efficiency, while consistent orientation of the sequences will offer the highest efficiency. Nonetheless, although having fewer of the contiguous sequences in the same orientation decreases the efficiency or reductive reassortment, it may still provide sufficient variation for the effective recovery of novel molecules.

5 [000167] Sequences can be assembled in a head-to-tail orientation using any of a variety of methods, including the following:

a) Primers can be utilized that include a poly-A head and poly-T tail which, when made single-stranded, would provide orientation. This is accomplished by having the first few bases of the primers made from RNA and hence easily removed by RNase H. b)

15 Primers can be utilized that include unique restriction cleavage sites. Multiple sites, a battery of unique sequences, and repeated synthesis and ligation steps would be required.

c) The inner few bases of the primer can be thiolated and an exonuclease used to produce properly tailed molecules.

[000168] The recovery of the reassorted sequences relies on the identification of cloning vectors with a reduced repetitive index (RI). The reassorted coding sequences can then be recovered by amplification. The products are recloned and expressed. The recovery of cloning vectors with reduced RI can be effected by:

1) The use of vectors only stably maintained when the construct is reduced in complexity.

2) The physical recovery of shortened vectors by physical procedures. In this case, the cloning vector would be recovered using standard plasmid isolation procedures and then size-fractionated using standard procedures (*e.g.*, agarose gel or column with a low molecular weight cut off).

3) The recovery of vectors containing interrupted genes can be selected when insert size decreases.

30 4) The use of direct selection techniques wherein an expression vector is used and the appropriate selection is carried out.

5 [000169] Coding sequences from related organisms may demonstrate a high degree of homology but nonetheless encode quite diverse protein products. These types of sequences are particularly useful in the present invention as quasi-repeats. However, while the examples illustrated below demonstrate the reassortment of coding sequences with a high degree of identity (quasi-repeats), this process is not limited to nearly identical repeats.

10 [000170] The following example demonstrates a method of the invention. Quasi-repetitive coding sequences derived from three different species are obtained. Each sequence encodes a protein with a distinct set of properties. Each of the sequences differs by one or more base pairs at unique positions in the sequences which are designated "A", "B" and "C". The quasi-repeated sequences are separately or collectively amplified and ligated into random assemblies such that all possible permutations and combinations are available in the population of ligated molecules. The number of quasi-repeat units can be controlled by the assembly conditions. The average number of quasi-repeated units in a construct is defined as the repetitive index (RI).

15 [000171] Once formed, the constructs can be size-fractionated on an agarose gel according to published protocols, inserted into a cloning vector, and transfected into an appropriate host cell. The cells can then be propagated to allow reductive reassortment to occur. The rate of the reductive reassortment process may be stimulated by the introduction of DNA damage if desired. Whether the reduction in RI is mediated by deletion formation between repeated sequences by an "intra-molecular" mechanism, or mediated by recombination-like events through "inter-molecular" mechanisms is immaterial. The end result is a reassortment of the molecules into all possible combinations.

[000172] In another aspect, prior to or during recombination or reassortment, polynucleotides of the invention or polynucleotides generated by the methods described
25 herein can be subjected to agents or processes which promote the introduction of mutations into the original polynucleotides. The introduction of such mutations would increase the diversity of resulting hybrid polynucleotides and polypeptides encoded therefrom. The agents or processes which promote mutagenesis include, but are not limited to: (+)-CC-1065, or a synthetic analog such as (+)-CC-1065-(N3-adenine) (Sun et al. (1992), *Biochemistry*
30 31(10):2822-9); an N-acetylated or deacetylated 4'-fluoro-4-aminobiphenyl adduct capable of inhibiting DNA synthesis (see, for example, van de Poll et al. (1992), *Carcinogenesis*
13(5):751-8); or a N-acetylated or deacetylated 4-aminobiphenyl adduct capable of inhibiting

DNA synthesis (see also, Van de Poll et al. (1992), *supra*); trivalent chromium, a trivalent chromium salt, a polycyclic aromatic hydrocarbon ("PAH") DNA adduct capable of inhibiting DNA replication, such as 7-bromomethyl-benz[a]anthracene ("BMA"), tris(2,3-dibromopropyl)phosphate ("Tris-BP"), 1,2-dibromo-3-chloropropane ("DBCP"), 2-bromoacrolein (2BA), benzo[a]pyrene-7,8-dihydrodiol-9-10-epoxide ("BPDE"), a platinum(II) halogen salt, N-hydroxy-2-amino-3-methylimidazo[4,5-f]-quinoline ("N-hydroxy-IQ"), and N-hydroxy-2-amino-1-methyl-6-phenylimidazo[4,5-f]-pyridine ("N-hydroxy-PhIP"). Especially preferred means for slowing or halting PCR amplification consist of UV light (+)-CC-1065 and (+)-CC-1065-(N3-Adenine). Particularly encompassed means are DNA adducts or polynucleotides comprising the DNA adducts from the polynucleotides or polynucleotides pool, which can be released or removed by a process including heating the solution comprising the polynucleotides prior to further processing.

[000173] GSSMTM - The invention also provides for the use of codon primers containing a degenerate N,N,G/T sequence to introduce point mutations into a polynucleotide, so as to generate a set of progeny polypeptides in which a full range of single amino acid substitutions is represented at each amino acid position, a method referred to as gene site-saturated mutagenesis (GSSMTM). The oligos used are comprised contiguously of a first homologous sequence, a degenerate N,N,G/T sequence, and possibly a second homologous sequence. The progeny translational products from the use of such oligos include all possible amino acid changes at each amino acid site along the polypeptide, because the degeneracy of the N,N,G/T sequence includes codons for all 20 amino acids.

[000174] In one aspect, one such degenerate oligo (comprising one degenerate N,N,G/T cassette) is used for subjecting each original codon in a parental polynucleotide template to a full range of codon substitutions. In another aspect, at least two degenerate N,N,G/T cassettes are used – either in the same oligo or not, for subjecting at least two original codons in a parental polynucleotide template to a full range of codon substitutions. Thus, more than one N,N,G/T sequence can be contained in one oligo to introduce amino acid mutations at more than one site. This plurality of N,N,G/T sequences can be directly contiguous, or separated by one or more additional nucleotide sequences. In another aspect, oligos serviceable for introducing additions and deletions can be used either alone or in combination with the codons containing an N,N,G/T sequence, to introduce any combination or permutation of amino acid additions, deletions, and/or substitutions.

[000175] In a particular exemplification, it is possible to simultaneously mutagenize two or more contiguous amino acid positions using an oligo that contains contiguous N,N,G/T triplets, *i.e.*, a degenerate (N,N,G/T)_n sequence.

[000176] In another aspect, the present invention provides for the use of degenerate cassettes having less degeneracy than the N,N,G/T sequence. For example, it may be desirable in some instances to use a degenerate triplet sequence comprised of only one N, where said N can be in the first second or third position of the triplet. Any other bases including any combinations and permutations thereof can be used in the remaining two positions of the triplet. Alternatively, it may be desirable in some instances to use a degenerate N,N,N triplet sequence, or an N,N, G/C triplet sequence.

[000177] It is appreciated, however, that the use of a degenerate triplet (such as N,N,G/T or an N,N, G/C triplet sequence) as disclosed in the instant invention is advantageous for several reasons. In one aspect, this invention provides a means to systematically and fairly easily generate the substitution of the full range of the 20 possible amino acids into each and every amino acid position in a polypeptide. Thus, for a 100 amino acid polypeptide, the invention provides a way to systematically and fairly easily generate 2000 distinct species (*i.e.*, 20 possible amino acids per position times 100 amino acid positions). It is appreciated that there is provided, through the use of an oligo containing a degenerate N,N,G/T or an N,N, G/C triplet sequence, 32 individual sequences that code for the 20 possible amino acids. Thus, in a reaction vessel in which a parental polynucleotide sequence is subjected to saturation mutagenesis using one such oligo, there are generated 32 distinct progeny polynucleotides encoding 20 distinct polypeptides. In contrast, the use of a non-degenerate oligo in site-directed mutagenesis leads to only one progeny polypeptide product per reaction vessel.

[000178] This invention also provides for the use of nondegenerate oligonucleotides, which can optionally be used in combination with degenerate primers disclosed. It is appreciated that in some situations, it is advantageous to use nondegenerate oligos to generate specific point mutations in a working polynucleotide. This provides a means to generate specific silent point mutations, point mutations leading to corresponding amino acid changes, and point mutations that cause the generation of stop codons and the corresponding expression of polypeptide fragments.

[000179] Thus, in one aspect, each saturation mutagenesis reaction vessel contains polynucleotides encoding at least 20 progeny polypeptide molecules such that all 20 amino acids are represented at the one specific amino acid position corresponding to the codon position mutagenized in the parental polynucleotide. The 32-fold degenerate progeny polypeptides generated from each saturation mutagenesis reaction vessel can be subjected to clonal amplification (*e.g.*, cloned into a suitable *E. coli* host using an expression vector) and subjected to expression screening. When an individual progeny polypeptide is identified by screening to display a favorable change in property (when compared to the parental polypeptide), it can be sequenced to identify the correspondingly favorable amino acid substitution contained therein.

[000180] It is appreciated that upon mutagenizing each and every amino acid position in a parental polypeptide using saturation mutagenesis as disclosed herein, favorable amino acid changes may be identified at more than one amino acid position. One or more new progeny molecules can be generated that contain a combination of all or part of these favorable amino acid substitutions. For example, if 2 specific favorable amino acid changes are identified in each of 3 amino acid positions in a polypeptide, the permutations include 3 possibilities at each position (no change from the original amino acid, and each of two favorable changes) and 3 positions. Thus, there are $3 \times 3 \times 3$ or 27 total possibilities, including 7 that were previously examined - 6 single point mutations (*i.e.*, 2 at each of three positions) and no change at any position.

[000181] In yet another aspect, site-saturation mutagenesis can be used together with shuffling, chimerization, recombination and other mutagenizing processes, along with screening. This invention provides for the use of any mutagenizing process(es), including saturation mutagenesis, in an iterative manner. In one exemplification, the iterative use of any mutagenizing process(es) is used in combination with screening.

[000182] Thus, in a non-limiting exemplification, polynucleotides and polypeptides of the invention can be derived by saturation mutagenesis in combination with additional mutagenization processes, such as process where two or more related polynucleotides are introduced into a suitable host cell such that a hybrid polynucleotide is generated by recombination and reductive reassortment.

[000183] In addition to performing mutagenesis along the entire sequence of a gene, mutagenesis can be used to replace each of any number of bases in a polynucleotide sequence, wherein the number of bases to be mutagenized can be each integer from about 15 to about 100,000. Thus, instead of mutagenizing every position along a molecule, one can
5 subject every or a discrete number of bases (*e.g.*, a subset totaling from about 15 to about 100,000) to mutagenesis. In one aspect, a separate nucleotide is used for mutagenizing each position or group of positions along a polynucleotide sequence. A group of 3 positions to be mutagenized can be a codon. In one aspect, the mutations are introduced using a mutagenic primer, containing a heterologous cassette, also referred to as a mutagenic cassette. For
10 example, cassettes can have from about 1 to about 500 bases. Each nucleotide position in such heterologous cassettes can be N, A, C, G, T, A/C, A/G, A/T, C/G, C/T, G/T, C/G/T, A/G/T, A/C/T, A/C/G, or E, where E is any base that is not A, C, G, or T.

[000184] In a general sense, saturation mutagenesis comprises mutagenizing a complete set of mutagenic cassettes (for example, each cassette is about 1-500 bases in length) in a defined
15 polynucleotide sequence to be mutagenized (for example, the sequence to be mutagenized is from about 15 to about 100,000 bases in length). Thus, a group of mutations (ranging from about 1 to about 100 mutations) is introduced into each cassette to be mutagenized. A grouping of mutations to be introduced into one cassette can be different or the same from a second grouping of mutations to be introduced into a second cassette during the application
20 of one round of saturation mutagenesis. Such groupings are exemplified by deletions, additions, groupings of particular codons, and groupings of particular nucleotide cassettes.

[000185] Defined sequences to be mutagenized include a whole gene, pathway, cDNA, entire open reading frame (ORF), promoter, enhancer, repressor/transactivator, origin of replication, intron, operator, or any polynucleotide functional group. Generally, a “defined
25 sequence” for this purpose may be any polynucleotide that a 15 base-polynucleotide sequence, and polynucleotide sequences of lengths between about 15 bases and about 15,000 bases (this invention specifically names every integer in between). Considerations in choosing groupings of codons include types of amino acids encoded by a degenerate mutagenic cassette.

[000186] In a particularly preferred exemplification a grouping of mutations that can be introduced into a mutagenic cassette, this invention specifically provides for degenerate codon substitutions (using degenerate oligos) that code for 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13,

14, 15, 16, 17, 18, 19, and 20 amino acids at each position, and a library of polypeptides encoded thereby.

[000187] One aspect of the invention is an isolated nucleic acid comprising one of the sequences of the Group A nucleic acid sequences, sequences substantially identical thereto, sequences complementary thereto, or a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases of one of the sequences of the Group A nucleic acid sequences. The isolated nucleic acids may comprise DNA, including cDNA, genomic DNA, and synthetic DNA. The DNA may be double-stranded or single-stranded, and if single stranded may be the coding strand or non-coding (anti-sense) strand. Alternatively, the isolated nucleic acids may comprise RNA.

[000188] As discussed in more detail below, the isolated nucleic acid sequences of the invention may be used to prepare one of the polypeptides of the Group B amino acid sequences, and sequences substantially identical thereto, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of one of the polypeptides of the Group B amino acid sequences, and sequences substantially identical thereto.

[000189] Alternatively, the nucleic acid sequences of the invention may be mutagenized using conventional techniques, such as site directed mutagenesis, or other techniques familiar to those skilled in the art, to introduce silent changes into the polynucleotides of the Group A nucleic acid sequences, and sequences substantially identical thereto. As used herein, "silent changes" include, for example, changes which do not alter the amino acid sequence encoded by the polynucleotide. Such changes may be desirable in order to increase the level of the polypeptide produced by host cells containing a vector encoding the polypeptide by introducing codons or codon pairs which occur frequently in the host organism.

[000190] The invention also relates to polynucleotides which have nucleotide changes which result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptides of the invention (*e.g.*, the Group B amino acid sequences). Such nucleotide changes may be introduced using techniques such as site-directed mutagenesis, random chemical mutagenesis, exonuclease III deletion, and other recombinant DNA techniques. Alternatively, such nucleotide changes may be naturally occurring allelic variants which are isolated by identifying nucleic acid sequences which specifically hybridize to probes

comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases of one of the sequences of the Group A nucleic acid sequences, and sequences substantially identical thereto (or the sequences complementary thereto) under conditions of high, moderate, or low stringency as provided herein.

5 Immobilized Enzyme Solid Supports

[000191] The enzymes, fragments thereof and nucleic acids which encode the enzymes and fragments can be affixed to a solid support. This is often economical and efficient in the use of the enzymes in industrial processes. For example, a consortium or cocktail of enzymes (or active fragments thereof), which are used in a specific chemical reaction, can be attached to a solid support and dunked into a process vat. The enzymatic reaction can occur. Then, the solid support can be taken out of the vat, along with the enzymes affixed thereto, for repeated use. In one aspect of the invention, the isolated nucleic acid is affixed to a solid support. In another aspect of the invention, the solid support is selected from the group of a gel, a resin, a polymer, a ceramic, a glass, a microelectrode and any combination thereof.

15 [000192] For example, solid supports useful in this invention include gels. Some examples of gels include sepharose, gelatin, glutaraldehyde, chitosan-treated glutaraldehyde, albumin-glutaraldehyde, chitosan-Xanthan, toyopearl gel (polymer gel), alginate, alginate-polylysine, carrageenan, agarose, glyoxyl agarose, magnetic agarose, dextran-agarose, poly(Carbamoyl Sulfonate) hydrogel, BSA-PEG hydrogel, phosphorylated polyvinyl alcohol (PVA),
20 monoaminoethyl-N-aminoethyl (MANA), amino, or any combination thereof.

[000193] Another solid support useful in the present invention are resins or polymers. Some examples of resins or polymers include cellulose, acrylamide, nylon, rayon, polyester, anion-exchange resin, AMBERLITE™ XAD-7, AMBERLITE™ XAD-8, AMBERLITE™ IRA-94, AMBERLITE™ IRC-50, polyvinyl, polyacrylic, polymethacrylate, or any
25 combination thereof. Another type of solid support useful in the present invention is ceramic. Some examples include non-porous ceramic, porous ceramic, SiO₂, Al₂O₃. Another type of solid support useful in the present invention is glass. Some examples include non-porous glass, porous glass, aminopropyl glass or any combination thereof. Another type of solid support which can be used is a microelectrode. An example is a polyethyleneimine-coated
30 magnetite. Graphitic particles can be used as a solid support. Another example of a solid support is a cell, such as a red blood cell.

Methods of immobilization

- [000194] There are many methods which would be known to one of skill in the art for immobilizing enzymes or fragments thereof, or nucleic acids, onto a solid support. Some examples of such methods include electrostatic droplet generation, electrochemical means, via adsorption, via covalent binding, via cross-linking, via a chemical reaction or process, via encapsulation, via entrapment, via calcium alginate, or via poly (2-hydroxyethyl methacrylate). Like methods are described in *Methods in Enzymology, Immobilized Enzymes and Cells*, Part C. 1987. Academic Press. Edited by S. P. Colowick and N. O. Kaplan. Volume 136; and *Immobilization of Enzymes and Cells*. 1997. Humana Press. Edited by G. F. Bickerstaff. Series: Methods in Biotechnology, Edited by J. M. Walker.
- [000195] Probes - The isolated nucleic acids of the Group A nucleic acid sequences, sequences substantially identical thereto, complementary sequences, or a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases of one of the foregoing sequences may also be used as probes to determine whether a biological sample, such as a soil sample, contains an organism having a nucleic acid sequence of the invention or an organism from which the nucleic acid was obtained. In such procedures, a biological sample potentially harboring the organism from which the nucleic acid was isolated is obtained and nucleic acids are obtained from the sample. The nucleic acids are contacted with the probe under conditions which permit the probe to specifically hybridize to any complementary sequences which are present therein.
- [000196] Where necessary, conditions which permit the probe to specifically hybridize to complementary sequences may be determined by placing the probe in contact with complementary sequences from samples known to contain the complementary sequence as well as control sequences which do not contain the complementary sequence. Hybridization conditions, such as the salt concentration of the hybridization buffer, the formamide concentration of the hybridization buffer, or the hybridization temperature, can be varied to identify conditions which allow the probe to hybridize specifically to complementary nucleic acids. Stringent hybridization conditions are recited herein.
- [000197] Hybridization may be detected by labeling the probe with a detectable agent such as a radioactive isotope, a fluorescent dye or an enzyme capable of catalyzing the formation of a detectable product. Many methods for using the labeled probes to detect the presence of complementary nucleic acids in a sample are familiar to those skilled in the art. These include Southern Blots, Northern Blots, colony hybridization procedures, and dot blots.

Protocols for each of these procedures are provided in Ausubel et al. (1997), Current Protocols in Molecular Biology, John Wiley & Sons, Inc., and Sambrook et al. (1989), Molecular Cloning: A Laboratory Manual 2d Ed., Cold Spring Harbor Laboratory Press, the entire disclosures of which are incorporated herein by reference.

- 5 [000198] In one example, a probe DNA is "labeled" with one partner of a specific binding pair (*i.e.*, a ligand) and the other partner of the pair is bound to a solid matrix to provide ease of separation of target from its source. For example, the ligand and specific binding partner can be selected from, in either orientation, the following: (1) an antigen or hapten and an antibody or specific binding fragment thereof; (2) biotin or iminobiotin and avidin or streptavidin; (3) a sugar and a lectin specific therefor; (4) an enzyme and an inhibitor therefor; (5) an apoenzyme and cofactor; (6) complementary homopolymeric oligonucleotides; and (7) a hormone and a receptor therefor. In one example, the solid phase is selected from: (1) a glass or polymeric surface; (2) a packed column of polymeric beads; and (3) magnetic or paramagnetic particles.
- 10 [000199] Alternatively, more than one probe (at least one of which is capable of specifically hybridizing to any complementary sequences which are present in the nucleic acid sample), may be used in an amplification reaction to determine whether the sample contains an organism containing a nucleic acid sequence of the invention (*e.g.*, an organism from which the nucleic acid was isolated). Typically, the probes comprise oligonucleotides. In one aspect, the amplification reaction may comprise a PCR reaction. PCR protocols are described in Ausubel et al. (1997), *supra*, and Sambrook et al. (1989), *supra*. Alternatively, the amplification may comprise a ligase chain reaction, 3SR, or strand displacement reaction. (See Barany (1991), *PCR Methods and Applications* 1:5-16; Fahy et al. (1991), *PCR Methods and Applications* 1:25-33; and Walker et al. (1992), *Nucleic Acid Research* 20:1691-1696, the disclosures of which are incorporated herein by reference in their entireties).
- 15 [000200] Probes derived from sequences near the ends of a sequence as set forth in the Group A nucleic acid sequences, and sequences substantially identical thereto, may also be used in chromosome walking procedures to identify clones containing genomic sequences located adjacent to the nucleic acid sequences as set forth above. Such methods allow the isolation of genes which encode additional proteins from the host organism.
- 20 [000201] An isolated nucleic acid sequence as set forth in the Group A nucleic acid sequences, sequences substantially identical thereto, sequences complementary thereto, or a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or
- 25
- 30

500 consecutive bases of one of the foregoing sequences may be used as probes to identify and isolate related nucleic acids. In some aspects, the related nucleic acids may be cDNAs or genomic DNAs from organisms other than the one from which the nucleic acid was isolated. For example, the other organisms may be related organisms. In such procedures, a nucleic acid sample is contacted with the probe under conditions which permit the probe to specifically hybridize to related sequences. Hybridization of the probe to nucleic acids from the related organism is then detected using any of the methods described above.

[000202] In nucleic acid hybridization reactions, the conditions used to achieve a particular level of stringency will vary, depending on the nature of the nucleic acids being hybridized.

For example, the length of the nucleic acids, the amount of complementarity between the nucleic acids, the nucleotide sequence composition (e.g., G-C rich v. A-T rich content), and the nucleic acid type (e.g., RNA v. DNA) can be considered in selecting hybridization conditions. Stringency may be varied by conducting the hybridization at varying temperatures below the melting temperatures of the probes. The melting temperature, T_m , is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly complementary probe. Stringent conditions are selected to be equal to or about 5°C lower than the T_m for a particular probe. The melting temperature of the probe may be calculated using the following formulas:

[000203] For probes between 14 and 70 nucleotides in length the melting temperature (T_m) is calculated using the formula: $T_m = 81.5 + 16.6(\log [Na^+]) + 0.41(\text{fraction G+C}) - (600/N)$ where N is the length of the probe.

[000204] If the hybridization is carried out in a solution containing formamide, the melting temperature may be calculated using the equation: $T_m = 81.5 + 16.6(\log [Na^+]) + 0.41(\text{fraction G+C}) - (0.63\% \text{ formamide}) - (600/N)$ where N is the length of the probe.

[000205] Expression Libraries - Expression libraries can be created using the polynucleotides of the invention in combination with expression vectors and appropriate host cells. The library allows for the *in vivo* expression of the polypeptides which are encoded by the polynucleotides of the invention. After such expression libraries have been generated one can include the additional step of "biopanning" such libraries prior to screening by cell sorting. The "biopanning" procedure refers to a process for identifying clones having a specified biological activity by screening for sequence identity in a library of clones prepared by (i) selectively isolating target DNA derived from at least one microorganism by use of at least one probe DNA comprising at least a portion of a DNA sequence encoding a

polypeptide having a specified biological activity (*e.g.*, nitrilase activity); and (ii) optionally transforming a host with the isolated target DNA to produce a library of clones which are screened for the specified biological activity.

5 [000206] The probe DNA used for selectively isolating the target DNA of interest from the DNA derived from at least one microorganism can be a full-length coding region sequence or a partial coding region sequence of DNA for an enzyme of known activity. The original DNA library can be probed using mixtures of probes comprising at least a portion of DNA sequences encoding enzymes having the specified enzyme activity. These probes or probe libraries are single-stranded and the microbial DNA which is probed has been converted into
10 single-stranded form. The probes that are particularly suitable are those derived from DNA encoding enzymes having an activity similar or identical to the specified enzyme activity that is to be screened.

[000207] Having prepared a multiplicity of clones from DNA selectively isolated from an organism, such clones are screened for a specific enzyme activity and to identify the clones
15 having the specified enzyme characteristics.

[000208] The screening for enzyme activity may be affected on individual expression clones or may be initially affected on a mixture of expression clones to ascertain whether or not the mixture has one or more specified enzyme activities. If the mixture has a specified enzyme activity, then the individual clones may be rescreened for such enzyme activity or for
20 a more specific activity. Thus, for example, if a clone mixture has nitrilase activity, then the individual clones may be recovered and screened to determine which of such clones has nitrilase activity.

[000209] As described with respect to one of the above aspects, the invention provides a process for enzyme activity screening of clones containing selected DNA derived from a
25 microorganism which process includes: screening a library for specified enzyme activity, said library including a plurality of clones, said clones having been prepared by recovering from genomic DNA of a microorganism selected DNA, which DNA is selected by hybridization to at least one DNA sequence which is all or a portion of a DNA sequence encoding an enzyme having the specified activity; and transforming a host with the selected
30 DNA to produce clones which are screened for the specified enzyme activity.

[000210] In one aspect, a DNA library derived from a microorganism is subjected to a selection procedure to select therefrom DNA which hybridizes to one or more probe DNA

sequences which is all or a portion of a DNA sequence encoding an enzyme having the specified enzyme activity by:

- (a) contacting the single-stranded DNA population from the DNA library with the DNA probe bound to a ligand under stringent hybridization conditions so as to produce a duplex between the probe and a member of the DNA library;
- (b) contacting the duplex with a solid phase specific binding partner for the ligand so as to produce a solid phase complex;
- (c) separating the solid phase complex from the non-duplexed members of the DNA library;
- (d) denaturing the duplex to release the member of the DNA library;
- (e) creating a complementary DNA strand of the member from step (d) so as to make the member a double-stranded DNA;
- (f) introducing the double-stranded DNA into a suitable host so as to express a polypeptide which is encoded by the member DNA; and
- (g) determining whether the polypeptide expressed exhibits the specified enzymatic activity.

[000211] In another aspect, the process includes a preselection to recover DNA including signal or secretion sequences. In this manner it is possible to select from the genomic DNA population by hybridization as hereinabove described only DNA which includes a signal or secretion sequence. The following paragraphs describe the protocol for this aspect of the invention, the nature and function of secretion signal sequences in general and a specific exemplary application of such sequences to an assay or selection process.

- [000212] A particularly aspect of this aspect further comprises, after (a) but before (b) above, the steps of:
- (i) contacting the single-stranded DNA population of (a) with a ligand-bound oligonucleotide probe that is complementary to a secretion signal sequence unique to a given class of proteins under hybridization conditions to form a double-stranded DNA duplex;
 - (ii) contacting the duplex of (i) with a solid phase specific binding partner for said ligand so as to produce a solid phase complex;
 - (iii) separating the solid phase complex from the single-stranded DNA population of (a);
 - (iv) denaturing the duplex so as to release single-stranded DNA members of the genomic population; and

(v) separating the single-stranded DNA members from the solid phase bound probe.

[000213] The DNA which has been selected and isolated to include a signal sequence is then subjected to the selection procedure hereinabove described to select and isolate therefrom DNA which binds to one or more probe DNA sequences derived from DNA encoding an enzyme(s) having the specified enzyme activity. This procedure is described and exemplified in U.S. Pat. No. 6,054,267, incorporated herein by reference in its entirety.

[000214] *In vivo* biopanning may be performed utilizing a (fluorescence activated cell sorter) FACS-based machine. Complex gene libraries are constructed with vectors which contain elements which stabilize transcribed RNA. For example, the inclusion of sequences which result in secondary structures such as hairpins which are designed to flank the transcribed regions of the RNA would serve to enhance their stability, thus increasing their half life within the cell. The probe molecules used in the biopanning process consist of oligonucleotides labeled with reporter molecules that only fluoresce upon binding of the probe to a target molecule. These probes are introduced into the recombinant cells from the library using one of several transformation methods. The probe molecules bind to the transcribed target mRNA resulting in DNA/RNA heteroduplex molecules. Binding of the probe to a target will yield a fluorescent signal that is detected and sorted by the FACS machine during the screening process.

[000215] In some aspects, the nucleic acid encoding one of the polypeptides of the Group B amino acid sequences, sequences substantially identical thereto, or fragments comprising at least about 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof is assembled in appropriate phase with a leader sequence capable of directing secretion of the translated polypeptide or fragment thereof. Optionally, the nucleic acid can encode a fusion polypeptide in which one of the polypeptides of the Group B amino acid sequences, sequences substantially identical thereto, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof is fused to heterologous peptides or polypeptides, such as N-terminal identification peptides which impart desired characteristics, such as increased stability or simplified purification.

[000216] The host cell may be any of the host cells familiar to those skilled in the art, including prokaryotic cells, eukaryotic cells, mammalian cells, insect cells, or plant cells. As representative examples of appropriate hosts, there may be mentioned: bacterial cells, such as *E. coli*, *Streptomyces*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, fungal cells, such as yeast,

insect cells such as *Drosophila* S2 and *Spodoptera* Sf9, animal cells such as CHO, COS or Bowes melanoma, and adenoviruses. The selection of an appropriate host is within the abilities of those skilled in the art.

[000217] Where appropriate, the engineered host cells can be cultured in conventional
5 nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the genes of the invention. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter may be induced by appropriate means (*e.g.*, temperature shift or chemical induction) and the cells may be cultured for an additional period to allow them to produce the desired polypeptide or
10 fragment thereof.

[000218] Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract is retained for further purification. Microbial cells employed for expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Such
15 methods are well known to those skilled in the art. The expressed polypeptide or fragment thereof can be recovered and purified from recombinant cell cultures by methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin
20 chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the polypeptide. If desired, high performance liquid chromatography (HPLC) can be employed for final purification steps.

[000219] Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines
25 of monkey kidney fibroblasts (described by Gluzman (1981), *Cell* 23:175.), and other cell lines capable of expressing proteins from a compatible vector, such as the C127, 3T3, CHO, HeLa and BHK cell lines.

[000220] The invention also relates to variants of the polypeptides of the Group B amino acid sequences, sequences substantially identical thereto, or fragments comprising at least 5,
30 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof. In particular, the variants may differ in amino acid sequence from the polypeptides of the Group B amino acid sequences, and sequences substantially identical thereto, by one or more substitutions, additions, deletions, fusions and truncations, which may be present in any combination.

[000221] The variants may be naturally occurring or created *in vitro*. In particular, such variants may be created using genetic engineering techniques such as site directed mutagenesis, random chemical mutagenesis, Exonuclease III deletion procedures, and standard cloning techniques. Alternatively, such variants, fragments, analogs, or derivatives may be created using chemical synthesis or modification procedures.

[000222] Other methods of making variants are also familiar to those skilled in the art. These include procedures in which nucleic acid sequences obtained from natural isolates are modified to generate nucleic acids which encode polypeptides having characteristics which enhance their value in industrial or laboratory applications. In such procedures, a large number of variant sequences having one or more nucleotide differences with respect to the sequence obtained from the natural isolate are generated and characterized. Typically, these nucleotide differences result in amino acid changes with respect to the polypeptides encoded by the nucleic acids from the natural isolates.

Error Prone PCR

[000223] For example, variants may be created using error prone PCR. In error prone PCR, PCR is performed under conditions where the copying fidelity of the DNA polymerase is low, such that a high rate of point mutations is obtained along the entire length of the PCR product. Error prone PCR is described in Leung et al. (1989), *Technique* 1:11-15 and Caldwell et al. (1992), *PCR Methods Applic.* 2:28-33, the disclosures of which are incorporated herein by reference in their entirety. Briefly, in such procedures, nucleic acids to be mutagenized are mixed with PCR primers and reagents (e.g., reaction buffer, MgCl₂, MnCl₂, Taq polymerase and an appropriate concentration of dNTPs) for achieving a high rate of point mutation along the entire length of the PCR product. For example, the reaction may be performed using 20 fmoles of nucleic acid to be mutagenized, 30 pmoles of each PCR primer, a reaction buffer comprising 50mM KCl, 10mM Tris HCl (pH 8.3) and 0.01% gelatin, 7mM MgCl₂, 0.5mM MnCl₂, 5 units of Taq polymerase, 0.2mM dGTP, 0.2mM dATP, 1mM dCTP, and 1mM dTTP. PCR may be performed for 30 cycles of 94°C for 1 min, 45°C for 1 min, and 72°C for 1 min. However, it will be appreciated that these parameters may be varied as appropriate. The mutagenized nucleic acids are cloned into an appropriate vector and the activities of the polypeptides encoded by the mutagenized nucleic acids are evaluated.

[000224] Variants also may be created using oligonucleotide directed mutagenesis to generate site-specific mutations in any cloned DNA of interest. Oligonucleotide mutagenesis

is described in Reidhaar-Olson et al. (1988), *Science*, 241:53-57, the disclosure of which is incorporated herein by reference in its entirety. Briefly, in such procedures a plurality of double stranded oligonucleotides bearing one or more mutations to be introduced into the cloned DNA are synthesized and inserted into the cloned DNA to be mutagenized. Clones
5 containing the mutagenized DNA are recovered and the activities of the polypeptides they encode are assessed.

Assembly PCR

[000225] Another method for generating variants is assembly PCR. Assembly PCR involves the assembly of a PCR product from a mixture of small DNA fragments. A large
10 number of different PCR reactions occur in parallel in the same vial, with the products of one reaction priming the products of another reaction. Assembly PCR is described in U.S. Pat. No. 5,965,408, the disclosure of which is incorporated herein by reference in its entirety.

Sexual PCR mutagenesis

[000226] Still another method of generating variants is sexual PCR mutagenesis. In sexual
15 PCR mutagenesis, forced homologous recombination occurs between DNA molecules of different but highly related DNA sequence *in vitro*, as a result of random fragmentation of the DNA molecule based on sequence homology, followed by fixation of the crossover by primer extension in a PCR reaction. Sexual PCR mutagenesis is described in Stemmer (1994), *Proc. Natl. Acad. Sci. USA* 91:10747-10751, the disclosure of which is incorporated herein by
20 reference in its entirety. Briefly, in such procedures a plurality of nucleic acids to be recombined are digested with DNase to generate fragments having an average size of about 50-200 nucleotides. Fragments of the desired average size are purified and resuspended in a PCR mixture. PCR is conducted under conditions which facilitate recombination between the nucleic acid fragments. For example, PCR may be performed by resuspending the
25 purified fragments at a concentration of 10-30 ng/ μ l in a solution of 0.2mM of each dNTP, 2.2mM MgCl₂, 50mM KCl, 10mM Tris HCl, pH 9.0, and 0.1% Triton X-100. 2.5 units of Taq polymerase per 100 μ l of reaction mixture is added and PCR is performed using the following regime: 94°C for 60 seconds, 94°C for 30 seconds, 50-55°C for 30 seconds, 72°C for 30 seconds (30-45 times) and 72°C for 5 minutes. However, it will be appreciated that
30 these parameters may be varied as appropriate. In some aspects, oligonucleotides may be included in the PCR reactions. In other aspects, the Klenow fragment of DNA polymerase I may be used in a first set of PCR reactions and Taq polymerase may be used in a subsequent

set of PCR reactions. Recombinant sequences are isolated and the activities of the polypeptides they encode are assessed.

In vivo Mutagenesis

[000227] Variants may also be created by *in vivo* mutagenesis. In some aspects, random mutations in a sequence of interest are generated by propagating the sequence of interest in a bacterial strain, such as an *E. coli* strain, which carries mutations in one or more of the DNA repair pathways. Such “mutator” strains have a higher random mutation rate than that of a wild-type parent. Propagating the DNA in one of these strains will eventually generate random mutations within the DNA. Mutator strains suitable for use for *in vivo* mutagenesis are described in PCT Publication No. WO 91/16427 the disclosure of which is incorporated herein by reference in its entirety.

Cassette Mutagenesis

[000228] Variants may also be generated using cassette mutagenesis. In cassette mutagenesis a small region of a double stranded DNA molecule is replaced with a synthetic oligonucleotide “cassette” that differs from the native sequence. The oligonucleotide often contains completely and/or partially randomized native sequence.

Recursive Ensemble Mutagenesis

[000229] Recursive ensemble mutagenesis may also be used to generate variants. Recursive ensemble mutagenesis is an algorithm for protein engineering (protein mutagenesis) developed to produce diverse populations of phenotypically related mutants whose members differ in amino acid sequence. This method uses a feedback mechanism to control successive rounds of combinatorial cassette mutagenesis. Recursive ensemble mutagenesis is described in Arkin et al. (1992), *Proc. Natl. Acad. Sci. USA*, 89:7811-7815, the disclosure of which is incorporated herein by reference in its entirety.

Exponential Ensemble Mutagenesis

[000230] In some aspects, variants are created using exponential ensemble mutagenesis. Exponential ensemble mutagenesis is a process for generating combinatorial libraries with a high percentage of unique and functional mutants, wherein small groups of residues are randomized in parallel to identify, at each altered position, amino acids which lead to functional proteins. Exponential ensemble mutagenesis is described in Delegrave et al. (1993), *Biotechnology Research* 11:1548-1552, the disclosure of which incorporated herein by reference in its entirety.

Random and site-directed mutagenesis

[000231] Random and site-directed mutagenesis is described in Arnold (1993), *Current Opinions in Biotechnology* 4:450-455, the disclosure of which is incorporated herein by reference in its entirety.

5 Shuffling Procedures

[000232] In some aspects, the variants are created using shuffling procedures wherein portions of a plurality of nucleic acids which encode distinct polypeptides are fused together to create chimeric nucleic acid sequences which encode chimeric polypeptides as described in U.S. Patent. Nos. 5,965,408 and 5,939,250, each of which is hereby incorporated by reference
10 in their entirety.

[000233] The variants of the polypeptides of the Group B amino acid sequences may be variants in which one or more of the amino acid residues of the polypeptides of the Group B amino acid sequences are substituted with a conserved or non-conserved amino acid residue (e.g, a conserved amino acid residue) and such substituted amino acid residue may or may
15 not be one encoded by the genetic code.

[000234] Conservative substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. Typically seen as conservative substitutions are the following replacements: replacements of an aliphatic amino acid such as Alanine, Valine, Leucine and Isoleucine with another aliphatic amino acid; replacement of a
20 Serine with a Threonine or vice versa; replacement of an acidic residue such as Aspartic acid and Glutamic acid with another acidic residue; replacement of a residue bearing an amide group, such as Asparagine and Glutamine, with another residue bearing an amide group; exchange of a basic residue such as Lysine and Arginine with another basic residue; and replacement of an aromatic residue such as Phenylalanine, Tyrosine with another aromatic
25 residue.

[000235] Other variants are those in which one or more of the amino acid residues of the polypeptides of the Group B amino acid sequences includes a substituent group.

[000236] Still other variants are those in which the polypeptide is associated with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol).
30

[000237] Additional variants are those in which additional amino acids are fused to the polypeptide, such as a leader sequence, a secretory sequence, a proprotein sequence or a sequence which facilitates purification, enrichment, or stabilization of the polypeptide.

[000238] In some aspects, the fragments, derivatives and analogs retain the same biological function or activity as the polypeptides of the Group B amino acid sequences, and sequences substantially identical thereto. In other aspects, the fragment, derivative, or analog includes a proprotein, such that the fragment, derivative, or analog can be activated by cleavage of the proprotein portion to produce an active polypeptide.

[000239] Another aspect of the invention is polypeptides or fragments thereof which have at least about 85%, at least about 90%, at least about 95%, or more than about 95% homology to one of the polypeptides of the Group B amino acid sequences, sequences substantially identical thereto, or a fragment comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof. Percent identity may be determined using any of the programs described above which aligns the polypeptides or fragments being compared and determines the extent of amino acid homology or similarity between them. It will be appreciated that amino acid "homology" includes conservative amino acid substitutions such as those described above. In one aspect of the invention, the fragments can be used to generate antibodies. These antibodies can be used to immobilize nitrilases can be used in industrial processes. Polynucleotides encoding the nitrilases of the present invention can be used in a similar way.

[000240] Alternatively, the homologous polypeptides or fragments may be obtained through biochemical enrichment or purification procedures. The sequence of potentially homologous polypeptides or fragments may be determined by proteolytic digestion, gel electrophoresis and/or microsequencing. The sequence of the prospective homologous polypeptide or fragment can be compared to one of the polypeptides of the Group B amino acid sequences, sequences substantially identical thereto, or a fragment comprising at least about 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof using any of the programs described herein.

[000241] Another aspect of the invention is an assay for identifying fragments or variants of the Group B amino acid sequences, or sequences substantially identical thereto, which retain the enzymatic function of the polypeptides of the Group B amino acid sequences, and sequences substantially identical thereto. For example, the fragments or variants of the polypeptides, may be used to catalyze biochemical reactions, which indicate that said fragment or variant retains the enzymatic activity of the polypeptides in Group B amino acid sequences.

[000242] The assay for determining if fragments of variants retain the enzymatic activity of the polypeptides of the Group B amino acid sequences, and sequences substantially identical thereto includes the steps of: contacting the polypeptide fragment or variant with a substrate molecule under conditions which allow the polypeptide fragment or variant to function, and
5 detecting either a decrease in the level of substrate or an increase in the level of the specific reaction product of the reaction between the polypeptide and substrate.

[000243] The polypeptides of the Group B amino acid sequences, sequences substantially identical thereto or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof may be used in a variety of applications. For example,
10 the polypeptides or fragments thereof may be used to catalyze biochemical reactions. In accordance with one aspect of the invention, there is provided a process for utilizing a polypeptide of the Group B amino acid sequences, and sequences substantially identical thereto or polynucleotides encoding such polypeptides for hydrolyzing aminonitriles. In such procedures, a substance containing a haloalkane compound is contacted with one of the
15 polypeptides of the Group B amino acid sequences, and sequences substantially identical thereto under conditions which facilitate the hydrolysis of the compound.

[000244] Antibodies - The polypeptides of Group B amino acid sequences, sequences substantially identical thereto or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof, may also be used to generate antibodies
20 which bind specifically to the enzyme polypeptides or fragments. The resulting antibodies may be used in immunoaffinity chromatography procedures to isolate or purify the polypeptide or to determine whether the polypeptide is present in a biological sample. In such procedures, a protein preparation, such as an extract, or a biological sample is contacted with an antibody capable of specifically binding to one of the polypeptides of the Group B
25 amino acid sequences, sequences substantially identical thereto, or fragments of the foregoing sequences.

[000245] In immunoaffinity procedures, the antibody is attached to a solid support, such as a bead or column matrix. The protein preparation is placed in contact with the antibody under conditions under which the antibody specifically binds to one of the polypeptides of the
30 Group B amino acid sequences, sequences substantially identical thereto, or fragments thereof. After a wash to remove non-specifically bound proteins, the specifically bound polypeptides are eluted.

[000246] The ability of proteins in a biological sample to bind to the antibody may be determined using any of a variety of procedures familiar to those skilled in the art. For example, binding may be determined by labeling the antibody with a detectable label such as a fluorescent agent, an enzymatic label, or a radioisotope. Alternatively, binding of the antibody to the sample may be detected using a secondary antibody having such a detectable label thereon. Particular assays include ELISA assays, sandwich assays, radioimmunoassays, and Western Blots.

[000247] The antibodies of the invention can be attached to solid supports and used to immobilize nitrilases of the present invention. Such immobilized nitrilases can be used, as described above, in industrial chemical processes for the conversion of nitriles to a wide range of useful products and intermediates.

[000248] Polyclonal antibodies generated against the polypeptides of the Group B amino acid sequences, and sequences substantially identical thereto, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof can be obtained by direct injection of the polypeptides into an animal or by administering the polypeptides to an animal. The antibody so obtained will then bind the polypeptide itself. In this manner, even a sequence encoding only a fragment of the polypeptide can be used to generate antibodies which may bind to the whole native polypeptide. Such antibodies can then be used to isolate the polypeptide from cells expressing that polypeptide.

[000249] For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler and Milstein (1975), *Nature*, 256:495-497, the disclosure of which is incorporated herein by reference), the trioma technique, the human B-cell hybridoma technique (Kozbor et al. (1983), *Immunology Today* 4:72, the disclosure of which is incorporated herein by reference), and the EBV-hybridoma technique (Cole et al. (1985), in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96, the disclosure of which is incorporated herein by reference in its entirety).

[000250] Techniques described for the production of single chain antibodies (U.S. Pat. No. 4,946,778, the disclosure of which is incorporated herein by reference in its entirety) can be adapted to produce single chain antibodies to the polypeptides of, for example, the Group B amino acid sequences, or fragments thereof. Alternatively, transgenic mice may be used to express humanized antibodies to these polypeptides or fragments.

[000251] Antibodies generated against a polypeptide of the Group B amino acid sequences, sequences substantially identical thereto, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof may be used in screening for similar polypeptides from other organisms and samples. In such techniques, polypeptides from the organism are contacted with the antibody and those polypeptides which specifically bind to the antibody are detected. Any of the procedures described above may be used to detect antibody binding. One such screening assay is described in "Methods for Measuring Cellulase Activities", *Methods in Enzymology*, 160:87-116, which is hereby incorporated by reference in its entirety.

10 Use of Whole Cells Comprising A Nucleic Acid

[000252] The invention provides for the use of whole cells which have been transformed with nucleic acid (or an active fragment thereof) encoding one or more of the nitrilases of the invention. The invention also provides for the use of such a whole cell in performing a nitrilase reaction on a substrate. Therefore, this invention provides for methods of hydrolyzing a cyanohydrin or aminonitrile linkage using a whole cell comprising at least one nucleic acid or polypeptide disclosed herein (SEQ ID NOS:1-386). For example, a whole cell which is stably transfected (the invention also encompasses transiently transfected or transformed whole cells) with a nucleic acid encoding a nitrilase is one aspect of the invention. Such a cell is useful as a reagent in a reaction mixture to act on a substrate and exhibit nitrilase activity.

Sequence Analysis Software

[000253] Percent identity or homology between two or more sequences is typically measured using sequence analysis software (e.g., Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, Madison, WI). Such software matches similar sequences by assigning a percent identity or homology to various deletions, substitutions and other modifications. The term "percent identity," in the context of two or more nucleic acids or polypeptide sequences, refers to the percentage of nucleotides or amino acid residues that are the same when compared after being aligned for maximum correspondence over a designated region or comparison "window." Under some algorithms, a conservative amino acid substitution can be considered "identical" and a change at a wobble site of a codon can be considered "identical."

[000254] "Alignment" refers to the process of lining up two or more sequences to achieve maximal correspondence for the purpose of assessing the degree of identity or homology, as defined within the context of the relevant alignment algorithm.

[000255] For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated for a particular algorithm. Default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent identity or homology for the test sequences relative to the reference sequence, based on the program parameters.

[000256] A "comparison window", as used herein, is a segment of the contiguous positions in a nucleic acid or an amino acid sequence consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 nucleotides or residues, which may be compared to a reference sequence of the same or different number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith and Waterman (1981), *Adv. Appl. Math.* 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970), *J. Mol. Biol.* 48:443, by the search for similarity method of Pearson and Lipman (1988), *Proc. Natl. Acad. Sci. USA* 85:2444-2448, by computerized implementations of these algorithms, or by manual alignment and visual inspection. Other algorithms for determining homology or identity include, for example, the BLAST program (Basic Local Alignment Search Tool, National Center for Biological Information), BESTFIT, FASTA, and TFASTA (Wisconsin Genetics Software Package, Genetics Computer Group, Madison, WI), ALIGN, AMAS (Analysis of Multiply Aligned Sequences), AMPS (Alignment of Multiple Protein Sequence), ASSET (Aligned Segment Statistical Evaluation Tool), BANDS, BESTSCOR, BIOSCAN (Biological Sequence Comparative Analysis Node), BLIMPS (BLOCKS IMPROVED Searcher), Intervals and Points, BMB, CLUSTAL V, CLUSTAL W, CONSENSUS, LCONSENSUS, WCONSENSUS, Smith-Waterman algorithm, DARWIN, Las Vegas algorithm, FNAT (Forced Nucleotide Alignment Tool), Framealign, Framesearch, DYNAMIC, FILTER, FSAP (Fristensky Sequence Analysis Package), GAP (Global Alignment Program), GENAL, GIBBS, GenQuest, ISSC (Sensitive Sequence Comparison), LALIGN (Local Sequence

Alignment), LCP (Local Content Program), MACAW (Multiple Alignment Construction and Analysis Workbench), MAP (Multiple Alignment Program), MBLKP, MBLKN, PIMA (Pattern-Induced Multi-sequence Alignment), SAGA (Sequence Alignment by Genetic Algorithm) and WHAT-IF. Such alignment programs can also be used to screen genome

5 databases to identify polynucleotide sequences having substantially identical sequences. A number of genome databases are available, for example, a substantial portion of the human genome is available as part of the Human Genome Sequencing Project (J. Roach, http://weber.u.washington.edu/~roach/human_genome_progress2.html) (Gibbs, 1995). At least twenty-one other genomes have already been sequenced, including, for example, *M.*

10 *genitalium* (Fraser et al., 1995), *M. jannaschii* (Bult et al., 1996), *H. influenzae* (Fleischmann et al., 1995), *E. coli* (Blattner et al., 1997), and yeast (*S. cerevisiae*) (Mewes et al., 1997), and *D. melanogaster* (Adams et al., 2000). Significant progress has also been made in sequencing the genomes of model organism, such as mouse, *C. elegans*, and *Arabidopsis sp.* Several databases containing genomic information annotated with some functional

15 information are maintained by different organizations, and are accessible via the internet, for example, <http://www.tigr.org/tdb>; <http://www.genetics.wisc.edu>; <http://genome-www.stanford.edu/~ball>; <http://hiv-web.lanl.gov>; <http://www.ncbi.nlm.nih.gov>; <http://www.ebi.ac.uk>; <http://Pasteur.fr/other/biology>; and <http://www.genome.wi.mit.edu>.

[000257] Examples of useful algorithms are the BLAST and the BLAST 2.0 algorithms,

20 which are described in Altschul et al. (1977), *Nuc. Acids Res.* 25:3389-3402, and Altschul et al. (1990), *J. Mol. Biol.* 215:403-410, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which

25 either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased.

30 Cumulative scores are calculated using the parameter M (reward score for a pair of matching residues; always >0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the

cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. For nucleotide sequences, the BLASTN program uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989), *Proc. Natl. Acad. Sci. USA* 89:10915).

[000258] The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993), *Proc. Natl. Acad. Sci. USA* 90:5873). One measure of similarity provided by BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a references sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, less than about 0.01, or less than about 0.001.

[000259] In one aspect, protein and nucleic acid sequence homologies are evaluated using the Basic Local Alignment Search Tool ("BLAST"). In particular, five specific BLAST programs are used to perform the following task:

- (1) BLASTP and BLAST3 compare an amino acid query sequence against a protein sequence database;
- (2) BLASTN compares a nucleotide query sequence against a nucleotide sequence database;
- (3) BLASTX compares the six-frame conceptual translation products of a query nucleotide sequence (both strands) against a protein sequence database;
- (4) TBLASTN compares a query protein sequence against a nucleotide sequence database translated in all six reading frames (both strands); and
- (5) TBLASTX compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

[000260] The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which may be obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are identified (*i.e.*, aligned) by

means of a scoring matrix, many of which are known in the art. In one example, the scoring matrix used is the BLOSUM62 matrix (Gonnet et al. (1992), *Science* 256:1443-1445; Henikoff and Henikoff (1993), *Proteins* 17:49-61). In another example, the PAM or PAM250 matrices may also be used (see, e.g., Schwartz and Dayhoff, eds. (1978), *Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure*, Washington: National Biomedical Research Foundation). BLAST programs are accessible through the U.S. National Library of Medicine, e.g., at www.ncbi.nlm.nih.gov.

[000261] The parameters used with the above algorithms may be adapted depending on the sequence length and degree of homology studied. In some aspects, the parameters may be

the default parameters used by the algorithms in the absence of instructions from the user.

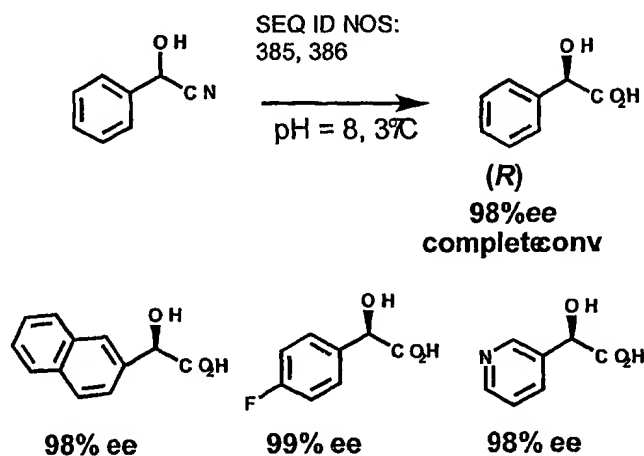
[000262] In a particular aspect, the invention provides a method for modifying small molecules, comprising contacting a polypeptide encoded by a polynucleotide described herein or enzymatically active fragments thereof with a small molecule to produce a modified small molecule. A library of modified small molecules is tested to determine if a modified small molecule is present within the library which exhibits a desired activity. A specific biocatalytic reaction which produces the modified small molecule of desired activity is identified by systematically eliminating each of the biocatalytic reactions used to produce a portion of the library, and then testing the small molecules produced in the portion of the library for the presence or absence of the modified small molecule with the desired activity.

The specific biocatalytic reactions, which produce the modified small molecule of, desired activity is optionally repeated. The biocatalytic reactions are conducted with a group of biocatalysts that react with distinct structural moieties found within the structure of a small molecule, each biocatalyst is specific for one structural moiety or a group of related structural moieties; and each biocatalyst reacts with many different small molecules which contain the distinct structural moiety.

[000263] Some aspects of the use of the nitrilases are:

α -hydroxy acid - Nitrilases produce α -hydroxy acids through hydrolysis of cyanohydrins. Production of mandelic acid and derivatives thereof is an example of this. A significant application of this type involves commercial production of (*R*)-mandelic acid in both high yield and high enantioselectivity from mandelonitrile. Mandelic acid and derivatives have found broad application as intermediates and resolving agents for the production of many chiral pharmaceutical and agricultural products. Previous attempts to

employ the few known nitrilases in processes using analogous substrates have been plagued by significantly lower activity, productivity, and selectivity.

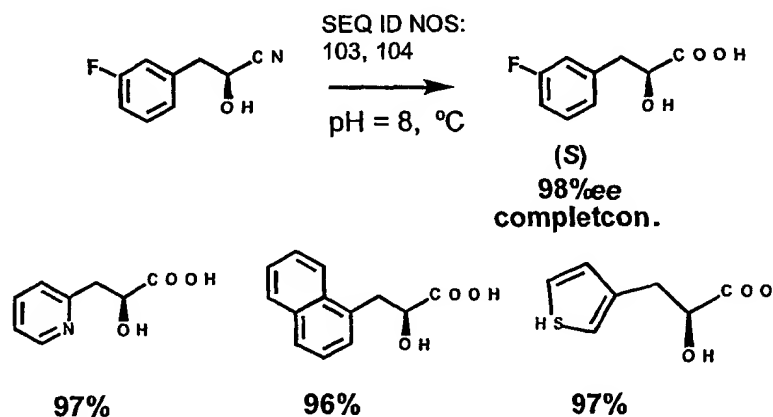


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Phenylactic acid derivatives

[000264] An additional application is in the production of (*S*)-phenyl lactic acid derivatives in both high yield and high enantioselectivity. Phenyl lactic acid derivatives have found broad application in the production of many chiral pharmaceutical and agricultural products.

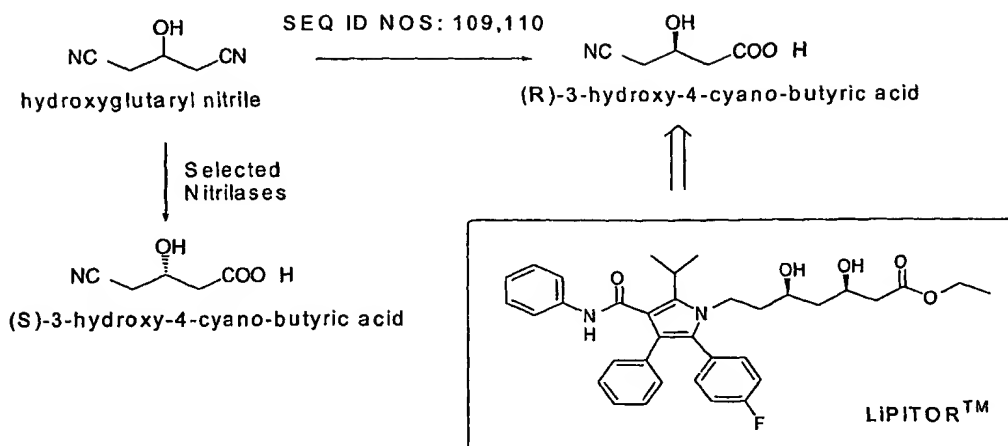
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β-hydroxy acid

[000265] With important commercial considerations, nitrilases are provided produce either enantiomer of 4-cyano-3-hydroxybutyric acid, the (*R*)-enantiomer of which is a key intermediate in the synthesis of the drug LIPITOR™.

15



[000266] The following nitrilases are more examples of nitrilases useful in converting hydroxyglutaryl nitrile to (R)-3-hydroxy-4-cyano-butyric acid: SEQ ID NOS:205, 206, SEQ ID NOS:207, 208, SEQ ID NOS:195, 196, SEQ ID NOS:43, 44, SEQ ID NOS:321, 322, and SEQ ID NOS:237, 238. The above schematic indicates that "selected nitrilases" can be used to convert hydroxyglutaryl nitrile to (S)-3-hydroxy-4-cyano-butyric acid: SEQ ID NOS:107, 108, SEQ ID NOS:109, 110, SEQ ID NOS:111, 112, SEQ ID NOS:127, 128, SEQ ID NOS:129, 130, SEQ ID NOS:133, 134, SEQ ID NOS:113, 114, SEQ ID NOS:145, 146, SEQ ID NOS:101, 102, SEQ ID NOS:179, 180, SEQ ID NOS:201, 202, SEQ ID NOS:159, 160, SEQ ID NOS:177, 178, SEQ ID NOS:181, 182, SEQ ID NOS:183, 184, SEQ ID NOS:185, 186, SEQ ID NOS:57, 58, SEQ ID NOS:197, 198, SEQ ID NOS:59, 60, SEQ ID NOS:67, 68, and SEQ ID NOS:359, 360.

[000267] The invention will be further described with reference to the following examples; however, it is to be understood that the invention is not limited to such examples. Rather, in view of the present disclosure which describes the current best mode for practicing the invention, many modifications and variations would present themselves to those of skill in the art without departing from the scope and spirit of this invention. All changes, modifications, and variations coming within the meaning and range of equivalency of the claims are to be considered within their scope.

EXAMPLES

Example 1: Phagemid infections

[000268] For each library to be screened for nitrilases, an infection was set up as follows: 5ml of an OD_{600nm}=1 resuspension of SEL700 cells and 1ml of the phagemid library to be screened were combined. The combination was incubated in a 37°C waterbath for 45 min.

- 5 [000269] Using the infection, serial dilutions were made in 10mM MgSO₄, using 10μl aliquots of the infection.

	<u>titer of library</u>	<u>dilutions to make</u>
	~10 ⁵ cfu/ml	10 ⁻¹ dilution
	~10 ⁶ cfu/ml	10 ⁻¹ , 10 ⁻² dilution
10	~10 ⁷ cfu/ml	10 ⁻¹ , 10 ⁻² , 10 ⁻³ dilution

[000270] 60μl of each of the following dilutions were deposited onto a small LB-kan⁵⁰ plate:

	<u>titer of library</u>	<u>dilutions to make</u>
	~10 ⁵ cfu/ml	undiluted infection, 10 ⁻¹ dilution
	~10 ⁶ cfu/ml	10 ⁻¹ , 10 ⁻² dilutions
15	~10 ⁷ cfu/ml	10 ⁻² , 10 ⁻³ dilutions

- [000271] The cells in the infection were centrifuged in a tabletop centrifuge at 4°C, 4.6k rpm, 10 min to form pellets. The supernatant was decanted from the resulting pellets. The cells were resuspended in residual liquid. All of the resuspended cells were deposited onto a single large LB-kan⁵⁰ plate. All plates were incubated at 30°C overnight.

Example 2: Selection Screenings

- [000272] The cells of each infection plate were resuspended with ~4mls 10mM MgSO₄.
 25 The resuspensions were placed in a tube. The remaining cells on each plate were resuspended with ~3mls 10mM MgSO₄ and combined with the first resuspension from the same plate. The volume of each tube was brought to 12ml with 10mM MgSO₄. The tubes were vortexed vigorously. The tubes were centrifuged in a tabletop centrifuge at 4°C and 4.6k for 10min to form pellets. The supernatant was decanted from each resuspension. The
 30 washed cells in each tube were resuspended with 10ml 10mM MgSO₄. The resuspensions from each library were stored at 4°C until the selection cultures were ready to be set up.

[000273] For each resuspension, selection cultures were set up using the following process:

- 1) The nitrilase selection medium was prepared, using: 1XM9 medium with 0.2% glucose, no nitrogen and 50µg/ml kanamycin (for pBK phagemid libraries only; use ampicillin for pBS libraries).
- 2) 5ml of the medium was aliquoted into a 50ml screw top conical tube.
- 5 3) 25µl of the stored resuspension was added to the tube.
- 4) 5µl of adiponitrile was added to the tube, to bring the final concentration to 8.8mM. Additional nitrile substrates may be used, in place of adiponitrile.
- 5) The resulting combination was cultured at 30°C.

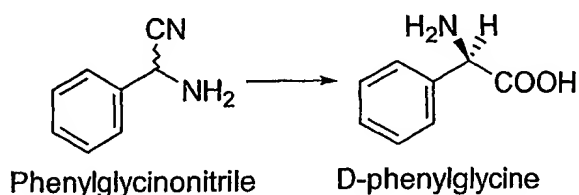
10 Steps 1-5 were repeated for each nitrile substrate.

Example 3: Isolation of a positive nitrilase clone from selection cultures

[000274] Ten (10) µl of selection culture with growth was streaked out onto a small LB-kan⁵⁰ plate and allowed to grow for 2 nights at 30°C. Five isolated cfu were picked and each was grown in 2ml nitrilase selection medium at 30°C. Each culture was monitored (where
15 growth indicates positive cfu was picked), and was removed when monitoring indicated that it was in a stationary phase of growth. One (1) ml of culture was used to do a plasmid preparation and was eluted with 40µl elution buffer. Five to eight (5-8) µl DNA was cut with Pst I/Xho I or Sac I/Kpn I restriction enzymes to remove insert from vector. A restriction
fragment length polymorphism (RFLP) determination was carried out to identify the size of
20 the insert. The insert was sequenced.

Example 4: Screening and Characterization of Nitrilases

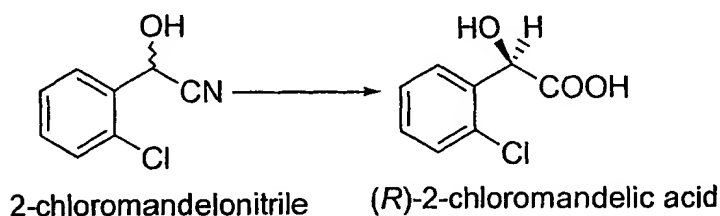
[000275] Nitrilases of the invention were screened against target substrates. Of those showing hydrolytic activity in a primary screen, enzymes with enantioselectivities above 20% enantiomeric excess (*ee*) were selected for further characterization. Those enzymes were
25 selected based on: 1) having activity against one of the substrates of interest and 2) exhibition of greater than 35% *ee* (enantiomeric excess). The results of this screening process are set forth in Table 1 above. The products used for screening were: D-Phenylglycine, L-Phenyllactic acid, (*R*) 2-chloromandelic acid, (*S*)- Cyclohexylmandelic acid, L-2-methylphenylglycine, (*S*)-2-amino-6-hydroxy hexanoic acid, and 4-methyl-L-
30 leucine.

Screening of nitrilases against target substrate D-Phenylglycine

5 [000276] The hydrolysis of phenylglycinonitrile was performed. Some of these enzymes showed an *ee* higher than 20% and those were selected for preliminary characterization.

[000277] Based on the preliminary characterization experiments, a number of putative hits were identified on phenylglycinonitrile and a large amount of data was accumulated on these enzymes. The data revealed many common properties: the majority of the enzymes had pH optima for activity at pH 7 and, in general, the enantioselectivity was enhanced at the lower pH values. The enzymes were found to be more active at higher temperature, particularly 10 38°C, although this temperature often resulted in lower enantioselectivities. The use of water-miscible co-solvents in the reaction was shown to be a practical option. The inclusion of 10-25% methanol (v/v) in the enzyme reactions did not substantially affect enzyme activity and in many cases, led to an increase in enantioselectivity. The use of biphasic 15 systems has also shown some promise, with the enzymes maintaining their level of activity with the addition of up to 70% (v/v) of hexane and, in some cases, toluene. The use of ethyl acetate in the biphasic systems, however, led to lower activity.

[000278] Of the enzymes identified active on phenylglycinonitrile, the enantioselectivity of several enzymes was shown to remain above the success criterion of 35% *ee*. The 20 preliminary characterization data indicated that some of the enzymes exhibited high enantioselectivities for D-phenylglycine, with corresponding conversion to product of 40-60%. Further investigation suggested that the rate of activity of some of these enzymes was faster than the rate of racemization of the substrate. Reducing the concentration of enzyme led to improved enantioselectivity; therefore, it appears that some benefit could be gained by 25 control of the relative rates of the chemical racemization and the enzyme activity.

Screening of nitrilases against target substrate (*R*)-2-chloromandelic acid

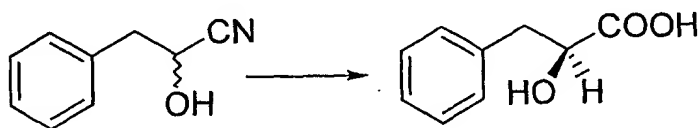
[000279] Enzymes were identified which showed activity on 2-chloromandelonitrile. A high degree of overlap existed between the enzymes which were active on 2-chloromandelonitrile and phenylglycinonitrile. Many of these enzymes also formed a distinct sequence family.

[000280] Higher temperatures and neutral pH appeared to lead to the highest activity for the active enzymes. For the majority of the nitrilases, the enantioselectivity also increased at higher temperatures, particularly 38°C. The enzymes retained their activity in the presence of up to 25% methanol or 10% isopropanol; in many of these cases, the enantioselectivity was also enhanced. Activity in biphasic systems was largely comparable to aqueous conditions, particularly with hexane as the non-aqueous phase; varying tolerances to toluene were observed between the different nitrilases.

Table 2. Summary of optimal conditions determined from characterization experiments for enantioselective hydrolysis of 2-chloromandelonitrile.

SEQ ID NOS:	Optimum pH	Optimum Temp °C	Solvent Tolerance
385, 386	7	38	25% MeOH
169, 170	5	38	25% MeOH, 10% IPA
185, 186	7	38	25% MeOH, 10% IPA
47, 48	7	38	10% MeOH
197, 198	6	55	25% MeOH, 10% IPA
187, 188	7	38	10% MeOH; 40% IPA
217, 218	7	38	25% MeOH, 10% IPA, 70% hexane, 40% toluene
55, 56	7	38	10% MeOH, IPA, 70% hexane
167, 168	9	38	10% MeOH, IPA, 70% hexane
15, 16	7	38	25% MeOH, 10% IPA, 70% hexane, 40% toluene

Screening of nitrilases against target substrate (S)-phenyllactic acid:



Phenylacetaldehyde
cyanohydrin

(S)-Phenyllactic acid

5

[000281] Many of the nitrilases tested were active on phenylacetaldehyde cyanohydrin. Many of these enzymes were part of two related sequence families and were distinct from those enzymes that were active on phenylglycinonitrile and chloromandelonitrile.

10 [000282] The pH optima of the enzymes was generally above pH 7 (*i.e.* pH 8 or 9), with higher enantioselectivities being exhibited at these levels. Most of the enzymes showed superior activity at higher temperature, particularly 38°C. The effect of temperature on the enantioselectivities of the enzymes varied; in most cases, this property was slightly lower at

higher temperatures. While the enzymes were tolerant towards the addition of co-solvents, particularly 10% (v/v) methanol, no advantage in activity or enantioselectivity was gained by such additions. The use of a biphasic system was again shown to be feasible.

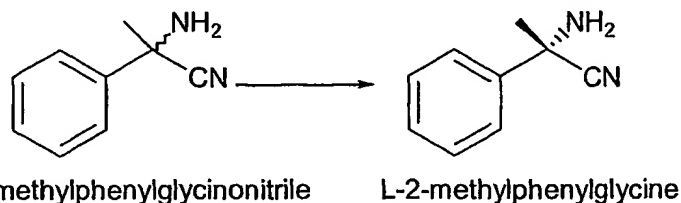
[000283] Table 3. Summary of optimal conditions determined from characterization

5 experiments for enantioselective hydrolysis of phenylacetaldehyde cyanohydrin

SEQ ID NOS:	Optimum pH	Optimum Temp °C	Solvent Tolerance
103, 104	7	55	10% MeOH, IPA
99, 100	8	38	10% MeOH, 70% hexane, toluene
183, 184	9	38	10% MeOH, IPA, 70% toluene, hexane
173, 174	5	38-55	25% MeOH, IPA, 70% hexane, toluene
213, 214	7	38	10% MeOH, 25% IPA, 70% hexane, toluene
61, 62	7	38	10% MeOH, 70% hexane, toluene
205, 206	8	38-55	10% MeOH, IPA, 40% hexane, toluene
207, 208	8	38	10% MeOH, 70% hexane
309, 210	8	38	10% MeOH, 40% hexane, toluene
195, 196	8	38	10% MeOH, 40% hexane, toluene
43, 44	9	38	10% MeOH, 40% hexane
161, 162	9	38	25% MeOH, IPA, 10% hexane, toluene
175, 176	6	38-55	10% MeOH, IPA, 40% hexane

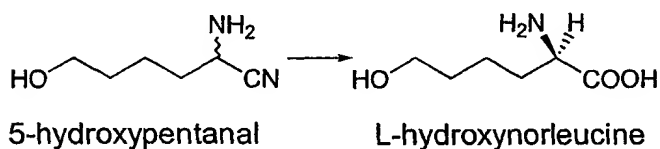
SEQ ID NOS:	Optimum pH	Optimum Temp °C	Solvent Tolerance
293, 294	6	38	10% MeOH, IPA, 40% hexane

Screening of nitrilases against target substrate L-2-methylphenylglycine



[000284] Nitrilases have shown activity on this substrate and preferentially yielded the D-2-methylphenylglycine, rather than the required L-2-methylphenylglycine.

Screening of nitrilases against target substrate L-hydroxynorleucine ((S)-2-amino-6-hydroxy hexanoic acid)



[000285] A number of nitrilases, which showed activity on 2-amino-6-hydroxy hexanenitrile, were isolated. All of these enzymes showed enantioselectivity towards the L-isomer of the product.

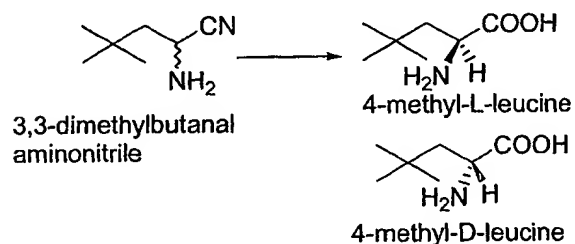
[000286] The enzymes all showed higher enantioselectivities at higher pH and appeared to more susceptible to the addition of solvents than the other nitrilases tested. Although activity was detected in the presence of organic solvents, it was generally lower than that of the aqueous control. Once again, the activity of the enzymes was negatively affected by the acid product and aldehyde starting material.

Table 4. Summary of optimal conditions determined from characterization experiments for enantioselective hydrolysis of 2-amino-6-hydroxy hexanenitrile.

SEQ ID NOS:	Optimum pH	Optimum Temp °C	Solvent
217, 218	9	38	10% MeOH
55, 56	9	38	None
187, 188	9	38	10% MeOH
167, 168	9	38	None
221, 222	9	38	

[000287] A range of hydrolytic activities was observed among the confirmed hit enzymes for 2-amino-6-hydroxy hexanenitrile.

5 Screening of nitrilases against target substrate 4-methyl-D-leucine and 4-methyl-L-leucine

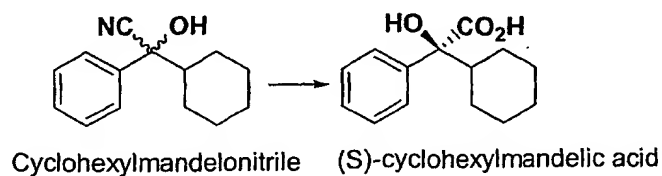


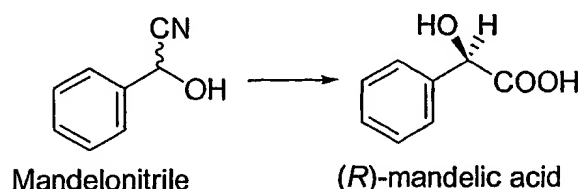
[000288] Hydrolysis of 2-amino-4,4-dimethyl pentanenitrile was performed by several of the nitrilases. Of these, some were shown to hydrolyse the nitrile to the L-isomer of the corresponding acid and were selected for further characterization.

10 Table 5. Summary of optimal conditions determined from characterization experiments for enantioselective hydrolysis of 2-amino-4,4-dimethyl pentanenitrile

SEQ ID NOS:	Optimum pH	Optimum Temp °C	Solvent Tolerance
103, 104	7	23	25% MeOH, 10% IPA
59, 60	8	23	25% MeOH
221, 222	6	38	25% MeOH, 10% IPA

Screening of nitrilases against target substrate (S)-cyclohexylmandelic acid



Screening of nitrilases against target substrate Mandelonitrile

- 5 [000289] The nitrilase collection was also screened on mandelonitrile. The nitrilases actively hydrolyzed both phenylglycinonitrile and chloromandelonitrile.

Enzymatic assay for determination of enantioselectivity

- [000290] In the design of a spectroscopic system for determination of the chiral α -hydroxy acids and α -amino acids, an enzyme based assay which permits the detection of product
10 formation and enantioselectivity was developed and used.

- [000291] Spectroscopic systems for the detection of α -hydroxy- and for α -amino- acids based on lactate dehydrogenase (L-LDH & D-LDH) and on amino acid oxidase (L-AA Oxid & D-AA Oxid) are described in Figures 6 and 7. These enzymes were chosen because they are reported to have reasonably broad substrate ranges while still retaining near absolute
15 enantiospecificity.

- [000292] The overall feasibility of this system has been established (Table 12). Neither the parent hydroxynitrile nor the aminonitrile is metabolized by the secondary or detection enzyme and thus starting material does not interfere. Cell lysate which is not heat treated results in background activity for the LDH system; however, heat inactivation eliminates the
20 background activity. Cell lysate does not appear to interfere in the AA Oxidase assay. One concern is the inactivation of the AA Oxidase, which utilizes a FMN co-factor, by residual cyanide. However, the control studies indicated that at 2 mM PGN (which could release up to 2 mM HCN) inactivation is not a problem. This assay is suitable for automation of 384 well (or possibly greater density) microtiter plates.

- 25 Table 6: Summary of Identification of Secondary Enzyme to Chiral Detection of Acid Product.

SUBSTRATE	ENZYME WITH SUITABLE ACTIVITY FOUND FROM COMMERCIAL SOURCE
Hydroxy Acid Products:	
L-lactic acid	YES
D-lactic acid	YES
L-phenyl lactic acid	YES
D-phenyl lactic acid	YES
S-cyclohexylmandelic acid ¹	<i>Not applicable</i>
R-cyclohexylmandelic acid ¹	<i>Not applicable</i>
Amino Acid Products:	
4-methyl-L-leucine	YES
4-methyl-L/D-leucine	YES (D-unknown)
D-phenylalanine	YES
R-phenylglycine	YES
L-homophenyllactic acid	YES
D-homophenyllactic acid	YES
L-homophenylalanine	YES
D-homophenylalanine	YES
(S)-2-amino-6-hydroxy hexanoic acid	YES
(R/S)-2-amino-6-hydroxy hexanoic acid	YES (D-unknown)
L-methylphenylglycine ¹	1. <i>Not Applicable</i>
D-methylphenylglycine ¹	<i>Not Applicable</i>

¹: The assay will not be applicable to cyclohexylmandelic acid and 2-methylphenylglycine, as tertiary alcohols are not amenable to this particular oxidation

5 Example 5: Standard assay conditions

[000293] The following solutions were prepared:

- Substrate stock solution: 50 mM of the aminonitrile substrate in 0.1 M phosphate buffer (pH 7) or 50 mM of the cyanohydrin substrate in 0.1 M Na Acetate buffer (pH 5)
- Enzyme stock solution: 3.33 ml of 0.1 M phosphate buffer (pH 7) to each vial of 20 mg of lyophilized cell lysate (final concentration 6 mg protein/ml)

[000294] Procedure:

- Add 100 µl of the 50 mM substrate solution to the appropriate number of wells of a 96-well plate
- Add 80 µl of buffer to each well
- Add 20 µl of enzyme solution to each well
- Blank controls were set up by substitution of 20 µl of buffer for the enzyme solution

• Negative controls consisting of 20 µl of enzyme solution in 180 µl of buffer were also included in many of the experiments. Once it had been established that the cell lysate did not interfere with the detection of the products, these controls were not included.

[000295] Sampling of reactions:

5 • The reactions were sampled by removing an aliquot from each well (15-50 µl) and diluting the samples as follows:

• Samples for non-chiral HPLC analysis:

• Phenylglycine, 2-chloromandelic acid and phenyllactic acid: initially, the samples were diluted 2-fold with water and a further 2-fold with methanol or acetonitrile (final
10 dilution: 4-fold). It was found that an 8-fold dilution of these samples led to improved chromatographic separation

• (S)-2-amino-6-hydroxy hexanoic acid, 4-methylleucine, *t*-leucine, 2-methylphenylglycine and cyclohexylmandelic acid: samples were diluted 1:1 with methanol or acetonitrile. The choice of solvent was based on the solvent used in the HPLC analysis
15 method.

[000296] • Samples for chiral HPLC analysis:

• Phenylglycine, 2-chloromandelic acid and phenyllactic acid: as described above for the non-chiral analyses, the samples for chiral analyses were initially diluted 2-fold and in the later stages of the project, at 4-fold.

20 • (S)-2-amino-6-hydroxy hexanoic acid, 4-methylleucine, *t*-leucine, 2-methylphenylglycine: samples were diluted 1:1 with methanol or acetonitrile.

[000297] • For each experiment, a standard curve of the product was included in the HPLC run. The curve was plotted on an X-Y axis and the concentration of product in the samples calculated from the slope of these curves.

25 **[000298]** • For the preliminary characterization experiments, samples were taken such that the activity of the enzymes was in the linear phase; this was performed so that differences in the effects of the parameters on the rate of reaction, rather than the complete conversion, could be determined. The sampling times are denoted in the tables included in the text.

[000299] • The samples were analyzed by HPLC, using the methods outlined in Table 20
30 and 21.

Example 6: Determination of the Effect of pH on enzyme activity and enantioselectivity

[000300] The effect of pH on the enzyme activity and enantioselectivity was studied by performance of the standard assay in a range of different buffers:

- 0.1 M Citrate Phosphate pH 5
- 5 0.1 M Citrate Phosphate pH 6
- 0.1 M Sodium Phosphate pH 7
- 0.1 M Tris-HCl pH 8
- M Tris-HCl pH 9

- 10 [000301] The samples were analyzed by non-chiral and chiral HPLC methods and examples of the results are presented in Tables 5, 8 and 11 herein.

Example 7: Determination of the effect of temperature on enzyme activity and enantioselectivity

- 15 [000302] The effect of temperature on the activity and enantioselectivity was investigated by performing the standard assay at room temperature, 38°C and 55°C. The samples were analyzed by non-chiral and chiral HPLC methods and examples of the results are given in Tables 5, 8 and 11 herein.

Example 8: Determination of the Effect of solvents on enzyme activity and enantioselectivity

- 20 [000303] The enzyme reactions were performed in the presence of cosolvents and as biphasic systems, in order to investigate the effect of water-miscible and water-immiscible solvents on the enzymes. In the presence of cosolvents, the reactions were run under standard conditions, with substitution of the buffer with methanol or isopropanol. The final concentrations of solvent in the reactions was 0, 10, 25 and 40% (v/v).
- 25 [000304] The biphasic reactions were also carried out under standard conditions, with a layer of water-immiscible organic solvent forming the nonaqueous phase. The solvent was added at the following levels: 0%, 10%, 40% and 70% (v/v) of the aqueous phase. The samples from these reactions were evaporated by centrifugation under vacuum and redissolved in a 50:50 mixture of methanol or acetonitrile and water. The samples were
- 30 analyzed by non-chiral and chiral HPLC methods.

Example 9: Determination of the Effect of process components on enzyme activity and enantioselectivity

Activity

[000305] The effect of the process components on the activity of the enzymes was established by addition of the individual components to the enzymatic reaction. These components included the starting materials for the nitrile synthesis, aldehyde, cyanide and ammonium, as well as triethylamine, which is added in catalytic amounts to the nitrile synthesis reaction. The concentrations of the reactants were selected with possible process conditions in mind and were adapted to the levels of reactants used in the enzyme assays. In some cases, the solubility of the aldehydes and products was relatively low; in these cases, the highest level of solubility was added to the reactions as the highest level and 10% of this level as the lower value.

[000306] The enzymatic reactions were carried out under standard conditions, with addition of one or more of the following components: benzaldehyde, phenylglycine, phenylacetaldehyde, phenyllactic acid, 2-chlorobenzaldehyde, 2-chloromandelic acid, 5-hydroxypentanal, (S)-2-amino-6-hydroxy hexanoic acid, 4-methyllucine, KCN, Triethylamine, NH_4Cl . Control reactions were performed under standard conditions, with no additive. The samples were analyzed by non-chiral HPLC.

Stability

[000307] The stability of the enzymes to process conditions was monitored by incubation of the enzymes in the presence of the individual reaction components for predetermined time periods, prior to assay of the enzyme activity under standard conditions. In these experiments, the enzymes were incubated at a concentration of 1.2 mg protein/ml in the presence of each of the following reaction components: methanol, benzaldehyde, phenylglycine, phenylacetaldehyde, phenyllactic acid, 2-chlorobenzaldehyde, 2-chloromandelic acid, 5-hydroxypentanal, (S)-2-amino-6-hydroxy hexanoic acid, KCN, NH_4Cl .

Assay conditions:

[000308] At 0, 2, 6 and 24 hours of incubation in the particular additive, 50 μl of the enzyme solution was removed, 50 μl of a 50 mM substrate stock solution added and the enzyme activity assayed under standard conditions. After substrate addition, the reactions were sampled at the following times: Phenylglycine nitrile: 10 mins; Phenylacetaldehyde cyanohydrin: 1 hour; 2-chloromandelonitrile: 2 hours. Control reactions were performed by

incubation of the enzyme in buffer only. The samples were analyzed using non-chiral HPLC methods.

Example 10: Confirmation of putative hit enzymes

[000309] Following the preliminary characterization experiments, the enzymes which were identified as putative hits were assayed under the optimal conditions determined, in order to evaluate their performance, especially in terms of enantioselectivity, when higher conversions were attained. The enzymes were assayed with 25 mM substrate, under the conditions of pH and temperature noted in the tables included in the text. A standard concentration of 0.6 mg/ml protein was used for each of the enzymes, unless otherwise stated.

Example 11: Selected examples of chromatograms from enzyme reactions

[000310] In this section, representative examples of chromatograms for each substrate and product combination will be shown, together with a discussion of some of the challenges encountered with the methods and how they were addressed.

D-Phenylglycine

[000311] Non-chiral analysis showing the substrate peak eluting at 2.6 min and 3.2 min. See Figures 8A-8E. The two peaks were present in all samples containing higher concentrations of the nitrile; the second peak is thought to be a product associated with the nitrile; it decreased with time and was no longer present once complete conversion to the product had taken place. The chromatogram shown in Figure 8A is a blank control, containing only nitrile and buffer; the samples were all diluted with water and solvent as explained in section 1 above. This was repeated for all samples discussed below. An enzymatic reaction sample is shown in the chromatogram in Figure 8B, with the product eluting at 0.4 min.

[000312] Of note in these chromatograms is the small solvent front peak eluting at 0.3 min. Further representation of this peak is given in the chromatogram shown in Figure 8C, in which a negative control consisting of cell lysate in buffer, was run. A very small peak coeluted with the product at 0.4 min. In the initial phase of the project, this peak was regarded as problematic, although the appropriate controls were run with each experiment for in order to maintain accuracy. In these experiments, the peak area resulting from the cell lysate, although it was relatively small, was subtracted from the peak areas of the product in the enzymatic reactions. Improvement of this analysis was obtained by further dilution of the samples and the use of lower injection volumes on the HPLC. Following the implementation

of these improvements, interference by this peak was shown to be minimal, as shown in the chromatogram illustrated in Fig. 6C.

[000313] The chiral analysis of phenylglycine is shown in chromatogram in Fig. 6D with the L-enantiomer eluting at 6 min and the D-enantiomer at 11 min. Good resolution between the two isomers was obtained. However, the column used was very sensitive and the characteristics of the column appeared to change over time, resulting in changes in the elution times of the acids. While this was easily detected by the use of the proper controls and standards, a greater problem existed in the coelution of the nitrile peak with the D-enantiomer (chromatogram shown in Fig. 6E). The cause of this coelution was unclear; however, it was easily detected by the use of appropriate standards; in addition, the UV spectrum of the acid was very distinctive, making the use of this tool effective in detecting the coelution. The problem was also easily resolved by adjusting the methanol content in the mobile phase.

(R)-2-chloromandelic acid

[000314] The HPLC analysis of chloromandelic acid and chloromandelonitrile offered many of the challenges associated with the analysis of the phenylglycine samples. From the chromatogram shown in Fig. 7A, which contains only chloromandelonitrile in buffer, it is evident that a peak eluted at the same time as the product in the chromatogram shown in Fig. 7B, which represents a chloromandelic acid standard. The contribution of the cell lysate to this peak was found to be small; it would appear that the greatest contribution to this peak was from the chloromandelonitrile, either from a breakdown product or a contaminant in the nitrile preparation. The peak area remained constant throughout each experiment and, using the appropriate controls, it was found that subtraction of the peak area from that of the product yielded sufficient accuracy. Many attempts were made to change the HPLC conditions so that the product peak eluted at a later time; however, these attempts were not successful. Chromatogram shown in Fig. 7C illustrates the appearance of product and the reduction of the substrate peaks.

[000315] The chiral analysis of chloromandelic acid was almost problem-free. The elution of a small peak at the same time as the (S)-enantiomer presented some concern (the peak at 2.4 min in chromatogram shown in Fig. 7D). However, once it was established that this peak was present in all the samples at the same level, including the blank control, and that it had a different UV spectrum to that of the chloromandelic acid peak, it was not regarded as a problem. Consequently, it was subtracted from the peak eluting at 2.4 min in each sample. The (R)-enantiomer eluted at 3 minutes.

(S)-phenyllactic acid

[000316] The analysis of phenyllactic acid was initially plagued with the same problems discussed for phenylglycine and 2-chloromandelic acid. However, in this case, adjustment of the solvent concentration in the nonchiral HPLC method led to a shift in the retention time of the acid, so that it no longer coeluted with the cell lysate peak. Following this, no problems were encountered with either the nonchiral or chiral methods. Representative nonchiral chromatograms of the product (1.9 min) and cyanohydrin substrate (3.7 min) are shown in Fig. 8A, while the chiral analysis of the acid is shown in Fig. 8B, with the L-enantiomer eluting at 2 min and the opposite enantiomer at 6 min.

10 L-2-methylphenylglycine

[000317] The analysis of methylphenylglycine was unproblematic, although the nonchiral method did not provide baseline separation between a cell lysate peak and the product peak, as shown in the chromatogram illustrated in Fig. 9A. The amino acid standard for this method was provided in the final stages of the project, thus minimizing the time for method development. In the chromatogram shown in Fig. 9A the amino acid elutes at 0.7 min and the aminonitrile at 5.0 min. Sufficient separation between the two initial peaks was obtained to allow the calculation of approximate conversion to product.

[000318] The chiral analysis of this compound provided good separation between the two enantiomers, as shown in the chromatogram illustrated in Fig. 9B. The L-enantiomer elutes at 5 min and the D-enantiomer at 8 min.

20 L-tert-leucine

[000319] For the nonchiral analysis of *t*-leucine, the cell lysate presented the most serious problem amongst the group of products for this project. This was compounded by the low spectroscopic properties of the amino acid, leading to difficulty in differentiating the product peak from the cell lysate. Good separation of the individual product enantiomers was obtained by chiral analysis as shown in Fig. 10A. During the primary screen, a small peak eluted at the same time as the L-amino acid standard in certain samples (see Fig. 10B) and was thought to be the amino acid. However, further development of the method and the use of the appropriate controls established that this peak was actually a cell lysate peak.

0 [000320] The aminonitrile eluted between the two *t*-leucine peaks, as shown in Fig. 10C; this chromatogram also shows the cell lysate peak at 4.8 min. The UV spectrum of the nitrile was distinct from that of the amino acid, making it easier to differentiate from the acid peaks.

L-hydroxynorleucine ((S)-2-amino-6-hydroxy hexanoic acid)

[000321] The chiral analysis of (S)-2-amino-6-hydroxy hexanoic acid was consistent and reliable. By contrast, the nonchiral method presented many problems, primarily as a result of non-separation between the nitrile and the acid peaks. Towards the latter half of the project, a method was developed and used successfully for the confirmation of activities. Prior to this, most of the analysis was performed using the chiral method; standard curves of the products were run in order to quantify the reactions. A representative chromatogram of (S)-2-amino-6-hydroxy hexanoic acid is shown in Figure 11A, with (S)-2-amino-6-hydroxy hexanoic acid eluting at 6 min. The aminonitrile was not detected by this method.

[000322] Separation of the individual 2-amino-6-hydroxy hexanoic acid enantiomers is shown in Fig. 11B. The L-enantiomer elutes first, at 2 min, followed by the D-enantiomer at 3 min. In Fig. 11C, an enzymatic sample is represented; the only area of slight concern is the negative peak preceding the elution of the L-enantiomer. However, it did not appear to interfere significantly with the elution of this enantiomer; method development did not eliminate the negative peak.

4-methyl-D-leucine and 4-methyl-L-leucine

[000323] For the detection of 4-methylleucine, the chiral HPLC method again proved more reliable. The combination of low activities, together with the low sensitivity of the method to the compound led to difficulties in detection using nonchiral HPLC. A 2.5 mM standard of the amino acid is shown in Fig. 12A, with a peak height of approximately 40 mAU; this was substantially lower than those detected for the aromatic compounds. Chromatogram in Fig. 12B shows an enzymatic sample, in which conversion was detected using the chiral HPLC method; while it is not clear, it would appear that the 4-methylleucine peak elutes at 2.7 min and is extremely low in both peak height and area. This peak did not appear in samples which were negative by chiral HPLC analysis.

[000324] The chiral analysis of 4-methyl-L-leucine and 4-methyl-D-leucine did not present any problems. The L-enantiomer eluted at 5 min and the D-enantiomer at 7 min, although some peak shift did occur, as a result of the sensitivity to the column, described in section (i) for phenylglycine. In chromatograms shown in Figs. 14C-14D, the separation of these amino acids is shown; the first sample represents an enzyme which produced both enantiomers and in the second sample, the enzyme preferentially hydrolyzed the L-enantiomer, with a small amount D-amino acid forming.

(S)-cyclohexylmandelic acid

[000325] Chromatograms of the standards for cyclohexylmandelic acid (Fig. 13A) and the corresponding nitrile (Fig. 13B) are shown. The acid eluted at 1.3 min, while the cyanohydrin was observed at 2.5 min. The peak eluting at 2.1 min is thought to be the cyclohexylphenylketone, as shown by the elution of a ketone standard at this point.

Example 12: An Enzyme Library Approach to Biocatalysis: Development of a Nitrilase Platform for Enantioselective Production of Carboxylic Acid Derivatives

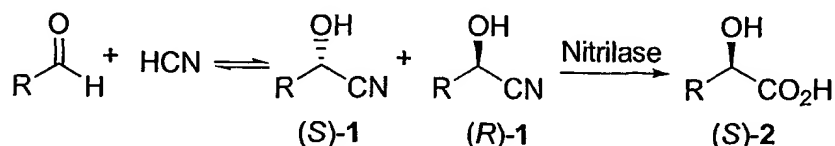
[000326] Biocatalytic processes can offer unique advantages in transformations that are challenging to accomplish through conventional chemical methods (Wong, C.-H.; Whitesides, G.M. *Enzymes in Synthetic Organic Chemistry*; Pergamon, New York, 1994; Drauz, K.; Waldmann, H., Roberts, S.M. Eds. *Enzyme Catalysis in Organic Synthesis*; VCH: Weinheim, Germany, 2nd ed., 2002). Nitrilases (EC 3.5.5.1) promote the mild hydrolytic conversion of organonitriles directly to the corresponding carboxylic acids (Kobayashi, M.; Shimizu, S. *FEMS Microbiol. Lett.* **1994**, 120, 217; Bunch, A.W. In *Biotechnology*; Rehm, H.-J.; Reed, G.; Puhler, A.; Stadler, P., Eds.; Wiley-VCH: Weinheim, Germany, Vol. 8a, Chapter 6, pp 277-324; Wieser, M.; Nagasawa, T. In *Stereoselective Biocatalysis*; Patel, R.N., Ed.; Marcel Dekker: New York, 2000, Chapter 17, pp 461-486.) Fewer than fifteen microbially-derived nitrilases have been characterized and reported to date. (Harper, D.B. *Int. J. Biochem.* **1985**, 17, 677; Levy-Schil, S.; Soubrier, F.; Crutz-Le Coq, A.M.; Faucher, D.; Crouzet, J.; Petre, D. *Gene* **1995**, 161, 15; Yu, F. 1999, US Patent 5872000; Ress-Loschke, M.; Friedrich, T.; Hauer, B.; Mattes, R.; Engels, D. PCT Appl. WO 00/23577, April 2000.). Several nitrilases previously have been explored for the preparation of single-enantiomer carboxylic acids, although little progress has been made in the development of nitrilases as viable synthetic tools. This application describes the discovery of a large and diverse set of nitrilases and herein demonstrate the utility of this nitrilase library for identifying enzymes that catalyze efficient enantioselective production of valuable hydroxy carboxylic acid derivatives.

[000327] In an effort to access the most diversified range of enzymes that can be found in Nature, we create large genomic libraries by extracting DNA directly from environmental samples that have been collected from varying global habitats. (For a description of these methods, see: Short, J.M. *Nature Biotech.* **1997**, 15, 1322; Handelsman, J.; Rondon, M.J.; Brady, S.F.; Clardy, J.; Goodman, R.M. *Chem. Biol.* **1998**, 5, R245; Henne, A.; Daniel, R.; Schmitz, R.A.; Gottschalk, G. *Appl. Environ. Microbiol.* **1999**, 65, 3901.). We have

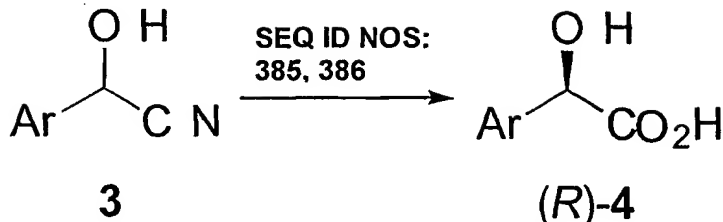
established a variety of methods for identifying novel activities through screening mixed populations of uncultured DNA. (Robertson, D.E.; Mathur, E.J.; Swanson, R.V.; Marrs, B.L.; Short, J.M. *SIM News* **1996**, 46, 3; Short, J.M. US Patent 5,958,672, 1999; Short J.M. US Patent 6,030,779, 2000.) Through this approach, nearly 200 new nitrilases have been
 5 discovered and characterized. (For a concise description of the studies, see Materials and Methods section below.) All nitrilases were defined as unique at the sequence level and were shown to possess the conserved catalytic triad Glu-Lys-Cys which is characteristic for this enzyme class. (Pace, H.; Brenner, C. *Genome Biology* **2001**, 2, 0001.1-0001.9.) Each nitrilase in our library was overexpressed and stored as a lyophilized cell lysate in order to
 10 facilitate rapid evaluation of the library for particular biocatalytic functions.

[000328] The initial investigations focused upon the efficacy of nitrilases for production of α -hydroxy acids **2** formed through hydrolysis of cyanohydrins **1**. Cyanohydrins are well-documented to racemize readily under basic conditions through reversible loss of HCN. (Inagaki, M.; Hiratake, J.; Nishioka, T.; Oda, J.; *J. Org. Chem* **1992**, 57, 5643. (b) van
 15 Eikeren, P. US Patent 5,241,087, 1993.) Thus, a dynamic kinetic resolution process is possible whereby an enzyme selectively hydrolyzes only one enantiomer of **1**, affording **2** in 100% theoretical yield and with high levels of enantiomeric purity.

[000329] One important application of this type involves commercial production of (*R*)-mandelic acid from mandelonitrile. (Ress-Loschke, M.; Friedrich, T.; Hauer, B.; Mattes, R.;
 20 Engels, D. PCT Appl. WO 00/23577, April 2000; Yamamoto, K.; Oishi, K.; Fujimatsu, I.; Komatsu, K. *Appl. Environ. Microbiol.* **1991**, 57, 3028; Endo, T.; Tamura, K. US Patent 5,296,373, March 1994.) Mandelic acid and derivatives find broad use as intermediates and resolving agents for production of many pharmaceutical and agricultural products. (Coppola, G.M.; Schuster, H.F. *Chiral α -Hydroxy Acids in Enantioselective Synthesis*; Wiley-VCH: Weinheim, Germany: 1997.) However, the few known nitrilases derived from cultured
 25 organisms have not been found useful for efficient and selective hydrolysis of analogous substrates.



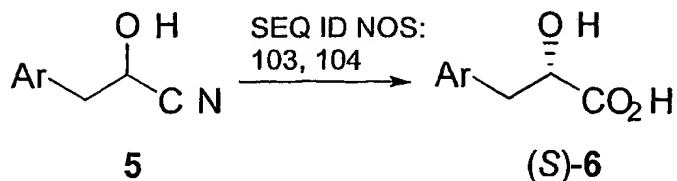
[000330] The nitrilase library was screened for activity and enantioselectivity in the
 30 hydrolysis of mandelonitrile (3a, Ar = phenyl) to mandelic acid. Preliminary results revealed



that 27 enzymes afforded mandelic acid in >90% ee. One enzyme, SEQ ID NOS:385, 386, was studied in greater detail and was found to be very active for hydrolysis of mandelonitrile. Under standard conditions using 25 mM 3a and 0.12 mg/mL enzyme in 10% MeOH (v/v) 0.1 M phosphate buffer at 37°C and pH 8, (R)-mandelic acid was formed quantitatively within 10 min and with 98% ee. To confirm synthetic utility, the reaction was performed using 1.0 g 3a (50 mM) and 9 mg nitrilase (0.06 mg/mL nitrilase I); after 3 h (R)-mandelic acid was isolated in high yield (0.93 g, 86%) and again with 98% ee.

(a) Reactions were conducted under standard conditions (see text). Reaction time for complete conversion to 4 was 1-3 h. Entries 8-9 were conducted at pH 9 and 5 mM substrate concentration. (b) Specific activities were measured at 5 min transformation timepoints and are expressed as $\mu\text{mol mg}^{-1} \text{ min}^{-1}$. (c) TOF = turnover frequency, mol product/mol catalyst/sec. (d) Enantioselectivities were determined by chiral HPLC analysis. Hydroxy acids were isolated and absolute configurations were determined to be (R) in all cases.

[000331] The substrate scope of SEQ ID NOS:385, 386 was next explored. As shown in Table 13, a broad range of mandelic acid derivatives as well as aromatic and heteroaromatic analogues (4) may be prepared through this method. SEQ ID NOS:385, 386 tolerates aromatic ring substituents in the *ortho*-, *meta*-, and *para*-positions of mandelonitrile derivatives and products of type 4 were produced with high enantioselectivities. Other larger aromatic groups such as 1-naphthyl and 2-naphthyl also are accommodated within the active site, again affording the acids 4 with high selectivity (Table 13, entries 8-9). Finally, 3-pyridyl and 3-thienyl analogues of mandelic acid were prepared readily using this process (Table 13, entries 10-11). This is the first reported demonstration of a nitrilase that affords a range of mandelic acid derivatives and heteroaromatic analogues of type 4. High activity on the more sterically encumbered *ortho*-substituted and 1-naphthyl derivatives is particularly noteworthy.



[000332] We next examined the preparation of aryllactic acid derivatives **6** through hydrolysis of the corresponding cyanohydrins **5**. Phenyllactic acid and derivatives serve as versatile building blocks for the preparation of numerous biologically active compounds.

(Coppola, G.M.; Schuster, H.F. *Chiral α -Hydroxy Acids in Enantioselective Synthesis*;

- 5 Wiley-VCH: Weinheim, Germany: 1997.) Upon screening our nitrilase library against the parent cyanohydrin **5a** (Ar = phenyl), we found several enzymes that provided **6a** with high enantiomeric excess. One enzyme, SEQ ID NOS: 103, 104, was further characterized. After optimization, SEQ ID NOS:103, 104, was shown to provide (*S*)-phenyllactic acid (**6a**) with complete conversion (50 mM) and very high enantioselectivity (98% ee) over 6 h. The
- 10 highest enantioselectivity previously reported for biocatalytic conversion of **5** to **6** was 75% ee achieved through a whole cell transformation using a *Pseudomonas* strain. (Hashimoto, Y.; Kobayashi, E.; Endo, T.; Nishiyama, M.; Horinouchi, S. *Biosci. Biotech. Biochem.* **1996**, *60*, 1279.)

Table 7. Nitrilase II-catalyzed production of aryllactic acid derivatives and analogues **6**^a

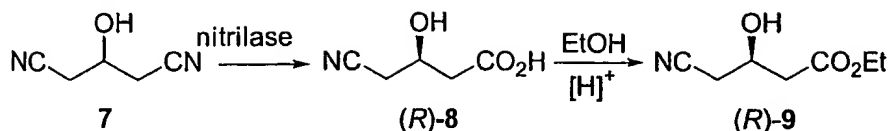
Entry	Ar in 6	Spec. Act. ^b	TOF ^c	% ee ^d
1	C ₆ H ₅	25	16	99
2	2-Me-C ₆ H ₅	160	100	95
3	2-Br-C ₆ H ₅	121	76	95
4	2-F-C ₆ H ₅	155	97	91
5	3-Me-C ₆ H ₅	21	13	95
6	3-F-C ₆ H ₅	22	14	99

7	1-naphthyl	64	40	96
8	2-pyridyl	10.5	6.6	99
9	3-pyridyl	11.6	7.2	97
10	2-thienyl	3.4	2.1	96
11	3-thienyl	2.3	1.4	97

(a) Reaction conditions as in Table 13, except 0.016 mg/mL nitrilase was used. Full conversion to **6** was observed within 6 h. (b)-(d) See Table 13. The absolute configuration was determined to be (*S*) for phenyllactic acid and entries 2-11 were assigned (*S*) based upon identical chiral HPLC peak elution order.

5 [000333] *Ortho* and *meta* substituents appear to be tolerated well by nitrilase II, with *ortho* substituted derivatives surprisingly being converted with higher rates relative to the parent substrate **5a**. Novel heteroaromatic derivatives, such as 2-pyridyl-, 3-pyridyl-, 2-thienyl- and 3-thienyllactic acids, were prepared with high conversions and enantioselectivities (entries 8-11). Unexpectedly, *para* substituents greatly lowered the rates
10 of these reactions, with full conversion taking over two weeks under these conditions.

[000334] The final transformation that we examined was desymmetrization of the readily available prochiral substrate 3-hydroxyglutarylnitrile (**7**) (Johnson, F.; Panella, J.P.; Carlson, A.A. *J. Org. Chem.* **1962**, *27*, 2241) to afford hydroxy acid (*R*)-**8** which, once esterified to (*R*)-**9**, is an intermediate used in the manufacture of the cholesterol-lowering
15 drug LIPITORTM. Previously reported attempts to use enzymes for this process were unsuccessful and **8** was produced with low selectivity (highest: 22% ee) and the undesired (*S*)-configuration. (Crosby, J.A.; Parratt, J.S.; Turner, N.J. *Tetrahedron: Asymmetry* **1992**, *3*, 1547; Beard, T.; Cohen, M.A.; Parratt, J.S.; Turner, N.J. *Tetrahedron: Asymmetry* **1993**, *4*, 1085; Kakeya, H.; Sakai, N.; Sano, A.; Yokoyama, M.; Sugai, T.; Ohta, H. *Chem. Lett.* **1991**,
20 1823.)



[000335] The nitrilase library was screened and unique enzymes were discovered and isolated that provided the required product (R)-8 with high conversion (>95%) and >90% *ee*. Using one of the (R)-specific nitrilases, this process was operated on a 1.0 g scale (240 mM 7, 30 mg enzyme, 22°C, pH 7) and after 22 h, (R)-8 was isolated in 98% yield and 95% *ee*. Interestingly, the same screening program also identified nitrilases that afford the opposite enantiomer (S)-8 with 90-98% *ee*. Thus, the extensive screen of biodiversity has uncovered enzymes that provide ready access to either enantiomer of the intermediate 8 with high enantioselectivities. Our discovery of the first enzymes that furnish (R)-8 underscores the advantage of having access to a large and diverse library of nitrilases.

[000336] By plumbing our environmental genomic libraries created from uncultured DNA, we have discovered a large array of novel nitrilases. This study has revealed specific nitrilases that furnish mandelic and aryl lactic acid derivatives, as well as either enantiomer of 4-cyano-3-hydroxybutyric acid in high yield and enantiomeric excess.

15 Procedures and Analytical Data:

[000337] Hydroxyglutarylnitrile was purchased from TCI America and used as received. Amino acids used for the preparation of aryl lactic acid standards were purchased from PepTech (Cambridge, MA). (R)-3-hydroxy-4-cyanobutyric acid was obtained from Gateway Chemical Technology (St. Louis, MO). Both (R)- and (S)- mandelic acid and (R)- and (S)- phenyl lactic acid standards were purchased from Sigma Aldrich. All other reagents were purchased from Sigma Aldrich and utilized without further purification. Silica Gel, 70-230 mesh, 60 Å, purchased from Aldrich, was used for chromatographic purifications. All ¹H NMRs and ¹³C NMRs were run on Bruker model AM-500 machines, set at room temperature, 500 MHz and 125MHz respectively for ¹H and ¹³C. Mass analyses and unit mass resolution was achieved by flow injection analysis (FIA) using a Perkin-Elmer Sciex API-4000 TURBOION™ Spray LC/MS/MS system. The LC flow was provided by Shimadzu LC-10Advp pumps, with 0.05% acetic acid and MeOH. Injections were accomplished via a Valco injector valve. The HPLC analysis was done on an Agilent 1100 HPLC with Astec's Chirobiotic R column (100 x 4.6 mm, cat no. 13022 or 150 x 4.6 mm, cat no. 13023) or Daicel's Chiralcel OD column (50 x 4.6 mm, cat no. 14022) and the DAD detector set at 210,

220, 230, and 250 nm. For specific rotations, a Perkin Elmer Model 341 Polarimeter was used, set at 589 nm, Na lamp, at room temperature, with a 100 mm path length cell.

Concentrations for specific rotation are reported in grams per 100 mL of solvent.

Microbiology techniques were executed in accordance to published protocols. (Sambrook, J.

- 5 Fritsch, EF, Maniatis, T. (1989) *Molecular Cloning: A Laboratory Manual* (2nd ed.), Cold Spring Harbor Laboratory Press, Plainview NY.) Glycolic acid products were isolated and absolute configurations were determined to be (*R*) in all cases by comparison with literature optical rotation data on configurationally defined compounds except for (-)-3-pyridylglycolic acid, which to our knowledge is not known as a single enantiomer. (For mandelic, 2-chloromandelic, 2-methyl mandelic, 3-chloromandelic, 3-bromomandelic and 4-fluoromandelic acid see Hoover, J.R. E.; Dunn, G. L.; Jakas, D.R.; Lam, L.L.; Taggart, J. J.; Guarini, J.R.; Phillips, L. *J. Med. Chem.* **1974**, 17(1), 34-41; For 2-bromo mandelic acid see Collet, A.; Jacques, J.; *Bull. Soc. Chem. Fr.* **1973**, 12, 3330-3331; For 1- and 2-naphthylglycolic acid see Takahashi, I; Y. Aoyagi, I. Nakamura, Kitagawa, A., Matsumoto, K., Kitajima, H. Isa, K. Odashima, K. Koga, K. *Heterocycles* **1999**, 51(6), 1371-88; For 3-thienylglycolic acid Gronowitz, S. *Ark. Kemi*, **1957**, 11, 519-525.)

- [000338] For the aryl lactic acid products, absolute configuration was established to be (*S*) for phenyl lactic acid by comparison with literature optical rotation and for all other phenyl lactic acid products, absolute configurations were predicted based upon elution order using chiral HPLC. Absolute configuration for 3-hydroxy-4-cyano-butanoic acid was established by derivatization to (*R*)-(-)-Methyl (3-O-[benzoyl]-4-cyano)-butanoate and comparison to literature optical rotation data on configurationally defined compound. (3. Beard, T. Cohen, M. A. Parratt, J.S. Turner, N. J. *Tetrahedron:Asymm.* **4**(6), 1993, 1085-1104.)

25 Nitrilase Discovery and Characterization Methods:

1. Nitrilase Selection.

- [000339] An *Escherichia coli* screening host strain, SEL700, was optimized for nitrilase selections on a nitrile substrate. An Abs_{600nm} = 1, resuspension of SEL700 screening host in 10 mM MgSO₄ was infected with kanamycin-resistant environmental DNA library for 45 minutes at 37°C, such that complete screening coverage of the library was achieved. Infected cells, now denoted by kanamycin resistance, were plated on kanamycin LB plates and allowed to grow overnight at 30°C. Titer plates were also made to determine infection

efficiency. Cells were pooled, washed, and resuspended the next morning with 10 mM MgSO₄. Transformed clones were inoculated into M9 media (without nitrogen) with 10 mM of nitrile substrate. M9 media consisted of 1X M9 salts (NH₄Cl omitted), 0.1mM CaCl₂, 1 mM MgSO₄, 0.2 % glucose, and approximately 10 mM of a nitrile selection substrate. The selection cultures were then incubated at 30°C, shaking at 200 rpm, for up to five weeks. Positive nitrilase cultures were identified by growth, due to positive clone's ability to hydrolyze nitrile substrate. Positive clones were isolated by streaking out a selection culture with growth and subsequent secondary culturing of isolated colonies in the same defined media. The DNA from any positive secondary cultures exhibiting re-growth was then isolated and sequenced to confirm discovery of a nitrilase gene and to establish the unique nature of that gene.

2. Nitrilase Biopanning.

[000340] Traditional filter lift hybridization screening protocols are limited to libraries with approximately 10⁶ to 10⁷ members. Attempting to screen one library would require approximately 5,000 filter lifts. Therefore, solution phase and other biopanning formats have been developed for ultra high throughput sequence based screening permitting rapid screening of up to 10⁸ member environmental libraries. In the solution format, the DNA from a large number of library clones is mixed with tagged molecules of interest under conditions which promote hybridization. The tagged clones and hybridized DNA are then removed from solution and washed at some level of stringency to remove clones which do not have sequence identity with the probe. The hybridized DNA is then eluted and recovered. Clones of interest are sequenced and cloned to provide enzyme activities of interest. This method has been demonstrated to achieve up to 1,000-fold enrichment per round for sequences of interest.

3. High Throughput Nitrilase Activity Assay.

[000341] Activity assays were conducted using 25 mM (~3 mg/mL) substrate, 0.1 mg/mL nitrilase in 0.25 mL of assay solution. Assay solutions consisted of 0-10% (v/v) MeOH in 0.1 M sodium phosphate buffer solution at pH 7 to 9 and temperatures 37°C or 22°C. Specific activities were measured at 5 min transformation time point, unless otherwise noted, and are expressed in units $\mu\text{mol mg}^{-1} \text{ min}^{-1}$. Enantiomeric excess and conversion rates were determined by high throughput HPLC analysis comparing enzyme product concentration to standard curves of racemic acid products. Analytical conditions for the products are tabulated below.

Analytical Methods:

	Acid Product	Column	Liquid Chromatography Method	Retention Times of enantiomers (min)
1.1	mandelic acid	Chirabiotic R 100 x 4.6 mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.4 (<i>S</i>); 2.9 (<i>R</i>)
1.2	2-Cl-mandelic acid	Chirabiotic R 100 x 4.6 mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.3 (<i>S</i>); 2.9 (<i>R</i>)
1.3	2-Br-mandelic acid	Chirabiotic R 100 x 4.6 mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.8; 4.0
1.4	2-CH ₃ -mandelic acid	Chirabiotic R 100 x 4.6 mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	3.1; 3.8
1.5	3-Cl-mandelic	Chirabiotic R 100 x 4.6 mm	10%[0.5% AcOH], 90% CH ₃ CN 1 ml/min	3.1; 3.8
1.6	3-Br-mandelic	Chirabiotic R 100 x 4.6 mm	10%[0.5% AcOH], 90% CH ₃ CN 1 ml/min	3.3; 3.9
1.7	4-F-mandelic	Chirabiotic R 150 x 4.6 mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	3.7; 4.8
1.8	1-naphthylglycolic acid	Chirabiotic R 100 x 4.6 mm	4%[0.5% AcOH], 96% CH ₃ CN 1 ml/min	3.1; 3.7
1.9	2-naphthylglycolic acid	Chirabiotic R 100 x 4.6 mm	4%[0.5% AcOH], 96% CH ₃ CN 1 ml/min	3.7; 4.7
1.10	3-pyridylglycolic acid	Chirabiotic R 100 x 4.6 mm	5% [0.5% AcOH], 65% H ₂ O, 30% CH ₃ CN, 2 ml/min	4.4; 5.5
1.11	3-thienylglycolic acid	Chirabiotic R 100 x 4.6 mm	20%[0.5% AcOH], 80% CH ₃ CN 2 ml/min	1.4; 2.5
2.1	phenyl lactic acid	Chirabiotic R 150 x 4.6 mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.8 (<i>S</i>); 4.0 (<i>R</i>)
2.2	2-methylphenyl lactic acid	Chirabiotic R 150 x 4.6 mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.5; 2.8
2.3	2-bromophenyl lactic acid	Chirabiotic R 150 x 4.6 mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.8; 3.2
2.4	2-fluorophenyl lactic acid	Chirabiotic R 150 x 4.6 mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.6; 2.9
2.5	3-methylphenyl lactic acid	Chirabiotic R 150 x 4.6 mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.4; 3.2
2.6	3-fluorophenyl lactic acid	Chirabiotic R 150 x 4.6mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.8; 3.6
2.7	1-naphthyllactic acid	Chirabiotic R 150 x 4.6mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.7; 3.1
2.8	2-pyridyllactic acid	Chirabiotic R 150 x 4.6mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.5; 2.9
2.9	3-pyridyllactic acid	Chirabiotic R 150 x 4.6mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	2.9; 3.6
2.10	2-thienyllactic acid	Chirabiotic R 150 x 4.6mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	3.6; 4.6
2.11	3-thienyllactic acid	Chirabiotic R 150 x 4.6mm	20%[0.5% AcOH], 80% CH ₃ CN 1 ml/min	3.5; 4.6
	Methyl(3-O [benzoyl]-4-cyano)-butanoate	Daicel OD 50 x 4.6 mm	5% isopropanol, 95% hexane 1 ml/min	4.5 (<i>R</i>); 5.4(<i>S</i>)

Cyanohydrin (Substrate) Synthesis:

- 5 [000342] Mandelonitrile Synthesis Method A: Acetone cyanohydrin (685 μ L, 7.5 mmol), aldehyde (5 mmol), and catalytic DIEA (13 μ L, 0.075 mmol) were mixed at 0 °C. The

reactions were stirred on ice for 45 minutes. To drive the equilibrium toward the product, acetone was removed *in vacuo*. Subsequently, crude reactions were acidified with H₂SO₄ (3 μ L) and stored at -20°C. TLC was used to monitor reaction progress (3:1 hexane/ethylacetate (EtOAc)).

- 5 [000343] Mandelonitrile Synthesis Method B: To a solution of KCN (358 mg, 5.5 mmol) in MeOH (1 mL) at 0°C was added aldehyde (5 mmol) and acetic acid (315 μ L, 5.5 mmol). After stirring for one hour on ice, MeOH was removed *in vacuo*, and the crude mixture was partitioned using EtOAc and H₂O. The organic fraction was retained and concentrated *in vacuo*. TLC analysis was used to monitor reaction progress (3:1 Hexanes/EtOAc).
- 10 [000344] Aryl Acetaldehyde Cyanohydrin: Arylacetic acid (50 mmol) was dissolved in 50 ml anhydrous tetrahydrofuran (THF) in a two-neck 500 ml round-bottom flask under N₂(g) atmosphere. To this solution cooled to 0 °C, under vigorous mixing, was added slowly 105 mmol of thexylchloroborane-dimethyl sulfide (2.55 M in methylene chloride). The reaction was allowed to proceed overnight. Excess acetic acid (10 ml) was added to quench and
- 15 acidify the reaction followed by the addition 10 ml water. After stirring at room temperature for 1 hour, solvent was removed *in vacuo* and the residue was dissolved in 100 ml water and extracted with 200 ml EtOAc. The EtOAc layer was dried over sodium sulfate, filtered and then concentrated *in vacuo*. Subsequently, 60 mmol of KCN, followed by 100 ml methanol was added to the residue. The solution was then cooled to 0 °C and acetic acid (60 mmol)
- 20 added. The reaction was stirred for 1-2 hours after all KCN dissolved. Solvents were removed *in vacuo* and residue was dissolved in 100 ml water and 200 ml EtOAc. The aqueous layer was extracted with EtOAc one more time. Combined EtOAc extracts were washed with saturated brine and dried over sodium sulfate, filtered and then concentrated *in vacuo* to obtain crude cyanohydrin product. The cyanohydrin was purified by silica-gel column
- 25 (hexane/EtOAc), as necessary.

[000345] 2-chloro mandelonitrile: ¹H NMR (CDCl₃, 500 MHz) δ 7.69 (m, 1H), 7.41 (m, 1H), 7.36 (m, 2H), 5.84 (s, 1H), 3.07 (br, 1H). ¹³C NMR (CDCl₃, 125 MHz) δ 132.89, 132.73, 131.22, 130.19, 128.48, 127.84, 118.24, 60.87. MS calc'd for [C₈H₆ClNO] 167.01 found 167.9 (LC-MS +).

- 30 [000346] 2-bromomandelonitrile: ¹H NMR (CDCl₃, 500 MHz) δ 7.72 (d, 1H, *J*= 6.58), 7.62 (d, 1H, *J*= 8.35), 7.43 (t, 1H, *J*= 8.42), 7.30 (t, 1H, *J*= 7.00), 5.85 (s, 1H). ¹³C NMR (CDCl₃, 125 MHz) δ 134.550, 133.584, 131.564, 128.819, 128.535, 122.565, 118.153, 63.379.

- [000347] 2-methylmandelonitrile: ^1H NMR (CDCl_3 , 500 MHz) δ : 7.60 (d, 1H, $J = 7.4$), 7.23-7.35 (m, 3H), 5.66 (s, 1H), 2.44 (s, 3H). ^{13}C NMR (CDCl_3 , 298 K, 125 MHz) δ : 136.425, 133.415, 131.450, 130.147, 127.204, 126.894, 118.952, 18.916. MS calc'd for $[\text{C}_9\text{H}_9\text{NO}]$ 147.07, found 147.2 (ESI +).
- 5 [000348] 3-chloromandelonitrile: ^1H NMR (CDCl_3 , 500 MHz) δ 7.55 (s, 1H), 7.43-7.37 (m, 3H), 5.54 (s, 1H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 137.183, 135.480, 130.718, 130.303, 127.047, 124.891, 118.395, 63.156. MS calc'd for $[\text{C}_8\text{H}_6\text{ClNO}]$ 167.01 found 167.9 (LC-MS +).
- [000349] 3-bromomandelonitrile: ^1H NMR (CDCl_3 , 500 MHz) δ 7.69 (s, 1H), 7.56 (d, $J = 6.2$ Hz, 1H), 7.45 (d, $J = 5.5$ Hz, 1H), 7.32 (t, $J = 6.4$ Hz, 1H), 5.53 (s, 1H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 137.376, 133.201, 130.934, 129.208, 125.359, 123.380, 118.458, 63.006. MS calc'd for $[\text{C}_8\text{H}_6\text{BrNO}]$ 212.0 found 211.9 (LC-MS +).
- 10 [000350] 4-fluoromandelonitrile: ^1H NMR (CDCl_3 , 500 MHz) δ 5.54 (s, 1H), 7.13 (m, 2H), 7.51-7.53 (m, 2H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 63.02, 116.44, 118.97, 128.90, 131.54, 132.51, 162.575.
- 15 [000351] 4-chloromandelonitrile: ^1H NMR (CDCl_3 , 500 MHz) δ 7.47 (d, $J = 7.0$ Hz, 2H), 7.42 (d, $J = 7.0$ Hz, 2H), 5.53 (s, 1H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 136.209, 133.845, 129.647, 128.232, 118.630, 63.154. MS calc'd for $[\text{C}_8\text{H}_6\text{ClNO}]$ 167.01 found 167.9 (LC-MS +).
- 20 [000352] 1-naphthyl cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 8.14 (d, 1H, $J = 8.5$), 7.92 (t, 2H, $J = 6.1$), 7.82 (d, 1H, $J = 5.7$), 7.62 (t, 1H, $J = 6.1$), 7.56 (t, 1H, $J = 6.1$), 7.50 (t, 1H, $J = 6.1$), 6.18 (s, 1H); ^{13}C NMR (CDCl_3 , 125 MHz) δ 137.0, 135.7, 134.2, 131.1, 129.2, 127.5, 126.7, 125.8, 125.3, 123.1, 119.0, 62.4; MS calc'd for $[\text{C}_{12}\text{H}_9\text{O}]$ 183.21, found 183.2 (ESI +).
- 25 [000353] 2-naphthyl cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 8.03 (s, 1H), 7.92 (d, 1H, $J = 8.6$), 7.87-7.91 (m, 2H), 7.61 (dd, 1H, $J = 6.7, 1.2$), 7.55-7.60 (m, 2H), 5.72 (s, 1H); ^{13}C NMR (CDCl_3 , 125 MHz) δ 134.9, 133.9, 132.7, 129.6, 128.6, 128.0, 127.4, 127.2, 126.4, 123.9, 118.9, 64.1; MS calc'd for $[\text{C}_{12}\text{H}_9\text{O}]$ 183.21, found 183.2 (ESI +).
- [000354] 3-pyridyl cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ : 8.62 (d, 1H, $J = 1.8$), 8.57 (d, 1H, $J = 5.1$), 7.94 (d, 1H, $J = 8.1$), 7.41 (dd, 1H, $J = 8.1, 5.1$), 5.64 (s, 1H); ^{13}C NMR (CDCl_3 , 125 MHz) δ 149.921, 147.355, 135.412, 133.044, 124.443, 118.980, 61.085. MS calc'd for $[\text{C}_7\text{H}_6\text{N}_2\text{O}]$ 134.05, found 135.2 (ESI +).
- 30

- [000355] 3-thienyl cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 7.45 (d, $J = 2.2$ Hz, 1H), 7.56 (dd, $J = 6.2$ Hz, 1H), 7.45 (d, $J = 5.5$ Hz, 1H), 7.32 (t, $J = 6.4$ Hz, 1H), 5.53 (s, 1H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 137.376, 133.201, 130.934, 129.208, 125.359, 123.380, 118.458, 63.006. MS calc'd for $[\text{C}_6\text{H}_5\text{NOS}]$ 139.01 found 139.9 (LC-MS +).
- 5 [000356] phenyl acetaldehyde cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 7.34 (m, 5H), 4.64 (t, $J = 6.75$ Hz, 1H), 3.11 (d, $J = 6.75$ Hz, 2H), 2.75 (br, 1H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 133.96, 129.91, 129.16, 128.08, 119.47, 62.33, 41.55.
- [000357] 2-methylphenyl acetaldehyde cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 7.11 (m, 4H), 4.61 (t, $J = 6.62$ Hz, 1H), 3.12 (d, $J = 6.62$ Hz, 2H), 2.14 (s, 3H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 136.94, 136.47, 132.57, 130.48, 127.61, 125.75, 120.11, 62.95, 44.73 MS calc'd for $[\text{C}_{10}\text{H}_{11}\text{NO}]$: 161.08, found 162.2 (M+Na, ESI +)
- 10 [000358] 2-bromophenyl acetaldehyde cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 7.20 (m, 4H), 4.78 (t, $J = 6.5$ Hz, 1H), 3.26 (d, $J = 6.5$ Hz, 2H). ^{13}C NMR (CDCl_3 , 100 MHz) δ 133.93, 132.82, 131.72, 129.21, 128.12, 124.86, 119.41, 63.02, 44.89.
- 15 [000359] 2-fluorophenyl acetaldehyde cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 7.2 (m, 2H), 7.02 (m, 2H), 4.50 (dd, $J = 4.62$ Hz, $J = 7.88$ Hz, 1H), 3.23 (dd, $J = 4.62$ Hz, $J = 14.12$ Hz, 1H), 2.97 (dd, 7.88 Hz, 14.12 Hz, 1H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 132.18, 131.52, 129.66, 129.03, 128.07, 124.05, 115.8, 63.02, 44.79 MS calc'd for $[\text{C}_9\text{H}_8\text{FNO}]$ 165.06, found 164.2 (ESI +).
- 20 [000360] 3-methylphenyl acetaldehyde cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 7.18 (m, 1H), 7.02 (m, 3H), 4.54 (dd, $J = 4.62$ Hz, $J = 8$ Hz, 1H), 3.06 (dd, $J = 4.62$ Hz, $J = 14.38$ Hz, 1H), 2.83 (dd, $J = 8$ Hz, $J = 14.38$ Hz, 1H), 2.36 (s, 3H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 176.25, 138.18, 136.0, 130.97, 128.93, 127.68, 126.58, 76.42, 34.29, 37.69 MS calc'd for $[\text{C}_{10}\text{H}_{12}\text{O}_3]$ 180.08, found 180.0 (ESI +).
- 25 [000361] 3-fluorophenyl acetaldehyde cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 7.18 (m, 2H), 6.95 (m, 2H), 4.44 (dd, 1H), 3.11 (dd, 1H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 130.40, 125.53, 124.85, 116.92, 114.87, 114.50, 119.77, 61.97, 41.27.
- [000362] 1-naphthyl acetaldehyde cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 8.07 (m, 1H), 7.86 (m, 1H), 7.74 (m, 1H), 7.41 (m, 4H), 4.20 (t, $J = 7$ Hz, 1H), 3.33 (d, $J = 6.8$ Hz, 2H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 177.7, 140.31, 129.74, 129.24, 128.92, 128.26, 127.84, 125.63, 124.53, 124.05, 123.42, 70.58, 38.0 MS calc'd for $[\text{C}_{13}\text{H}_{11}\text{NO}]$ 197.08, found 197.1 (ESI +).
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- [000363] 2-pyridyl acetaldehyde cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 8.50 (m, 1H), 7.85 (m, 1H), 7.48 (m, 1H), 7.34 (m, 1H), 4.42 (m, 1H), 3.19 (dd, $J = 3.5$ Hz, $J = 13.7$ Hz, 2H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 157.44, 145.69, 140.24, 126.96, 126.16, 122.99, 60.30, 42.60 MS calc'd for $[\text{C}_8\text{H}_8\text{N}_2\text{O}]$ 148.06, found 149.1 (ESI +).
- 5 [000364] 3-pyridyl acetaldehyde cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 8.62 (d, 1H, $J = 1.8$), 8.57 (d, 1H, $J = 5.1$), 7.94 (d, 1H, $J = 8.1$), 7.41 (dd, 1H, $J = 8.1$, 5.1), 5.64 (s, 1H). ^{13}C NMR (CDCl_3 , 125 MHz) δ : 149.921, 147.355, 135.412, 133.044, 124.443, 118.980, 61.085. Exact Mass calculated for $[\text{C}_7\text{H}_6\text{N}_2\text{O}]$: 134.05, found: 135.2 (ESI +).
- [000365] 2-thienyl acetaldehyde cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 7.1 (m, 1H), 6.9 (m, 1H), 6.8 (m, 1H), 4.11 (t, $J = 7.0$ Hz, 1H), 2.86 (d, $J = 7.0$ Hz, 2H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 127.68, 127.41, 125.58, 124.60, 118.70, 63.25, 44.84.
- 10 [000366] 3-thienyl acetaldehyde cyanohydrin: ^1H NMR (CDCl_3 , 500 MHz) δ 7.09 (m, 3H), 4.60 (t, $J = 6.25$ Hz, 1H), 3.12 (d, $J = 6.25$ Hz, 2H). ^{13}C NMR (CDCl_3 , 125 MHz) δ 129.05, 127.16, 125.27, 122.65, 119.87, 61.58, 44.90.
- 15 [000367] Preparation of racemic mandelic acids standards from corresponding cyanohydrins: (Stoughton, R.W. J. Am. Chem. Soc. 1941, 63, 2376) 2-bromomandelonitrile (230 mg, 1.08 mmol) was dissolved in conc. HCl (1 mL) and stirred at room temperature for 18 h and then at 70 °C for 24 h. After cooling, the reaction mixture was extracted with diethyl ether (4 x 2 mL). Organic extracts were, combined, dried over MgSO_4 , filtered and
- 20 concentrated *in vacuo*. 2-bromomandelic acid was isolated as a colorless powder (180 mg, 0.78 mmol, 70 % yield).
- [000368] Preparation of racemic arylactic acids standards from corresponding amino acids: Phenylalanine (10 mmol, 1.65g) was dissolved in 30 ml 2N H_2SO_4 at room temperature under N_2 (g) atmosphere. Sodium nitrite (1.4 g in 3 ml aqueous solution, 2 eq) solution was added
- 25 slowly to the reaction mixture over a period of 3-4 hours with vigorous stirring at room temperature under N_2 (g) atmosphere. The reaction mixture was stirred overnight and the phenylactic acid product was then extracted into diethylether (3 x 30 ml). Combined ether extracts were dried over MgSO_4 and then filtered and concentrated *in vacuo*. (Kenji, I.; Susumu, A.; Masaru, M.; Yasuyoshi, U.; Koki, Y.; Koichi, K. Patent Number, WO0155074,
- 30 Publication date: 2001-08-02.)
- General Method for Enzymatic Preparation of α -hydroxy acids:
- [000369] (R)-(-)-Mandelic Acid To a solution of mandelonitrile (1.005 g, 7.56 mmol) in 150 mL of sodium phosphate (100 mM) buffer at pH 8 with 10% v/v methanol, that had been

N₂ (g) sparged, at 37 °C, was added 9 mg of nitrilase 1 (normalized for nitrilase content). The reaction was conducted under N₂ (g) atmosphere on a rotating platform shaker. Reaction progress was monitored by withdrawing aliquots for HPLC analysis. After 3 h incubation, the reaction mixture was acidified to pH 2 with 1 N HCl and extracted with diethyl ether (4 x 50 ml). Organic fractions were concentrated *in vacuo* and then the residue was taken up in 10% sodium bicarbonate solution. This aqueous solutions was then washed with diethyl ether (3 x 50 ml) and then acidified to pH 2 with 1 N HCl and extracted with diethyl ether (3 x 50 ml). Organic fractions were combined, washed with brine, dried over MgSO₄, filtered and then concentrated *in vacuo*. (R)-(-)-Mandelic acid (933 mg, 6.22 mmol) was isolated as a colorless powder in 86 % yield. ¹H NMR (DMSO-d₆, 500 MHz) δ 12.6 (br, s, 1H) 7.41 (m, 2H), 7.34 (m, 2H), 7.28 (m, 1H), 5.015 (s, 1H). ¹³C NMR DMSO-d₆, 125 MHz) δ 174.083, 140.216, 128.113, 127.628, 126.628, 72.359. MS calc'd for [C₈H₈O₃] 150.07, found 150.9 (ESI +); *ee* = 98 % [HPLC]. [α]_D²⁰₅₉₈ = -134.6 (*c* = 0.5, methanol).

[000370] (-)-2-chloromandelic acid ¹H NMR (DMSO-d₆, 500 MHz) δ 7.75 (m, 1H), 7.44 (m, 1H), 7.34 (m, 2H), 5.34 (s, 1H). ¹³C NMR (DMSO, 298K, 125MHz) δ 173.070, 137.985, 132.105, 129.399, 129.158, 128.705, 127.235. MS calc'd for [C₈H₇ClO₃] 186.0, found 185.0 (LC-MS -). *ee* = 96 % [HPLC]. 92 % yield. [α]_D²⁰₅₉₈ = -137.6 (*c* = 0.5, ethanol).

[000371] (-)-2-bromomandelic acid ¹H NMR (DMSO-d₆, 500 MHz) δ 7.60 (d, *J* = 7.93, 1H), 7.48 (m, 1H), 7.40 (m, 1H), 7.25 (m, 1H), 5.30 (s, 1H). ¹³C NMR DMSO-d₆, 125 MHz) δ 172.994, 139.61, 132.355, 129.652, 128.753, 127.752, 122.681, 71.644. MS calc'd for [C₈H₇BrO₃] 230.0, found 230.9. *ee* = 96% [HPLC]. 92% yield. [α]_D²⁰₅₉₈ = -116.4 (*c* = 0.5, ethanol).

[000372] (-)-2-methylmandelic acid ¹H NMR (DMSO-d₆, 500 MHz) δ 11.78 (bs, 1H) 7.38 (m, 1H), 7.16-7.38 (m, 3H), 5.18 (s, 1H), 2.35 (s, 3H). ¹³C NMR DMSO-d₆, 125 MHz) δ 174.229, 138.623, 135.649, 130.129, 127.491, 126.990, 125.698, 125.698, 69.733, 18.899. MS calc'd for [C₉H₁₀O₃] 166.1, found 165.2. *ee* = 91 % [HPLC]. 86 % yield. [α]_D²⁰₅₉₈ = -164.4 (*c* = 0.5, ethanol).

[000373] (-)-3-chloromandelic acid ¹H NMR (DMSO-d₆, 500 MHz) δ 7.46 (s, 1H), 7.36 (m, 3H), 5.07 (s, 1H). ¹³C NMR (DMSO, 298K, 125MHz) δ 173.554, 142.685, 132.813, 130.069, 127.568, 126.355, 125.289, 71.659. MS calc'd for [C₈H₇ClO₃] 186.0, found 185.34 (MALDI TOF -). *ee* = 98 % [HPLC]. 70 % yield. [α]_D²⁰₅₉₈ = -120.4 8 (*c* = 0.5, methanol).

- [000374] (-)-3-bromomandelic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 7.60 (s, 1H), 7.49 (m, 1H), 7.42 (m, 1H), 7.31 (m, 1H), 5.06 (s, 1H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 173.551, 142.917, 130.468, 130.379, 129.237, 125.687, 121.404, 71.605. MS calc'd for $[\text{C}_8\text{H}_7\text{BrO}_3]$ 229.98, found 229.1 (LC-MS). $ee = 98\%$ [HPLC]. 82 % yield. $[\alpha]^{20}_{598} = -84.8$ ($c = 0.5$, ethanol).
- [000375] (-)-4-fluoromandelic acid ^1H NMR (DMSO, 298K, 500MHz) δ 12.65 (s, 1H), 7.44 (m, 2H), 7.17 (m, 2H), 5.91 (s, 1H), 5.03 (s, 1H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 173.93, 162.57, 136.47, 128.61, 128.55, 114.96, 114.80, 71.61. MS calc'd for $[\text{C}_8\text{H}_7\text{FO}_3]$ 170.0, found 168.8. $ee = 99\%$ [HPLC]. 81% yield. $[\alpha]^{20}_{598} = -152.8$ ($c = 0.5$, methanol).
- [000376] (-)-1-naphthylglycolic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 8.28-8.26 (m, 1H), 7.87-7.93 (m, 2H), 7.47-7.58 (m, 4H), 5.66 (s, 1H). ^{13}C NMR DMSO- d_6 , 125 MHz) δ 174.288, 136.284, 133.423, 130.654, 128.353, 128.192, 125.926, 125.694, 125.613, 125.266, 124.558, 70.940. MS calc'd for $[\text{C}_{12}\text{H}_{10}\text{O}_3]$: 202.21 found 201.37 (MALDI TOF -). $ee = 95\%$ [HPLC]. 90 % yield $[\alpha]^{20}_{598} = -115.4$ ($c = 0.5$, ethanol).
- [000377] (-)-2-naphthylglycolic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 12.6 (bm, 1H), 7.88-7.93 (m, 4H), 7.48-7.56 (m, 3H), 5.20 (s, 1H). ^{13}C NMR DMSO- d_6 , 125 MHz) δ 174.005, 137.760, 132.644, 132.498, 127.811, 127.658, 127.506, 127.209, 125.993, 125.334, 124.761, 72.472. MS calc'd for $[\text{C}_{12}\text{H}_{10}\text{O}_3]$ 202.21, found 201.37 (MALDI TOF). $ee = 98\%$ [HPLC]. 68% yield. $[\alpha]^{20}_{598} = -115.4$ ($c = 0.5$, ethanol).
- [000378] (-)-3-pyridylglycolic acid This Reaction was performed in 100 mM ammonium formate buffer at pH 8. To isolate the product, the reaction mixture was filtered through a 10,000 MWCO membrane to remove enzyme and then concentrated *in vacuo*. ^1H NMR (DMSO- d_6 , 500 MHz) δ 8.56 (s, 1H), 8.36 (d, $J = 4.57$ Hz, 1H), 8.25 (s, 1H), 7.71 (m, 1H), 7.25 (dd, $J = 4.98, 4.80$ Hz 1H), 5.45 (s, 1H). ^{13}C NMR DMSO- d_6 , 125 MHz) δ 165.911, 147.862, 147.251, 139.118, 133.381, 122.746, 71.508. MS calc'd for $[\text{C}_7\text{H}_7\text{NO}_3]$ 153.04, found 154.0 ((MALDI TOF). $ee = 92\%$ [HPLC], 84% yield, $[\alpha]^{20}_{598} = -65.2$ ($c = 0.5$, H_2O).
- [000379] (-)-3-thienylglycolic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 7.48 (m, 1H), 7.45 (d, $J = 2.81$, 1H), 7.10 (m, 1H), 5.09 (s, 1H), 3.33 (s, 1H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 173.704, 141.109, 126.446, 126.042, 122.247, 68.915 MS calc'd for $[\text{C}_6\text{H}_6\text{O}_3\text{S}]$ 158.00, found 157.224 (MALDI TOF). $ee = 95\%$ [HPLC]. 70 % yield. $[\alpha]^{20}_{598} = -123.2$ ($c = 0.5$, methanol).

- [000380] (*S*)-(-)-phenyllactic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 7.28(m, 5H), 4.17(dd, $J = 4.5$ Hz, $J = 8.3$ Hz, 1H), 2.98(dd, $J = 4.5$ Hz, $J = 13.7$ Hz, 1H), 2.79 (dd, $J = 8.3$ Hz, $J = 13.7$ Hz, 1H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 178.16, 133.4, 129.27, 128.6, 127.3, 70.45, 44.12. *ee* = 97 % [HPLC], 84 % yield. $[\alpha]^{20}_{598} = -17.8$ ($c = 0.5$, methanol).
- 5 [000381] (-)-2-methylphenyllactic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 7.16 (m, 4H), 4.47 (dd, $J = 3.9$ Hz, $J = 8.8$ Hz, 1H), 3.25(dd, $J = 3.9$ Hz, 14.3 Hz, 1H), 2.94 (dd, $J = 8.8$ Hz, $J = 14.3$ Hz), 2.35(s, 3H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 178.61, 137.08, 134.74, 130.80, 130.25, 127.44, 126.34, 70.93, 37.67, 19.79. MS calc'd $[\text{C}_{10}\text{H}_{12}\text{O}_3]$ 180.08, found 180.0 (ESI +). 86 % yield. *ee* = 95 % [HPLC]. $[\alpha]^{20}_{598} = -13.2$ ($c = 0.5$, methanol).
- 10 [000382] (-)-2-bromophenyllactic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 7.28 (m, 4H), 4.60(dd, $J = 4.0$ Hz, $J = 9.1$ Hz, 1H), 3.45(dd, $J = 4.0$ Hz, $J = 14.1$ Hz, 1H), 3.04(dd, $J = 8.0$ Hz, $J = 14.1$ Hz, 1H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 178.70, 136.05, 133.21, 132.10, 128.99, 127.72, 125.0, 70.04, 40.76. MS calc'd for $[\text{C}_9\text{H}_9\text{BrO}_3]$ 243.9, found 243.3 (ESI +). 91 % yield. *ee* = 93 % [HPLC], $[\alpha]^{20}_{598} = -17.6$ ($c = 0.5$, methanol).
- 15 [000383] (-)-2-fluorophenyllactic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 7.10 (m, 4H), 4.64 (t, $J = 6.8$ Hz, 1H), 3.11(d, $J = 6.8$ Hz, 2H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 132.18, 131.52, 129.66, 129.03, 128.07, 124.05, 115.8, 63.02, 44.79. MS calc'd for $[\text{C}_9\text{H}_8\text{FNO}]$: 165.06, found 164.2 (ESI +). 91 % yield. *ee* = 88 % [HPLC]. $[\alpha]^{20}_{598} = -14.0$ ($c = 0.5$, methanol).
- 20 [000384] (-)-3-methylphenyllactic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 7.18 (m, 1H), 7.02 (m, 3H), 4.54 (dd, $J = 4.6$ Hz, $J = 8.0$ Hz, 1H), 3.06(dd, $J = 4.54$ Hz, $J = 14.4$ Hz, 1H), 2.83(dd, $J = 8.0$ Hz, $J = 14.4$ Hz, 1H), 2.36 (s, 3H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 175.88, 163.80, 130.33, 130.09, 125.7, 116.68, 113.75, 71.31, 34.28. MS calc'd for $[\text{C}_{10}\text{H}_{11}\text{NO}]$ 161.08, found 162.2 (ESI +). 80 % yield. *ee* = 98 % [HPLC]. $[\alpha]^{20}_{598} = -2.4$ ($c = 0.5$, methanol).
- 25 [000385] (-)-3-fluorophenyllactic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 7.2 (m, 1H), 6.9 (m, 3H), 4.56 (dd, 4.5 Hz, $J = 7.9$ Hz, 1H), 3.09(dd, $J = 4.5$ Hz, $J = 14.1$ Hz, 1H), 2.86 (dd, $J = 7.9$ Hz, $J = 14.1$ Hz, 1H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 175.88, 163.80, 130.33, 130.09, 125.7, 116.68, 113.75, 71.31, 34.28. MS calc'd for $[\text{C}_9\text{H}_9\text{O}_3\text{F}]$ 184.05, found 184.1 (ESI +). 82 % yield. *ee* = 97 % [HPLC]. $[\alpha]^{20}_{598} = -5.2$ ($c = 0.5$, methanol).
- 30 [000386] (-)-1-naphyllactic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 8.57 (m, 1H), 8.21(m, 1H), 8.08 (m, 1H), 7.61 (m, 4H), 4.64 (dd, 3.5 Hz, 8.5 Hz, 1H), 3.84 (dd, $J = 3.5$ Hz, $J = 14.5$

Hz, 1H), 3.38 (dd, $J = 8.5$ Hz, $J = 14.5$ Hz, 1H) ^{13}C NMR (DMSO, 298K, 125MHz) δ 177.7, 140.31, 129.74, 129.24, 128.92, 128.26, 127.84, 125.63, 124.53, 124.05, 123.42, 70.58, 38.0. MS calc'd for $[\text{C}_{13}\text{H}_{11}\text{NO}]$ 197.08, found 197.1 (ESI +). 87 % yield. $ee = 94$ % [HPLC]. $[\alpha]_{598}^{20} = -16.2$ ($c = 0.5$, methanol).

- 5 [000387] (-)-2-pyridylactic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 8.49 (m, 1H), 7.62 (m, 1H), 7.21 (m, 2H), 4.50 (t, $J = 5.0$ Hz, 1H), 3.01 (d, $J = 5.0$ Hz, 2H). ^{13}C NMR (DMSO, 298K, 125 MHz) δ 178.8, 159.79, 148.84, 136.89, 124.35, 121.75, 71.14, 44.09. MS calc'd for $[\text{C}_8\text{H}_9\text{NO}_3]$: 167.06, found 167.0. (ESI +). 62 % yield. $ee = 94$ % [HPLC], $[\alpha]_{598}^{20} = -3.6$ ($c = 0.5$, methanol).
- 10 [000388] (-)-3-pyridylactic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 8.43(m, 2H), 7.62(m, 1H), 7.28(m, 1H), 4.57(t, 5.37Hz, 1H), 2.85(d, 5.37Hz, 2H). ^{13}C NMR (DMSO, 298K, 125 MHz) δ 176.6, 150.03, 147.12, 136.41, 129.45, 123.26, 61.56, 31.46 MS calc'd for $[\text{C}_8\text{H}_9\text{NO}_3]$ 167.06, found 167.0 (ESI +). 59 % yield. $ee = 94$ % [HPLC]. $[\alpha]_{598}^{20} = -4.0$ ($c = 0.5$, methanol).
- 15 [000389] (-)-2-thienylactic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 7.18(m, 1H), 6.94(m, 1H), 6.90 (m, 1H), 4.49 (dd, $J = 4.1$ Hz, $J = 6.25$ Hz, 1H), 3.36 (dd, $J = 4.1$ Hz, $J = 15.0$ Hz, 1H), 3.26(dd, $J = 6.25$ Hz, $J = 15.0$ Hz, 1H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 127.68, 127.41, 125.58, 124.60, 118.70, 63.25, 44.84. MS calc'd for $[\text{C}_7\text{H}_7\text{NOS}]$ 153.02, found 153.0 (ESI +). 85 % yield. $ee = 95$ % [HPLC]. $[\alpha]_{598}^{20} = -13.0$ ($c = 0.5$, methanol).
- 20 [000390] (-)-3-thienylactic acid ^1H NMR (DMSO- d_6 , 500 MHz) δ 7.30(m, 1H), 7.13(m, 1H), 7.01(m, 1H), 4.50 (dd, $J = 4.25$ Hz, $J = 6.5$ Hz, 1H), 3.21(dd, $J = 4.25$ Hz, $J = 15.0$ Hz, 1H), 3.10 (dd, $J = 6.5$ Hz, $J = 15.0$ Hz, 1H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 127.50, 136.09, 128.83, 126.24, 123.32, 70.65, 34.84. MS calc'd for $[\text{C}_7\text{H}_8\text{O}_3\text{S}]$ 172.02, found 172.1 (ESI +). 81 % yield. $ee = 96$ % [HPLC]. $[\alpha]_{598}^{20} = -18.8$ ($c = 0.5$, methanol).
- 25 Enzymatic Hydrolysis of 3-Hydroxyglutarylnitrile:

[000391] 3-Hydroxyglutarylnitrile (1.0 g, 9.0 mmol, 240 mM) was suspended in N_2 (g) sparged sodium phosphate buffer (37.5 mL, pH 7, 100 mM) at room temperature. Cell lysate (30 mg, normalized for nitrilase content) was added to bring the concentration to 0.8 mg/ml enzyme and the reaction was at shaken at 100 rpm, room temperature. Reaction progress was

30 monitored by TLC (1:1 EtOAc:Hexanes, $R_f = 0.32$, nitrile; $R_f = 0.0$, acid) After 22 h, the reaction was acidified with 1M HCl. The reaction mixture was continuously extracted with diethyl ether. The acid product was isolated as a yellow oil (1.15 g, 98 % yield). ^1H NMR

(DMSO, 298K, 500MHz) δ 12.32 (s, 1H), 5.52 (s, 1H), 4.10 (m, 1H), 2.70 (dd, 1H, $J = 16.8$, 4.1 Hz), 2.61 (dd, 1H, $J = 16.9$, 6.3 Hz), 2.44 (dd, 1H, $J = 15.4$, 5.3 Hz), 2.37 (dd, 1H, $J = 15.6$, 7.8 Hz). ^{13}C NMR (DMSO, 298K, 125 MHz) δ 171.9, 118.7, 63.4, 41.2, 25.2 MS calc'd for $[\text{C}_5\text{H}_7\text{NO}_3]$: 129.0, found 130.0 $[\text{M}+\text{H}^+]$, (ESI +).

5 Preparation of (R)-(-)-Methyl (3-O-[benzoyl]-4-cyano)-butanoate

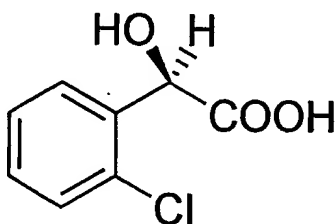
[000392] Benzoyl chloride (0.068 ml, 0.752 mmol) was added to a stirred solution of (R)-methyl-(3-hydroxy-4-cyano)-butanoate (71.7 mg, 0.501mmol) in pyridine (2.0 ml), at room temperature. After 19 hours, add an additional 0.5 equivalent of benzoyl chloride (0.023ml, 0.251mmol). Reaction was complete at 23 h, as determined by TLC. Add 1ml H_2O , extract with ether (3 x 10ml). Wash with brine (2 x 10ml). Dry combined aqueous extracts with MgSO_4 . Filter off drying agent and remove solvent by rotary evaporation. Purify by column chromatography (hexane:ethyl acetate [2:1]). Rotary evaporation of fractions yielded the product as a yellow oil (46 mg, 0.186 mmol, 37%). ^1H NMR (DMSO, 298K, 500MHz) δ 7.96 (d, 2H, $J = 7.8$), 7.70 (t, 1H, $J = 7.25$), 7.56 (t, 2H, $J = 7.8$), 5.55 (m, 1H), 3.59 (s, 3H), 3.13 (m, 2H), 2.90 (m, 2H). ^{13}C NMR (DMSO, 298K, 125MHz) δ 169.6, 164.5, 133.8, 129.3, 128.9, 128.5, 117.3, 66.0, 51.8, 37.5, 22.2 MS calc'd for $[\text{C}_{13}\text{H}_{13}\text{NO}_4]$: 247.25, found 270.3 $[\text{M}+\text{Na}^+]$ $ee = 95\%$ [HPLC]. $[\alpha]_{598}^{20} -32.4$ ($c = 0.5$, CHCl_3).

Synthesis of (R)-Ethyl-(3-hydroxy-4cyano)-butanoate

[000393] A 0.2 M solution of (R)-3-hydroxy-4-cyano-butanoic acid (50 mg, 0.387 mmol) in anhydrous ethanol (1.94 mL) was prepared. The ethanol solution was added dropwise to 1.0 ml of a 50:50 (v/v) mixture of anhydrous 1 M HCl ethereal solution and anhydrous ethanol over sieves. The reaction was stirred overnight at room temperature under N_2 (g) atmosphere. The reaction was monitored by TLC, (1:1 EtOAc:Hexanes, $R_f = 0.45$, ester; $R_f = 0.0$, acid, stained with p-anisaldehyde). After 30 hrs, solvent was removed by rotary evaporation. The crude product was taken up in 25 mL ether, washed with 5 mL saturated bicarbonate and then 5 mL brine. The organic extract was dried over MgSO_4 , filtered and then concentrated *in vacuo*, yielding the product as a clear oil. ^1H NMR (DMSO, 298K, 500MHz) δ 5.60 (d, 1H, $J = 5.58$ Hz), 4.12 (m, 1H), 4.07 (q, 2H, $J = 7.1$), 2.66 (m, 2H), 2.47 (m, 2H), 1.87 (t, 3H, $J = 7.0$). ^{13}C NMR (DMSO, 298K, 125 MHz) δ 170.21, 118.60, 63.40, 59.98, 41.10, 25.14, 14.02. MS calc'd for $[\text{C}_7\text{H}_{11}\text{NO}_3]$: 157.1, found 158.2. $[\text{M}+\text{H}^+]$

Example 13: Optimization Of Nitrilases For The Enantioselective Production Of
(R)-2-Chloromandelic Acid

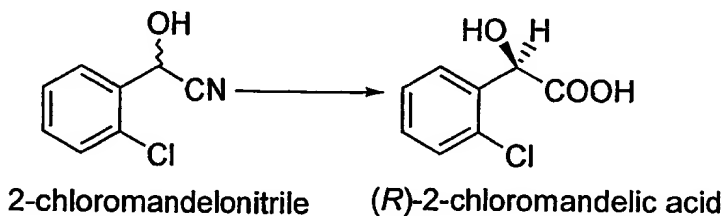
[000394] Chloromandelic acid has the structure:



5

[000395] Nitrilases were identified which selectively produced (*R*)-2-chloromandelic acid from (*R,S*)-2-chloromandelonitrile. Nitrilases were identified which were useful to improve the enantioselectivity of the enzymes and establishing the effects of process conditions on the enzymes. An examination of the reaction conditions for the enzymatic nitrile hydrolysis was carried out in order to improve the enantiomeric excess of the product. Additionally, further investigation into the effects of process conditions on the enzyme was performed.

10



- 15 [000396] In this aspect, the enantioselective production of (*R*)-2-chloromandelic acid was the target. One enzyme, SEQ ID NOS:385, 386, was selected for further confirmation of its enantioselectivity on 2-chloromandelonitrile. SEQ ID NOS:385, 386 was shown to be stable to process components, with a half-life of 8 hours. The enzyme was inhibited by 2-chlorobenzaldehyde and a contaminant in the cyanohydrin substrate, 2-chlorobenzoic acid.
- 20 The enzymatic reaction was scaled up to a substrate concentration of 45 mM 2-chloromandelonitrile. Over 90% conversion was obtained, with *ee* of 97%. The chiral HPLC method was improved, to remove a contaminating peak that was present in the substrate. Improved accuracy in the determination of enantioselectivity was obtained using this method.

[000397] Nitrilases were screened against 2-chloromandelonitrile, with 31 nitrilases exhibiting activity on this substrate. High enantioselectivities were shown by 9 enzymes. The optimization of 5 of these enzymes was undertaken and one of them was identified as a candidate for the next stage of development.

- 5 [000398] In an effort to improve the enantioselectivity of the selected enzymes for (*R*)-2-chloromandelic acid, a number of factors that are known to affect this property, together with the activity of the enzymes, were investigated. These included pH, temperature, buffer strength and addition of solvents to the reaction. Initially, 5 nitrilases were selected for these studies, based on the high enantioselectivities obtained by these enzymes. These enzymes
10 were: SEQ ID NOS:385, 386, SEQ ID NOS:197, 198, SEQ ID NOS:217, 218, SEQ ID NOS:55, 56, and SEQ ID NOS:167, 168.

Effect of pH

- [000399] The enzymatic reactions were run at a range of pH values, from pH 5 to pH 9. An increase in both activity and enantioselectivity with increasing pH was observed for all of
15 the enzymes. With the exception of SEQ ID NOS:385, 386, pH 9 (0.1 M Tris-HCl buffer) was determined as the optimum for activity and enantioselectivity. The optimum pH for SEQ ID NOS:385, 386 was pH 8 (0.1 M sodium phosphate buffer).

Effect of temperature

- [000400] The enzymes exhibited similar temperature profiles, with the highest activities
20 being measured at 37°C and 45°C. Although the latter temperature resulted in higher conversions, the enantioselectivity of most of the enzymes showed a clear preference for the lower temperatures, with ee values being 10-20% lower when the temperature was raised above 37°C. In the case of SEQ ID NOS:385, 386 a slight optimum for enantioselectivity was evident at 37°C. Therefore, this temperature was established as the optimum for
25 hydrolysis of 2-chloromandelonitrile by these enzymes.

Effect of enzyme concentration

- [000401] During the concurrent investigation into the enantioselective hydrolysis of phenylacetaldehyde cyanohydrin to L-phenyllactic acid, the concentration of the enzyme in the reaction was found to have a significant effect on the enantioselectivity of the reaction.
30 This provided an indication that the enzymatic hydrolysis rate was faster than the rate of racemization of the remaining cyanohydrin in the reaction. On this basis, the effect of enzyme concentration on the enantioselectivity of the enzymes towards (*R*)-2-chloromandelonitrile was investigated. Enzymatic reactions were performed with the

standard concentration of enzyme (0.6 mg protein/ml), half the standard concentration and one-tenth of the standard concentration.

[000402] The following Table indicates the highest conversions achieved for the reactions, with the corresponding ee. With the exception of SEQ ID NOS:385, 386, it appears that very little, if any, increased enantioselectivity is observed. Therefore, it appears that the rate of racemization of the remaining chloromandelonitrile is not a limiting factor to obtaining higher enantioselectivities.

Investigation of other positive enzymes

[000403] In addition to the enzymes in the above Table, a number of other nitrilases were screened for their enantioselectivities on 2-chloromandelonitrile. Some of these enzymes were newly discovered enzymes. Some were reinvestigated under conditions that have since been found to be optimal for these enzymes (pH 8 and 37°C). The results of this screening are shown below in the Table.

Effect of co-solvent concentration

[000404] The addition of methanol as a cosolvent in the enzymatic reactions was shown to enhance the ee. In order to establish the lowest level of methanol that could be added to the reactions, the enzyme reactions were performed at varying concentrations of methanol, ranging from 0-20% (v/v). No significant differences in enantioselectivity were evident between the various methanol concentrations. However, the ee in these reactions was 97-98%, while that of the control reaction, with no added methanol was 95-96%. While this difference in ee is small, the effect of the methanol was shown in more than one set of experiments during the course of this investigation and is therefore regarded as significant.

Effect of reaction components on activity of SEQ ID NOS:385, 386

[000405] A vital part of an investigation into process optimization of an enzyme involves the determination of the effects of any compounds which could be present in the enzymatic reaction. For SEQ ID NOS:385, 386, these components were established as the starting material and equilibrium product of the cyanohydrin, 2-chlorobenzaldehyde; the product, 2-chloromandelic acid and the contaminant detected in the substrate, 2-chlorobenzoic acid. The addition of cyanide to the reaction was found to have no effect on the enzyme activity. The presence of trace amounts of triethylamine was also found to be tolerable to the enzyme.

[000406] The effect of the various reaction components on the activity of SEQ ID NOS:385, 386 was assessed by addition of various levels of possible inhibitors to the enzyme reaction. From these experiments, it appeared that both the aldehyde and its oxidation product, 2-chlorobenzoic acid were detrimental to enzyme activity. Approximately 70% and 40% of the activity of SEQ ID NOS:385, 386 was lost upon addition of 5 mM 2-chlorobenzaldehyde or 5 mM 2-chlorobenzoic acid to the reaction, respectively.

Scale-up hydrolysis of 2-chloromandelonitrile

[000407] In order to confirm the conversion and enantioselectivity obtained by SEQ ID NOS:385, 386 for the production of (R)-2-chloromandelic acid, a larger scale reaction was performed and the product isolated from the aqueous mixture. The reaction was performed in a 20 ml reaction volume, with a substrate concentration of 45 mM 2-chloromandelonitrile. Complete conversion of the cyanohydrin was obtained, with 30 mM product formed. The ee of the product was 97% and the specific activity of the enzyme was 0.13 mmol product/mg nitrilase/h.

[000408] It is evident from this experiment, together with the other experiments performed, that the formation of product does not account for the complete loss of substrate. In all experiments, a nitrile-containing control sample was run, in order to determine the extent of breakdown of the cyanohydrin. Overall, it appears that approximately 50% of the substrate is lost over a period of 4 hours at 37°C. It is expected that this breakdown would be to its equilibrium products, cyanide and 2-chlorobenzaldehyde, which could undergo further oxidation. A larger scale reaction was also run at a substrate concentration of 90 mM 2-chloromandelonitrile. However, no product was detected in this reaction. At higher substrate concentrations, it is expected that the concentration of the equilibrium product, 2-chlorobenzaldehyde and the contaminant, 2-chlorobenzoic acid will be present in higher amounts. Based on the results above, it is possible that the enzyme will be completely inhibited under such conditions.

Reactions under biphasic conditions

[000409] The use of biphasic systems can facilitate product recovery following the enzymatic reaction step. These systems can be also be used for the removal of products or by-products which are inhibitory to the enzyme. The nitrilases were shown to be active under biphasic conditions using a variety of solvents. Following the low conversions obtained at the higher substrate concentration above, further investigation of a biphasic system was performed with the hit enzyme, SEQ ID NOS:385, 386. It was important to ascertain

whether any inhibitory factors could be removed by the solvent phase and whether any process advantages could be gained by the use of a biphasic system.

[000410] Promising results were obtained with hexane as the organic phase. Therefore, further investigations involved the use of this solvent at two different levels: 100% and 70% of the volume of the aqueous phase, with increasing substrate concentrations, up to 90 mM. The substrate was dissolved in the organic phase. The level of hexane did not appear to affect the level of product formation, particularly at the higher concentrations of 2-chloromandelonitrile.

[000411] Once again, high conversion was observed in a biphasic system, with a 76% yield of product being observed after 5 hours. The rate of product formation appeared to be slightly lower than in the corresponding monophasic system, where the reaction is complete within 1 hour. Lower enantioselectivity was observed in the biphasic system. Some possibilities which may account for these results are (i) the mass transfer rate is lower than the rate of enzyme activity or (ii) the non-polar solvent directly affects the enzyme.

[000412] At a higher substrate concentration, a very low conversion was observed, with 7 mM 2-chloromandelic acid being formed from 90 mM 2-chloromandelonitrile. This level of conversion, albeit low, was higher than that observed in the monophasic system with the same substrate concentration. These results suggest that some of the inhibitory 2-chlorobenzaldehyde or 2-chlorobenzoic acid is retained in the non-polar organic solvent.

Standard assay conditions:

[000413] The following solutions were prepared:

- Substrate stock solution: 50 mM of the cyanohydrin substrate in 0.1 M phosphate buffer (pH 8).

- Enzyme stock solution: 3.33 ml of 0.1 M phosphate buffer (pH 8) to each vial of 20 mg of lyophilized cell lysate (final concentration 6 mg protein/ml)

[000414] The reaction volumes varied between the different experiments, depending on the number of time points taken. Unless otherwise noted, all reactions consisted of 25 mM 2-chloromandelonitrile and 10% (v/v) of the enzyme stock solution (final concentration 0.6 mg protein/ml). The reactions were run at 37°C, unless otherwise stated. Controls to monitor the nitrile degradation were run with every experiment. These consisted of 25 mM 2-chloromandelonitrile in 0.1 M phosphate buffer (pH 8).

[000415] Sampling of reactions: The reactions were sampled by removing an aliquot from each reaction and diluting these samples by a factor of 8. Duplicate samples were taken for

analysis by chiral and achiral HPLC methods. The reactions were sampled at 0.5, 1, 1.5, 2, 3, and 4 hours, unless otherwise shown in the figures above.

HPLC methods

The achiral HPLC method was run on a SYNERGI-RP™ column (4 µm; 50 x 2 mm) with a mobile phase of 10 mM Na phosphate buffer (pH 2.5). A gradient of methanol was introduced at 3.5 min and increased to 50% over 1.5 min, following which the methanol was decreased to 0%. Elution times for 2-chloromandelic acid and 2-chloromandelonitrile were 2.5 and 6.1 minutes, with another peak appearing with the nitrile at 5.9 minutes.

[000416] As described above, the chiral HPLC method was optimized during the course of the investigation, to improve the separation between 2-chlorobenzoic acid and (S)-2-chloromandelic acid. The optimized method was used during the latter half of the investigation and was run on a CHIROBIOTIC-R™ column. The mobile phase was 80% Acetonitrile:20% of 0.5% (v/v) acetic acid. Elution times for (S)-2-chloromandelic acid and (R)-2-chloromandelic acid were 2.4 and 3.5 minutes respectively. A peak for 2-chlorobenzoic acid eluted at 1.9 minutes. For each experiment, a standard curve of the product was included in the HPLC run. The concentration of product in the samples was calculated from the slope of these curves.

Effect of pH

[000417] The effect of pH on the enzyme activity and enantioselectivity was studied by performance of the standard assay in a range of different buffers: 0.1 M Citrate Phosphate pH 5; 0.1 M Citrate Phosphate pH 6; 0.1 M Sodium Phosphate pH 6; 0.1 M Sodium Phosphate pH 7; 0.1 M Sodium Phosphate pH 8; 0.1 M Tris-HCl pH 8; and 0.1 M Tris-HCl pH 9. The standard enzyme concentration was used for all enzymes, with the exception of SEQ ID NOS:385, 386, where half the standard concentration was used (5% v/v of the enzyme stock solution).

Effect of temperature

[000418] The effect of temperature on the activity and enantioselectivity was investigated by performing the standard assay at a range of different temperatures: room temperature, 37°C, 45°C, 50°C and 60°C. The standard enzyme concentration was used for all enzymes, with the exception of SEQ ID NOS:385, 386, where half the standard concentration was used (5% v/v of the enzyme stock solution).

Effect of enzyme concentration

[000419] Reactions were run under standard conditions, with varying enzyme concentrations: 1%, 5% and 10% (v/v) of the enzyme stock solution. The reaction volume was normalized with the appropriate buffer.

5 Addition of solvents

[000420] The enzyme reactions were performed in the presence of methanol as a cosolvent. Methanol was added to the standard reaction mixture at the following levels: 0, 5, 10, 15 and 20% (v/v).

[000421] Biphasic reactions with hexane were also investigated. The aqueous phase
10 contained 10% (v/v) of the enzyme stock solution in 0.1 M phosphate buffer (pH 8). The cyanohydrin was dissolved in the hexane, prior to addition to the reaction. Two levels of organic phase were used: 1 equivalent and 0.7 equivalents of the aqueous phase volume. In addition, a range of nitrile concentrations was investigated: 25, 45 and 90 mM. These reactions were run at room temperature.

15 [000422] Samples from these reactions were taken both from the aqueous and the solvent phase. The hexane was evaporated by centrifugation under vacuum and redissolved in a 50:50 mixture of methanol and water, so that the samples were at the same dilution as the aqueous samples. Analysis of the samples was performed by non-chiral and chiral HPLC.

Effect of process components

20 [000423] (i) Activity: The effect of the process components on the activity of the enzymes was established by addition of the individual components, 2-chlorobenzaldehyde, 2-chlorobenzoic acid or 2-chloromandelic acid, to the enzymatic reaction. The enzymatic reactions were carried out under standard conditions, in the presence of one of the 2 possible inhibitors as follows: 5, 10, 20 and 25 mM 2-chlorobenzaldehyde; 1.5 and 5 mM 2-
25 chlorobenzoic acid; and 10, 20, 40 and 80 mM 2-chloromandelic acid. Control reactions were performed under standard conditions, with no additive. At each of the sampling times, the samples were diluted to a level of 1 in 10. Control samples containing the reaction components without enzyme were used and diluted to the same level. The samples were analysed by non-chiral HPLC.

30 [000424] (ii) Stability: The stability of the enzymes to process conditions was monitored by incubation of the enzymes in the presence of the reaction components, 2-chlorobenzaldehyde and 2-chloromandelic acid for predetermined time periods, prior to assay of the enzyme activity under standard conditions. In these experiments, the enzymes were

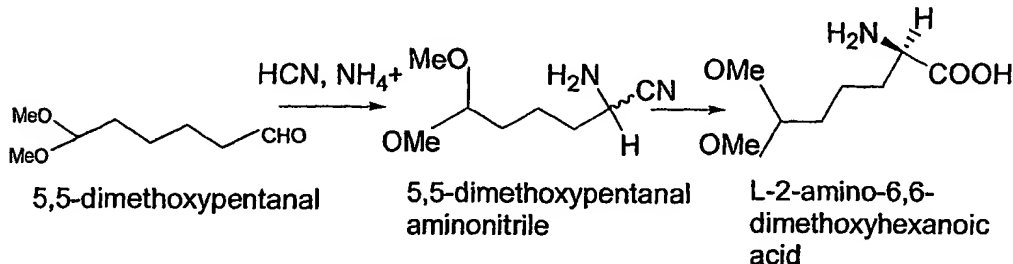
incubated at a concentration of 3 mg protein/ml in the presence of each of the following reaction components: 5, 10, 20 and 25 mM 2-chlorobenzaldehyde; and 10, 20, 40 and 80 mM 2-chloromandelic acid. Control reactions were performed by incubation of the enzyme in buffer only.

- 5 [000425] Assay conditions: At 0, 4, 8 and 24 hours of incubation in the particular additive, 20 μ l of the enzyme solution was removed and added to 60 μ l of a 41.6 mM substrate stock solution and 20 μ l buffer. The enzyme activity was thus assayed under standard conditions. The reactions were sampled 90 minutes after substrate addition and analyzed using the non-chiral HPLC method.

10 Scale-up of enzymatic reaction

[000426] The enzymatic reactions were run at two difference concentrations: 45 mM and 90 mM substrate. The reactions were run under standard conditions, i.e. pH 8 (0.1 M sodium phosphate buffer), 37°C and 10% (v/v) of the enzyme stock solution. The substrate was dissolved in 10% (v/v) methanol prior to addition of the buffer. The final reaction
15 volume was 20 ml and the reactions were performed with magnetic stirring.

Example 14: Optimization Of Nitrilases For The Enantioselective Production Of L-2-amino-6,6-dimethoxyhexanoic acid



- [000427] Four of the isolated enzymes were shown to hydrolyze 2-amino-6-hydroxy hexanenitrile to (S)-2-amino-6-hydroxy hexanoic acid, with selectivity towards the L-
20 enantiomer. A new target, with a similar structure to (S)-2-amino-6-hydroxy hexanoic acid was identified. A panel of the isolated nitrilases are screened against the target, 5,5-dimethoxypentanal aminonitrile. The positive enzymes are characterized on this substrate. Laboratory evolution techniques can be used to optimize these nitrilases for improved
25 enantiospecificity towards the specified target. A primary screen is used to identify putative up-mutants, which is confirmed using HPLC.

[000428] Optimization of enzymes: GSSM™ and GeneReassembly™ can be performed on selected nitrilases, in order to improve the enantioselectivity and activity of the enzymes

for the production of L-2-amino-6,6-dimethoxyhexanoic acid. Four enzymes were identified that can hydrolyze enantioselectively 2-amino-6-hydroxy hexanenitrile to L-(S)-2-amino-6-hydroxy hexanoic acid. However, a slight structural difference is present in the new target molecule, L-2-amino-6,6-dimethoxyhexanoic acid. In order to determine whether this
5 difference affects the activity and enantioselectivity of the enzymes, the complete spectrum of nitrilases is screened against the new target.

[000429] An enzyme exhibiting the highest combination of activity and enantioselectivity for the production of L-2-amino-6,6-dimethoxyhexanoic is selected for GSSM™. Following the mutation of the target enzyme, the resulting mutants will be
10 screened on 5,5-dimethoxypentanal aminonitrile, using high throughput screening technology. Following confirmation of the up-mutants by HPLC analysis, the individual up-mutants will be combined in order to further enhance the properties of the mutant enzymes.

[000430] In parallel to GSSM™, a GeneReassembly™ can be performed on a combination of parent enzymes, at least one of which can be selected for activity and enantioselectivity on L-2-amino-6,6-dimethoxyhexanoic acid. At least two other nitrilases,
15 with a high degree of homology, can be reassembled with the former enzyme(s); these enzymes will be selected in order to provide diversity to the reassembled sequences.

[000431] Crucial to the success of this evolution effort is the development of a high throughput assay for enantioselectivity. Such an assay is a novel enzyme-based
20 enantioselectivity assay that allows for the screening of >30,000 mutants in a significantly shorter time period than the traditionally used method of HPLC.

[000432] In one aspect, a non-stochastic method, termed synthetic ligation reassembly, that is related to stochastic shuffling, except that the nucleic acid building blocks are not shuffled or concatenated or chimerized randomly, but rather are assembled non-
25 stochastically, can be used to create variants. This method does not require the presence of high homology between nucleic acids to be shuffled. The ligation reassembly method can be used to non-stochastically generate libraries (or sets) of progeny molecules having at least 10^{100} or at least 10^{1000} different chimeras. The ligation reassembly method provides a non-stochastic method of producing a set of finalized chimeric nucleic acids that have an overall
30 assembly order that is chosen by design, which method is comprised of the steps of generating by design a plurality of specific nucleic acid building blocks having serviceable mutually compatible ligatable ends, as assembling these nucleic acid building blocks, such that a designed overall assembly order is achieved.

[000433] The mutually compatible ligatable ends of the nucleic acid building blocks to be assembled are considered to be "serviceable" for this type of ordered assembly if they enable the building blocks to be coupled in predetermined orders. Thus, in one aspect, the overall assembly order in which the nucleic acid building blocks can be coupled is specified by the design of the ligatable ends and, if more than one assembly step is to be used, then the overall assembly order in which the nucleic acid building blocks can be coupled is also specified by the sequential order of the assembly step(s). In a one aspect of the invention, the annealed building pieces are treated with an enzyme, such as a ligase (*e.g.*, T4 DNA ligase) to achieve covalent bonding of the building pieces.

[000434] In a another aspect, the design of nucleic acid building blocks is obtained upon analysis of the sequences of a set of progenitor nucleic acid templates that serve as a basis for producing a progeny set of finalized chimeric nucleic acid molecules. These progenitor nucleic acid templates thus serve as a source of sequence information that aids in the design of the nucleic acid building blocks that are to be mutagenized, *i.e.* chimerized, recombined or shuffled.

[000435] In one exemplification, the invention provides for the chimerization of a family of related genes and their encoded family of related products. In a particular exemplification, the encoded products are nitrilase enzymes. Nucleic acids encoding the nitrilases of the invention can be mutagenized in accordance with the methods described herein.

[000436] Thus, according to one aspect of the invention, the sequences of a plurality of progenitor nucleic acid templates encoding nitrilases are aligned in order to select one or more demarcation points, which demarcation points can be located at an area of homology. The demarcation points can be used to delineate the boundaries of nucleic acid building blocks to be generated. Thus, the demarcation points identified and selected in the progenitor molecules serve as potential chimerization points in the assembly of the progeny molecules.

[000437] Typically a serviceable demarcation point is an area of homology (comprised of at least one homologous nucleotide base) shared by at least two progenitor templates, but the demarcation point can be an area of homology that is shared by at least half of the progenitor templates, at least two thirds of the progenitor templates, at least three fourths of the progenitor templates, and preferably at almost all of the progenitor templates. Even more preferably still a serviceable demarcation point is an area of homology that is shared by all of the progenitor templates.

[000438] In a one aspect, the ligation reassembly process is performed exhaustively in order to generate an exhaustive library. In other words, all possible ordered combinations of the nucleic acid building blocks are represented in the set of finalized chimeric nucleic acid molecules. At the same time, the assembly order (*i.e.*, the order of assembly of each building block in the 5' to 3' sequence of each finalized chimeric nucleic acid) in each combination is by design (or non-stochastic, non-random). Because of the non-stochastic nature of the method, the possibility of unwanted side products is greatly reduced.

[000439] In another aspect, the method provides that, the ligation reassembly process is performed systematically, for example in order to generate a systematically compartmentalized library, with compartments that can be screened systematically, *e.g.*, one by one. Each compartment (or portion) holds chimeras or recombinants with known characteristics. In other words the invention provides that, through the selective and judicious use of specific nucleic acid building blocks, coupled with the selective and judicious use of sequentially stepped assembly reactions, an experimental design can be achieved where specific sets of progeny products are made in each of several reaction vessels. This allows a systematic examination and screening procedure to be performed. Thus, it allows a potentially very large number of progeny molecules to be examined systematically in smaller groups.

[000440] Because of its ability to perform chimerizations in a manner that is highly flexible, yet exhaustive and systematic, particularly when there is a low level of homology among the progenitor molecules, the invention described herein provides for the generation of a library (or set) comprised of a large number of progeny molecules. Because of the non-stochastic nature of the ligation reassembly method, the progeny molecules generated preferably comprise a library of finalized chimeric nucleic acid molecules having an overall assembly order that is chosen by design. In a particularly aspect, such a generated library is comprised of greater than 10^3 to greater than 10^{1000} different progeny molecular species.

[000441] In another exemplification, the synthetic nature of the step in which the building blocks are generated allows the design and introduction of nucleotides (*e.g.*, one or more nucleotides, which may be, for example, codons or introns or regulatory sequences) that can later be optionally removed in an *in vitro* process (*e.g.*, by mutagenesis) or in an *in vivo* process (*e.g.*, by utilizing the gene splicing ability of a host organism). It is appreciated that in many instances the introduction of these nucleotides may also be desirable for many other reasons in addition to the potential benefit of creating a serviceable demarcation point.

[000442] The synthetic ligation reassembly method of the invention utilizes a plurality of nucleic acid building blocks, each of which preferably has two ligatable ends. The two ligatable ends on each nucleic acid building block may be two blunt ends (i.e. each having an overhang of zero nucleotides), or preferably one blunt end and one overhang, or more preferably still two overhangs. On a double-stranded nucleic acid, a useful overhang can be a 3' overhang, or a 5' overhang. A nucleic acid building block can have a 3' overhang, a 5' overhang, two 3' overhangs, or two 5' overhangs. The overall order in which the nucleic acid building blocks are assembled to form a finalized chimeric nucleic acid molecule is determined by purposeful experimental design (*e.g.*, by designing sticky ends between building block nucleic acids based on the sequence of the 5' and 3' overhangs) and is not random.

[000443] According to one preferred aspect, a nucleic acid building block is generated by chemical synthesis of two single-stranded nucleic acids (also referred to as single-stranded oligos) and contacting them together under hybridization conditions so as to allow them to anneal to form a double-stranded nucleic acid building block. A double-stranded nucleic acid building block can be of variable size. The sizes of these building blocks can be small or large. Preferred sizes for building block range from 1 base pair (not including any overhangs) to 100,000 base pairs (not including any overhangs). Other preferred size ranges are also provided, which have lower limits of from 1 bp to 10,000 bp (including every integer value in between), and upper limits of from 2 bp to 100,000 bp (including every integer value in between).

[000444] According to one aspect, a double-stranded nucleic acid building block is generated by first generating two single stranded nucleic acids and allowing them to anneal to form a double-stranded nucleic acid building block. The two strands of a double-stranded nucleic acid building block may be complementary at every nucleotide apart from any that form an overhang; thus containing no mismatches, apart from any overhang(s). According to another aspect, the two strands of a double-stranded nucleic acid building block are complementary at fewer than every nucleotide apart from any that form an overhang. Thus, according to this aspect, a double-stranded nucleic acid building block can be used to introduce codon degeneracy. Preferably the codon degeneracy is introduced using the site-saturation mutagenesis described herein, using one or more N,N,GIT cassettes or alternatively using one or more N,N,N cassettes.

Example 15: Assays for Evaluation of Nitrilase Activity and Enantioselectivity

[000445] An assay method amenable to high throughput automation to increase the screening throughput both of the discovery and evolution efforts for nitrilases is described. The ideal assay is one that permits quantification of both product formation or substrate conversion and also enantiomeric excess. Two achiral and two chiral colorimetric assays that
5 are amenable to high throughput screening were developed.

Achiral Colorimetric Assays Developed:

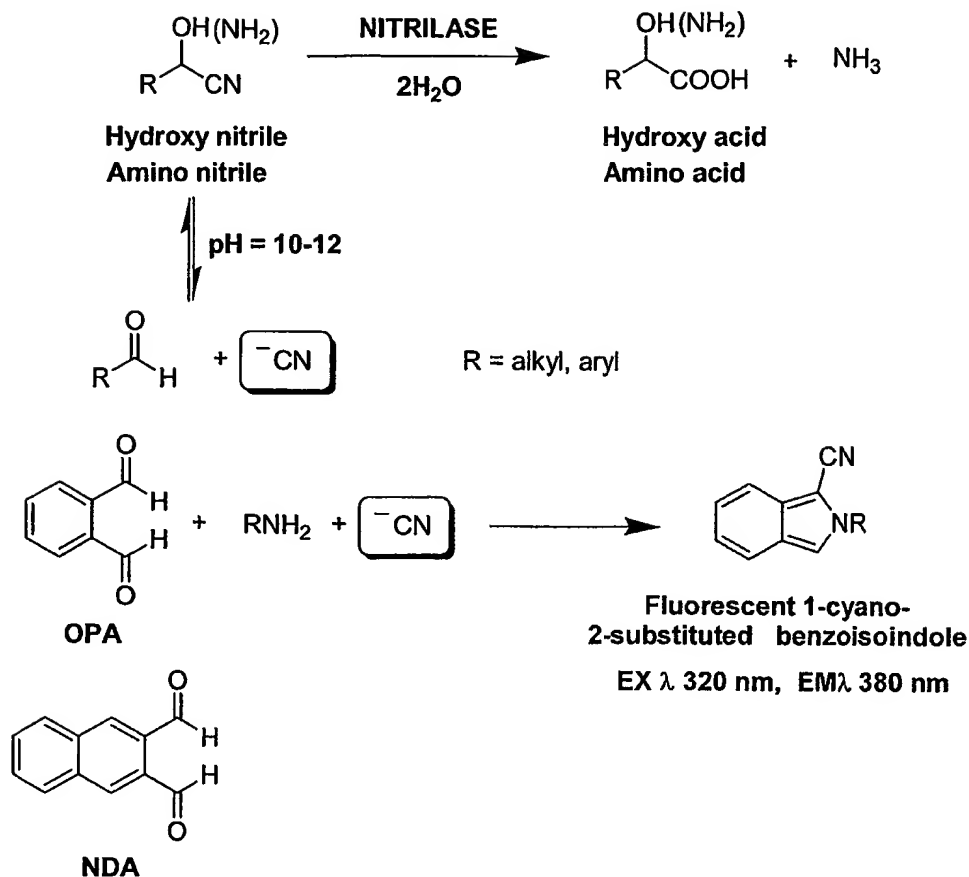
[000446] OPA assay for residual substrate. The OPA assay is Applicable to α -amino or α -hydroxy nitrile substrates. The lysis of whole cells is not necessary. These results were corroborated by HPLC for 2-chloromandelonitrile and phenyl acetaldehyde cyanohydrin.
10 The assay works best with aromatic nitriles. Aliphatic compounds exhibit a linear standard curve, fluorescence is reduced, reducing the efficacy of the assay.

[000447] LDH Assay for quantification and *ee* determination of hydroxyacid formed. The LDH assay is applicable to phenyl lactic acid but not to 2-chloromandelic acid. Use of a resazurin detection system increases sensitivity and reduces background. Background
15 fluorescence of whole cells was overcome either by centrifugation or heat inactivation prior to performing assay.

[000448] AAO Assay for quantification and *ee* determination of aminoacid formed. The AAO assay is applicable to phenylalanine and (S)-2-amino-6-hydroxy hexanoic acid. The use of the Amplex Red detection system increases sensitivity. Cell lysis was shown not be
20 necessary. Cells are grown in defined media in order to prevent background fluorescence.

OPA Assay

[000449] The *o*-phthalaldehyde (OPA) fluorescence based nitrilase assay is used to quantify the amount of α -hydroxynitrile substrate remaining. OPA reacts with the cyanide released from the pH controlled decomposition of α -hydroxynitriles to the corresponding
25 aldehyde and cyanide to yield a fluorescent, quantifiable product. OPA reacts with the cyanide released from the pH controlled decomposition of α -hydroxynitriles to the corresponding aldehyde and cyanide to yield the fluorescent 1-cyano-2-R benzoisindole.



[000450] Standard curves were established for the following substrates: 2-Chloromandelonitrile (CMN, 0.998), Cyclohexylmandelonitrile (CHMN, 0.99),

5 Acetophenone aminonitrile (APA, 0.99), and Phenylacetaldehyde cyanohydrin (PAC, 0.97), (Figure 5), (R^2 values in parentheses). A standard curve for Phenylglycine (PGN, 0.93) was also established. Three of the substrates tested, Dimethylbutanal aminonitrile (DMB) (2-amino-4,4-dimethyl pentanenitrile), Hydroxypivaldehyde aminonitrile (HPA) and Pivaldehyde aminonitrile (PAH), gave very low fluorescence readings and unreliable results

10 under the original assay conditions. For these compounds a number of parameters were adjusted, however the fluorescent signal strength of these compounds was not increased by these manipulations.

[000451] In an attempt to increase the fluorescent signal of these three compounds, naphthalene dicarboxaldehyde (NDA) was substituted for OPA. Standard curves for PAH,

15 HPA and DMB with either OPA or NDA were constructed. To determine sensitivity and background fluorescence, a lyophilized nitrilase lysate (SEQ ID NOS:189, 190) with

suspected catalytic activity on each of the substrates was added. Hydrolysis was detected in three out of four of the compounds. NDA sharply boosted the signal, often by an order of magnitude, though this reduced linearity is presumably due to signal saturation.

[000452] NDA was established as an alternative detection reagent for the aliphatic

5 compounds. However, it is desirable for the assay to utilize the same detection system for all of the substrates since this would facilitate the automated evaluation of multiple nitrilase substrates. The current OPA based assay is effective for the analysis of PAC, CMN, CHMN, APA, MN and PGN. While standard curves have been developed for the aliphatic compounds PAH, HPA, and DMB.

10 Whole cell optimization

[000453] The effect of addition of lyophilized nitrilase lysate to the assay components, either untreated or heat inactivated, was evaluated. Interfering background fluorescence was not observed in either case. The OPA assay was next evaluated and optimized for nitrilase activity detection in a whole cell format. Both nitrilase expressing whole cells and *in-situ*
15 lysed cells were evaluated. Lyophilized cell lysates were evaluated alongside their respective whole cell clones as controls. For this optimization study, mandelonitrile (MN) was chosen as a model substrate.

[000454] The lyophilized cell lysate of SEQ ID NOS:187, 188 was evaluated alongside whole cells expressing SEQ ID NOS:187, 188 and *in situ lysed* cells expressing SEQ ID

20 NOS:187, 188 The addition of whole cells did not affect fluorescence nor result in fluorescence quenching. Addition of any of the three cell lysis solutions improved permeability (and therefore conversion) of mandelonitrile in the whole cell systems. Three cell lysing solutions were evaluated: B-PER (Pierce), BugBuster (Novagen) and CellLytic B-II (Sigma) and were found not to have a deleterious affect on the OPA assay. The addition of
25 product α -hydroxyacid or α -aminoacid did not affect detection by the OPA assay.

[000455] The assay was modified from its original format, which required several liquid transfer steps, into a one plate process, where cell growth, nitrile hydrolysis and OPA assay reaction occurred in the same microtiter plate. Mandelonitrile was tested using this single well format. In this case, the *E. coli*. Gene site-saturation mutagenesis (GSSMTM) cell host
30 was evaluated. Three clones were tested: SEQ ID NOS:101, 102, SEQ ID NOS:187, 188, and an empty vector, which was used as a control. Hydrolysis was evaluated at four timepoints, at 10 and 20 mM, and also with a 0 mM control. In an earlier experiment, clone

SEQ ID NOS:187, 188 was evaluated against the phenylacetaldehyde cyanohydrin substrate (for which this enzyme does not exhibit activity), and no activity was observed.

5 [000456] The OPA assay was found to detect the presence of both α -hydroxy and α -amino nitrile substrate. Aromatic compounds were readily detectable with the assay, while aliphatic compounds posed some detection challenges. No background issues were evident when using lyophilized cell lysates, *in-situ* lysed whole cells or unlysed whole cells. The assay is amenable to one-plate analysis, where cells are grown, incubated with the substrate, and assayed on the same plate: no liquid transfers are required, easing automation. While all nitriles tested produced a linear response, aliphatic compounds gave a low fluorescent
10 response.

Chiral LDH Assay

[000457] A spectroscopic system based on lactate dehydrogenase (L-LDH) was developed for the analysis of the chiral α -hydroxy acids which are generated by the nitrilase catalyzed hydrolysis of cyanohydrins. The hydroxynitrile substrate is not metabolized by the
15 secondary or detection enzyme and thus starting material does not interfere. Cell lysate which is not heat treated results in background activity for the LDH system; however, heat inactivation or pelleting of the cell lysates eliminates the background activity. (See Figure 4.)

[000458] The activity and enantiomeric specificity of commercially available D- and L-lactate dehydrogenases against the nitrilases disclosed herein was evaluated. An LDH was identified which is suitable to both D- and L-phenyl lactic acid analysis. An enzyme suitable for 2-Chloromandelic acid analysis was not found. The chosen LDH enzymes exhibited virtually absolute stereoselectivity. The viability of the assay to detect D- and L-LDH produced from PAC using lyophilized cell lysate was established.

25 [000459] Originally, three colorimetric dyes were evaluated, all of which are tetrazolium salts: NBT (3,3'-dimethoxy-4,4'-biphenylene)bis[2,(4-nitrophenyl)-5-phenyl-2H]-, chloride) MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) INT (2-(4-Iodophenyl)-3-(4-nitrophenyl)-5-phenyl-2H-tetrazolium chloride). The insolubility of the product of these detection system posed an analytical challenge. To address this, another
30 tetrazolium salt with a reportedly soluble product, XTT (2,3-Bis-(2-methoxy-4-nitro-5-sulfophenyl)-2H-tetrazolium-5-carboxanilide, was evaluated. While XTT yielded a soluble bright red product, the substrate was insoluble which thus effected the same analytical challenges. As an alternative to the tetrazolium family of dyes, the dual

colorimetric/fluorometric dye resazurin was evaluated. Oxidation of resazurin produces resorfin. Both substrate and product are soluble, and the color change can be quantified colorimetrically or fluorimetrically, increasing accuracy. Due to the sensitivity of resazurin, 0.05 mM of lactic acid can be quantified. Optimal results were obtained when using the dye in the same range as the substrate, *e.g.* 0.5 mM resazurin can quantify a range of lactic (and analogs) from 0.05 to 0.5, though the best linearity is at the lower end of this scale. Resorfin was stable over 28 hours, and had a linear fluorescent response.

[000460] In the presence of the LDH assay components, lyophilized enzyme gave background fluorescence/absorption. To address this problem the lysate was boiled for 10 minutes and then centrifuged. This resulted in a 90% decrease in background signal. Interestingly, both centrifugation alone (5 minutes @ 14.1 rcf) or boiling followed by centrifugation (5 minutes @ 100°C) reduced the fluorescence to background levels. In a high-throughput format such as 1536 well plates, spinning would be preferable to boiling, as boiling would increase evaporation (8 µl well size) and potentially volatilize the nitrile substrates. No background signal resulting from growth media (LB and TB and M9) or cell lytic solutions (B-PER, CellLytic and BugBuster) was noted.

Chiral AAO Assay

[000461] A spectroscopic system based on amino acid oxidase (AAO) was developed for the analysis of the chiral α -amino acids which are generated by the nitrilase catalyzed hydrolysis of amino nitriles.

Assay Development and Validation

[000462] The initial assay validation utilized the 2,2'-azino-di-{3-ethylbenzothiazoline-6-sulfonic acid (ABTS) detection system as outlined above. However, since the color was not stable further investigations utilized the phenol amino antipyrine (PAAP) detection system which is analyzed at λ max 510nm. Enzymes with suitable activity were found for each enantiomer of 4-methyl- leucine, phenylalanine, (S)-2-amino-6-hydroxy hexanoic acid, and *tert*-leucine. The assay is not applicable to methylphenylglycine and does not work well with phenylglycine.

[000463] Standard curves were generated for phenylalanine from 0-15 mM. The curve is much more linear when the concentrations remained below 1 mM. The color remains stable for several days as long as it is kept in the dark. Three cell lysing solutions Bug Buster

(BB), Bacterial Protein Extracting Reagent (BPER), and Cell Lytic Reagent (CLR) were added to the standard curve and shown to have no affect on color development. The addition of cell lysate (cl) did not exhibit background color formation. Addition of the phenylacetaldehyde aminonitrile sulfate (PAS) starting material also showed no effect on color formation.

[000464] The AAO system exhibits greater linearity at up to 1 mM substrate. The concentration of the AAO enzymes and of the acid substrate were adjusted to try to move the intersection of the L-AAO and D-AAO curves closer to the middle of the graph. Premixing the PAAP, the HRP, and the AAO was demonstrated to be effective and caused no change in observed activity establishing that the assay components may be added to the assay in a cocktail format.

[000465] A high level of background was observed for the AAO assay of whole cells and this was attributed to the L-amino acids present in the TB and LB growth media. Washing and resuspension of the cells in M9 media eliminated background. For all future experiments cells were grown in M9 media with 0.2% glucose. The lysed cells gave only a slightly better response than unlysed cells. Therefore, cell lysis is not necessary. SEQ ID NOS:187, 188 demonstrated activity on HPA in primary screening based on HPLC analysis.

[000466] The use of a fluorescent detection system which would permits implementation of the assay in ultra high throughput fashion such as 1536 well or gigamatrix format was investigated. The fluorescent reagent most applicable to our system is Amplex Red from Molecular Probes which produces the highly fluorescent resorufin (λ_{ex} 545 nm; λ_{em} 590nm) Standard curves for phenylalanine and (S)-2-amino-6-hydroxy hexanoic acid were established (0-100 μM).

[000467] In preparation for assay automation, nitrilase expressing cells were added into microtiter plate containing M9 0.2% glucose, 0.25 mM IPTG media by fluorescence activated cell sorting (FACS). Three nitrilase expressing subclones, and the empty vector control were evaluated: SEQ ID NOS:101, 102, SEQ ID NOS:187, 188, SEQ ID NOS:29, 30 and the empty vector. The viability of the cells following cell sorting proved to be inconsistent. Thus colony picking is currently being evaluated as an alternative method to add cells into microtiter plates. The evaporative loss from an uncovered 1536-well microtiter plate is approximately 30% per day in the robot incubator (incubator conditions: 37°C at 85% relative humidity (RH)). Incubation in the 95% RH incubator reduced evaporative loss to 1% per day.

[000468] The ability of the three subclones to grow in the presence of up to 3.5 mM of nitrile was established using HPA nitrile. Growth rates were only slightly retarded (less than 30%). Subclones grown in the presence of HPA were shown to express a nitrilase that catalyzes the formation of hydroxy norleucine (HNL) as established using the Amplex Red detection system. Only *S* was evaluated as the enzymes are *S*-selective. The reaction plate was read at 10 minute intervals, with 40 minutes showing the best linearity. While cell growth is significantly inhibited above 5 mM of HPA when the cells were grown at pH 7, growth was inhibited above 0.1 mM HPA for cells grown at pH 8.

[000469] In order to verify the AAO results by HPLC, a reaction was performed using high concentrations of HPA, up to 40 mM (due to HPLC detection challenges for (S)-2-amino-6-hydroxy hexanoic acid) and lyophilized cell lysate SEQ ID NOS:187, 188.

Comparison AAO and HPLC data for HNL

[HNL] mM	%ee		%conversion	
	AAO	HPLC	AAO	HPLC
40	89%	100%	17%	18%
30	89%	97%	29%	36%
20	86%	97%	21%	34%
10	78%	98%	13%	35%

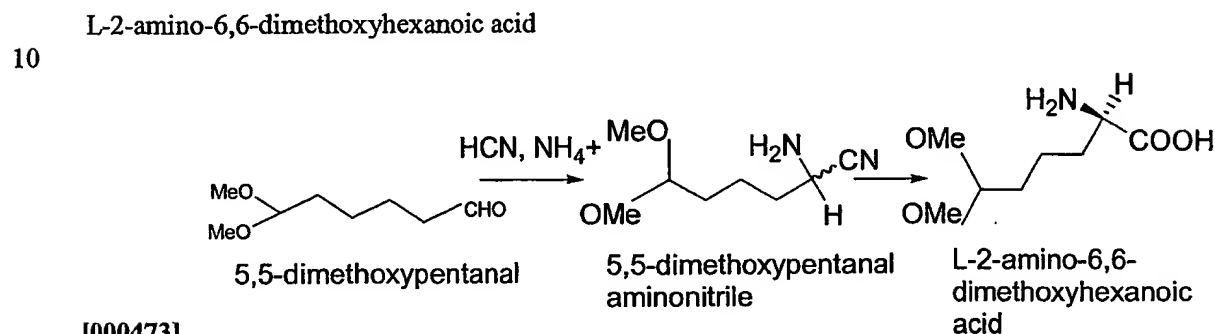
[000470] In order to determine if conducting the screen at a lower concentration introduces a bias in the results compared to the 20 mM substrate range that was used for HPLC based screens, an experiment was performed with SEQ ID NOS:187, 188 using three concentration ranges. Each experiment was done in triplicate in order to remove any nonsystematic error.

[000471] The AAO assay can be run on 384 or 1536 well format with cells sorted into an M9 0.2% glucose, 0.25 mM IPTG media. Cells can be grown in the presence of nitrile (in this case HPA), or the cells can be allowed to reach a certain density and the nitrile can then be added. Though cell lytic reagents do not interfere with the assay, when HPA was assayed, addition of the lytic reagents was found to be unnecessary. Either pre- or post- nitrile addition, the mother plate will have to be split into daughter plates, which are then assayed for the respective L- and D- enantiomer content. Incubation times with the AAO/Amplex Red reagents can be adjusted so that the D- and L- plate are read at separate times.

Example 16: Identification, Development and Production of Robust, Novel EnzymesTargeted for a Series of High-Value Enantioselective Bioprocesses

[000472] The invention provides for the development of nitrilases, through directed evolution, which provide significant technical and commercial advantages for the process

5 manufacturing of the following chemical target:



[000473]

Nitrilase enzymes were shown to hydrolyze 2-amino-6-hydroxy hexanenitrile to (S)-2-amino-6-hydroxy hexanoic acid, with selectivity towards the L-enantiomer. The panel of nitrilases was screened against the target, 5,5-dimethoxypentanal aminonitrile. The positive enzymes were characterized on this substrate. A primary screen is used to identify putative up-mutants, which is then confirmed using HPLC.

[000474] GSSM™ and GeneReassembly™ are performed on selected nitrilases, in order to improve the enantioselectivity and activity of the enzymes for the production of L-2-amino-6,6-dimethoxyhexanoic acid. Nitrilases were identified for the enantioselective hydrolysis of 2-amino-6-hydroxy hexanenitrile to L-(S)-2-amino-6-hydroxy hexanoic acid. However, a slight structural difference is presented by the new target molecule, L-2-amino-6,6-dimethoxyhexanoic acid. In order to determine whether this difference affects the activity and enantioselectivity of the enzymes, the complete spectrum of nitrilases was screened against the new target.

25 [000475] First, identification of the correct target gene for GSSM through more detailed characterization of the hit enzymes for the production of L-2-amino-6,6-dimethoxyhexanoic acid was carried out. This effort involves a more extensive investigation of the effects of pH

and temperature on activity and enantioselectivity and a more in-depth analysis of the stability of the enzyme to process conditions. Prior to initiation of the screening, the synthesis of a single enantiomer of an alkyl aminonitrile is done; the racemization of this nitrile is studied, in an effort to understand the relationship between this factor and

5 enantioselectivity of the enzymes.

An enzyme exhibiting the highest combination of activity and enantioselectivity for the production of L-2-amino-6,6-dimethoxyhexanoic acid is selected for GSSM. Following the mutation of the target enzyme, the resulting mutants are screened on 5,5-dimethoxypentanal aminonitrile, using high throughput screening technology. Following

10 confirmation of the up-mutants by HPLC analysis a decision point is reached, in order to evaluate the results of the GSSM on the target.

[000476] In parallel to GSSM™, a GeneReassembly™ is performed on a combination of parent enzymes, at least one of which is selected for activity and enantioselectivity on L-2-amino-6,6-dimethoxyhexanoic acid. At least two other nitrilases are reassembled with the

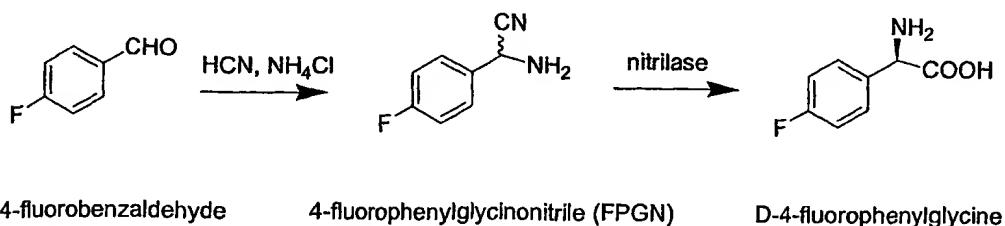
15 former enzyme(s); these enzymes are selected in order to provide diversity to the reassembled sequences.

[000477] The present invention provides for development of racemization conditions for the original substrate aminonitriles. In addition, the present invention provides for the identification of enzymes capable of the conversion of these aminonitriles to the target α-

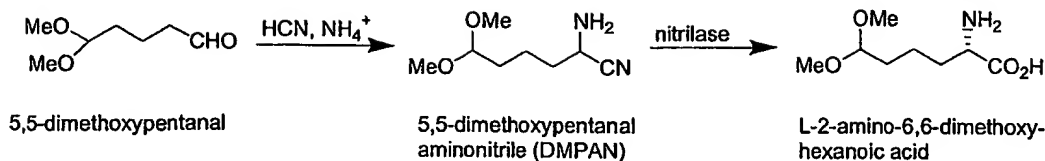
20 amino acids by dynamic kinetic resolution. The present invention also provides for screening and development of a nitrilase-catalyzed kinetic resolution process for (R)-2-amino-6,6-dimethoxy hexanoic acid (allysine) production. (S)-2-amino-6-hydroxy hexanoic acid will be used as a model substrate for development of the kinetic resolution.

The target α-amino acid products are shown below:

25 (i) D-4-Fluorophenylglycine



(ii) L-2-Amino-6,6-dimethoxyhexanoic acid (Allysine)



[000478] Conditions are developed for the racemization of the aminonitrile substrates for the nitrilase-catalyzed production of D-4-fluorophenylglycine and 2-amino-4,4-dimethyl pentanenitrile (allysine). Two model substrates, phenylglycinonitrile and pentanal

5 aminonitrile are used initially, and racemization is studied in the absence of the enzyme. Concurrently determination of the performance of one or more available nitrilases under a variety of possible racemization conditions is carried out. In addition, the nitrilases are screened against hydroxypentanal aminonitrile for the production of (S)-2-amino-6-hydroxy hexanoic acid, and the promising enzymes are optimized. Once racemization conditions are

10 established, the nitrilases are screened for activity. Further optimization for a kinetic resolution of the product is performed.

[000479] A number of enantioselective nitrilases were identified for the hydrolysis of α -aminonitriles to α -amino acids. While these enzymes were shown to have a preference for the required enantiomer of certain aminonitriles, a limiting factor in the further screening,

15 development and comparison of candidate nitrilases is the rate of racemization of the aminonitrile substrates under the reaction conditions.

Aromatic aminonitrile racemization

[000480] The first step is to establish conditions under which aromatic aminonitrile racemization occurs, using the model substrate, phenylglycinonitrile. Racemization strategies

20 include, but are not limited to the list below. Options are roughly prioritized according to their commercial applicability.

- (1) Manipulation of the pH of the reaction. Since it has been shown that racemization is rapid at high pH, this approach requires the discovery and optimization of nitrilases which are active and selective at $\text{pH} > 10$.
- 25 (2) Addition of known chemical racemizing agents, such as aldehydes, ketones, weak bases, resins, metal ions, Lewis acids etc., which can enhance racemization at lower pH.
- (3) Synthesis of N-acylated aminonitrile derivatives, e.g. N-acetyl phenylglycinonitrile, which may be more easily racemized. In the case of N-acetyl phenylglycinonitrile, a selective D-acylase which removes the acetyl group would enhance the optical purity of the nitrilase product.
- 30 (4) Use of a biphasic system in which base-catalyzed racemization occurs in the hydrophobic organic phase and enzymatic hydrolysis in the aqueous phase.

(5) Use of a 2-enzyme system comprised of a nitrilase and an aminonitrile racemase. One amino acid racemase is commercially available at present, and will be tested for activity against phenyl- and fluorophenylglycinonitrile. Gene libraries will be searched for genes showing homology to known amino acid amide racemases, hydantoin racemases or any other racemases which can be identified.

5 [000481] Once conditions for this racemization have been established, they provide the basis for development of conditions for racemization of the target aromatic substrate, 4-fluorophenylglycinonitrile (FPGN). The FPGN is expected to be less stable than the model substrate; thus, it may racemize more quickly, but degradation reactions may be faster as well. The ability of sample enzyme(s) to tolerate and/or function well under them is
10 evaluated. Final optimization of screening methods include the target substrates, sample nitrilases, and substrate racemization conditions.

[000482] Investigations carried out have shown that phenylglycinonitrile is easily racemized at pH 10.8. However, it does not appear that any of the existing enzymes can tolerate such harsh conditions of pH. Samples from highly alkaline environments are
15 screened for the presence of nitrilases which are tolerant to such conditions. Once discovered, the enzymes are sequenced and subcloned, and the enzymes are produced as lyophilized cell lysates ready for screening.

Aliphatic aminonitrile racemization

[000483] A model aliphatic aminonitrile, pentanal aminonitrile, is synthesized in its
20 racemic form. However optically enriched samples are prepared using one the following approaches: (i) preparative chiral HPLC; (ii) diastereomeric salt resolution; (iii) diastereomeric derivatization or column chromatography; (iv) synthesis from L-N-BOC norleucine. An HPLC assay is used for the detection of these compounds.

HPLC Assay

25 [000484] An HPLC assay for the detection of the (S)-2-amino-6-hydroxy hexanoic acid is used. An assay involving pre-column derivatization is used.

Screening/Characterization:

[000485] Nitrilases are screened against 2-amino-6-hydroxy hexanenitrile. For enzymes capable of performing well at greater than 25 mM substrate, scale up reactions are performed.
30 The substrate/product tolerance and stability profiles of the other enzymes are investigated.

[000486] The nitrilases are screened, and hits are characterized, focusing on pH and temperature optimum, enantioselectivity and stability under the reaction conditions.

Enzyme Evolution

[000487] A target enzyme exhibiting the desired properties is selected for GSSM™.

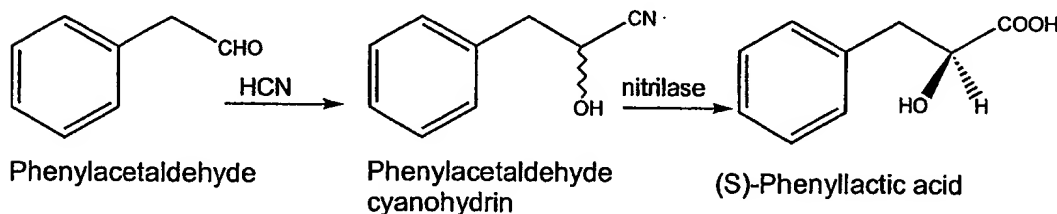
Following the mutation of the target enzyme, the resulting mutants are screened on the substrate using high throughput screening technology. Once the up-mutants have been

5 confirmed by HPLC analysis, the individual mutations responsible for increased performance may be combined and evaluated for possible additive or synergistic effects.

[000488] In addition, a GeneReassembly™ will be performed on a combination of lead enzymes, which are selected for their desirable characteristics, including activity, enantioselectivity and stability in the reaction.

10 Example 17: Optimization of Nitrilases for the Enantioselective
Production of (S)-Phenyllactic Acid

[000489] Nitrilases were identified for the enantioselective hydrolysis of 5 different nitrile substrates. These nitrilases were isolated and optimized for selected targets. The optimization involves process optimization and directed evolution. In particular, enzymes specific for the
15 production of (S)-phenyllactic acid were characterized and optimized. This was aimed primarily at improving the activity of the enzymes, while maintaining a high enantioselectivity. An investigation into the effects of process conditions on the enzymes was also performed.



20 [000490] The development of high throughput assays for screening of mutants from potential directed evolution efforts was accomplished. Two achiral and two chiral colorimetric assays that are amenable to high throughput screening were developed and used for nitrilase directed evolution.

[000491] SEQ ID NOS:103, 104 was identified as a highly enantioselective nitrilase for
25 the production of (S)- phenyllactic acid. Characterization of SEQ ID NOS:103, 104 shows the optimum reaction pH and temperature to be pH 8 and 37°C, respectively; the reaction starting material, phenylacetaldehyde, and the product, phenyllactic acid showed no effect on

the enzyme activity up to levels of 5 mM and 30 mM, respectively. The scaled-up enzymatic reaction with an enantiomeric excess (*ee*) of 95%.

Example 18: Directed Evolution of a nucleic acid encoding a nitrilase enzyme.

[000492] The *nitB* gene (GenBank Accession No. AX025996, from *Alcaligenes*
5 *faecalis*) was subjected to Gene Site Saturated Mutagenesis™ or GSSM™ to generate a library of single amino acid substitution mutants covering the entire enzyme. The sequence of the "parental" *nitB* gene used in the directed evolution is SEQ ID NO: 103, 104. A *nitB* mutant library was generated from carrying out GSSM™. This *nitB* mutant library was then screened for clones with increased whole cell hydroxymethylthiobutyronitrile (HMTBN,
10 which is a nitrilase substrate) activity. The product of the nitrilase reaction on that substrate is hydroxymethylthiobutyric acid (HMTBA).

[000493] Assays were run at 35°C with 100mM HMTBN and 100mM K₃PO₄, pH 7 to approximately 30-40% conversion. Two methods were used to quantitate HMTBN conversion, one being direct measurement of HMTBS produced by HPLC analysis and the
15 other being indirect detection of residual HMTBN using the fluorescent cyanide assay, which has previously been described.

[000494] Putative *nitB* up mutants were subjected to a secondary assay to confirm the increased activity. In the secondary assay, up mutants and the wild type control were induced in expression medium in shake flasks. Shake flask cultures are then washed with 100mM
20 K₃PO₄, pH7 and resuspended to the same optical density at 660nm. Kinetic assays were then performed with the normalized cell resuspensions under the same conditions used in the initial assays. Putative up mutants confirmed to have increased HMTBN activity were sequenced and tested for increased activity after transformation back into the same expression strain to ensure that increases in activity are not due to host mutations.

25 [000495] A confirmed *nitB* GSSM™ up-mutant is *nitB* G46P, which contains a glycine (GGT) to proline (CCG) substitution at amino acid 46. The whole cell HMTBN activity of this mutant is approximately 50% greater than that of wild type NitB at both 25°C and 35°C. Upon identification of the beneficial G46P mutation, GSSM™ was used again to generate a pool of double mutants using the *nitB* G46P template. These mutants all contain the G46P
30 mutation and an additional single amino acid substitution at a random site. The double mutants were assayed for HMTBN activity greater than that of *nitB* G46P. Double, triple and quadruple mutants were created in order to speed up the mutation process and identify beneficial mutations more quickly. After the first few beneficial mutations were identified

and isolated, they were combined to generate double mutants, the best of which was DM18. DM18 was used as a template to generate triple mutants. The most active triple mutant was TM3 and that was used as a template to generate quadruple mutants. The most active quadruple mutant was QM2. The table summarizes these mutations.

mutant	mutation 1	mutation 2	mutation 3	mutation 4
DM18	R (gcg) 29 C(tgt)	Y(tac) 207 M (atg)		
TM3	R (gcg) 29 C(tgt)	Y(tac) 207 M (atg)	L(ctt) 170 T(act)	
QM2	R (gcg) 29 C(tgt)	Y(tac) 207 M (atg)	L(ctt) 170 T(act)	A(gcg) 197 N9(aat)

5

[000496] The mutants were characterized first by studying their whole cell HMTBN activity. At 100 mM HMTBN, the HMTBS production rate of QM2 is 1.2 times greater than that of the parental gene. However, at 200 mM HMTBN, the rate of QM2 is 3.6 times that of the parental gene. The productivity of these mutants is increased considerably when the HMTBN concentration is raised from 100 mM to 300 mM. As to conversion rates, TM3 completely converted the substrate after 270 minutes and both DM18 and SM show greater than 75% conversion after this time. To further address the issue of HMTBN concentration effects on activity/productivity of NitB, several mutants were assayed at both 400 mM and 528 mM HMTBN. NitB is essentially inactive at these substrate concentrations, however the mutants retain significant activity at these concentrations. In particular, the activity at these high concentrations were essentially the same as their activity at 200 mM substrate. Therefore, the mutants can be used over a wide substrate concentration range and provide much more flexibility in utility than the NitB parental gene.

[000497] The mutants were shown to have higher expression levels than the parental gene and it also appeared that the QM2 and TM3 mutants contained a greater proportion of soluble enzyme than the wild type as seen in SDS-PAGE analysis. As to stability, all of the enzymes showed essentially the same stability pattern at both 25°C and 35°C.

[000498] Finally, the mutants were subjected to codon-optimization. The approach was to optimize the codons and therefore increase the expression levels in the particular host cell. That would, in turn, increase the activity per cell of the enzyme. This resulted in increased whole cell activity in the codon-optimized mutants as compared to controls. The increase in activity was approximately double the activity. An *E. coli* expression system was used.

Example 19: Selected Examples of Compounds Produced From a Nitrilase-Catalyzed Reaction

[000499] The compounds listed in Figure 15 are selected compounds that can be produced from a nitrilase-catalyzed reaction using an enzyme and/or a method of the invention.

[000500] In addition, the following are potential products which can be made via the nitrilase Strecker format. More than 100 amino acids and many new drugs can be produced
5 from their respective aldehydes or ketones utilizing the nitrilase enzymes of the invention. For example, large market drugs which can be synthesized using nitrilases of the invention include homophenylalanine, VASOTEC™, VASOTERIC™, TECZEM™, PRINIVIL™, PRINZIDE™, ZESTRIL™, ZESTORETIC™, RAMACE™, TARKA™, MAVIK™, TRANDOAPRIL™, TRANDOLAPRILAT™, ALTACE™, ODRIK™, UNIRETIC™,
10 LOTENSIN™, LOTREL™, CAPOTEN™, MONOPRIL™, TANATRIL™, ACECOL™, LONGEST™, SPIRAPRIL™, QUINAPRIL™, and CILAZAPRIL™. Other chiral drugs include DEMSER™ (alpha-methyl-L-Tyrosine), ALDOCHLOR™, LEVOTHROID™, SYNTHROID™, CYTOMEL™, THYOLAR™, HYCODAN™, CUPRIMINET™, DEPEN™, PRIMAXIN™, MIGRANOL™, D.H.E.-45, DIOVAN™, CEFOBID™, L-
15 DOPA, D-DOPA, D-alpha-methyl-DOPA, L-alpha-methyl-DOPA, L-gamma-hydroxyglutamate, D-gamma-hydroxyglutamate, 3-(2-naphthyl)-L-alanine, D-homoserine, and L-homoserine.

[000501] Furthermore, the nitrilase enzymes of the invention can be useful for synthesizing the following amino acids. Many of these amino acids have pharmaceutical applications. D-
20 phenylglycine, L-phenylglycine, D-hydroxyphenylglycine, L-hydroxyphenylglycine, L-tertiary leucine, D-tertiary leucine, D-isoleucine, L-isoleucine, D-norleucine, L-norleucine, D-norvaline, L-norvaline, D-2-thienylglycine, L-2-thienylglycine, L-2-aminobutyrate, D-2-aminobutyrate, D-cycloleucine, L-cycloleucine, D-2-methylphenylglycine, L-2-methylphenylglycine, L-thienylalanine, and D-thienylalanine.

[000502] The enzymes of the nitrilase enzymes of the invention can be useful for the synthesis of the following natural amino acids: glycine, L-alanine, L-valine, L-leucine, L-isoleucine, L-phenylalanine, L-tyrosine, L-tryptophan, L-cysteine, L-methionine, L-serine, D-serine, L-threonine, L-lysine, L-arginine, L-histidine, L-aspartate, L-glutamate, L-asparagine, L-glutamine, and L-proline. The following are examples of unnatural amino acids which can
30 be produced using the nitrilase enzymes of the invention. D-alanine, D-valine, D-leucine, D-isoleucine, D-phenylalanine, D-tyrosine, D-tryptophan, D-cysteine, D-methionine, D-threonine, D-lysine, D-arginine, D-histidine, D-aspartate, D-glutamate, D-asparagine, D-glutamine, and D-proline.

[000503] Furthermore, nitrilase enzymes of the invention can be used in non-Strecker chemical reactions including the synthesis of more chiral drugs such as TAXOTERE™ as well as chiral drugs containing 3-hydroxy-glutaronitrile (a \$5.5B market); LIPITOR™, BAYCOL™, and LESCOT™. Chiral product targets that are not drugs include

- 5 PANTENOL™, L-phosphinothricin, D-phosphinothricin, D-fluorophenylalanine, and L-fluorophenylalanine. Finally, nitrilase can be used to produce unnatural amino acid compounds lacking a chiral center such as sarcosine, iminodiacetic acid, EDTA, alpha-aminobutyrate, and beta-alanine.

Figure 16 examples of substrates and products produced by the nitrilases of the invention and/or the methods of the invention. The chemical structures of the substrates and of the products are shown. The chemical reactions shown here are non-limiting examples of activities of the nitrilases of the invention.

Example 20: Exemplary Preparation Using a Polypeptide of a Variant of SEQ ID NO:210

[000504] The variant, nitrilase 1506-83-H7A, is SEQ ID NO:210 with the Ala at residue 15 190 replaced with His. At the codon level, the mutation that occurred was GCT to CAT. This variant exhibits improved enantioselectivity in the conversion of 3-hydroxyglutaryl nitrile (HGN) to (R)-4-Cyano-3-hydroxybutyrate.

[000505] This variant has been demonstrated to perform this transformation in 100 mM pH 7 sodium phosphate buffer at room temperature. This mutant can perform in other buffer 20 systems and temperatures as well with the potential for providing additional altered properties. Exemplary properties include, but are not limited to, altered rates of the reaction, % ee, and stability. In particular, the altered properties can be a higher reaction rate, a higher % ee, and greater stability. Altered properties can be an increase or decrease of at least 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95% more than 25 wildtype.

[000506] This variant was shown to perform the transformation by producing products in high enantiomeric excess of 10 mM to 3 M substrate (HGN). Higher or lower substrate concentrations are also possible. Enantiomeric excess greater than or equal to 95% have been achieved. However, enantiomeric excess can be at least 25%, 30%, 35%, 40%, 45%, 50%, 30 55%, 60%, 65%, 70%, 75%, 80%, 85%, or 90% more than wildtype.

[000507] Variants of the SEQ ID NOs: of the invention, can be cloned into expression vectors. For example, variants of nucleic acid sequence SEQ ID NO:195, 205, 207, 209, OR 237, and nucleotides that encode the variants of amino acid sequence SEQ ID NO:210 can

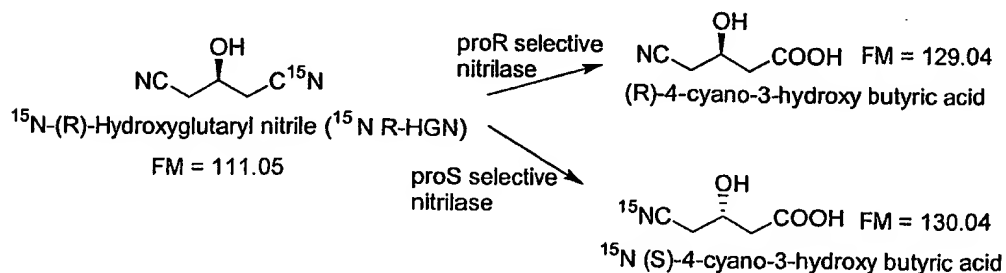
be cloned into exemplary vectors that include, but are not limited to, pSE420 (E. coli expression vector) and pMYC (pseudomonas expression vector).

Example 21: Preparation using variants of the invention:

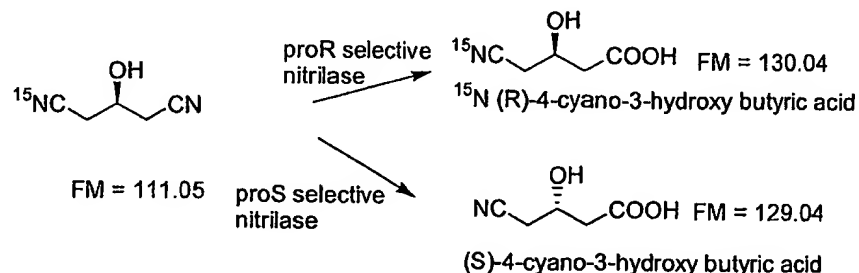
- [000508] Add 3-Hydroxyglutaronitrile (1 g, 9 mmol) drop-wise to a stirred solution of nitrilase cell lysate (normalized for 150 mg protein content) in 2.12 mL of 100 mM pH 7 sodium phosphate buffer at room temperature, ~22 °C. Stir this 3 M reaction by magnetic stir bar for 24 hours at room temperature. Monitor the progress of the reaction by TLC (Thin Layer Chromatography) and GC (Gas Chromatography). The reaction should be complete within 24 hours.
- [000509] Other variants contemplated herein include, but are not limited to the following: N111S; A190H, S, Y or T; F191L, V, M, D, G, E, Y or T; M199E, orL; D222L; A55K, G, or Q; I60E, or any combination thereof.

Example 22: Screening Assay for Enantioselective Transformation

- [000510] A new method to screen for enantioselective transformation, for example, of a prochiral substrate into a chiral one that affords the ability to monitor enantiomeric excess (% ee) of the resultant product is disclosed. This approach can also be applied to determine diastereomeric excess (% de).
- [000511] For example, by labeling one of the two prochiral or enantiotopic moieties in a molecule, for example by the use of a heavier or lighter isotope, the modification of one of the two moieties by a selective catalyst, for example, an enzyme, can be established by mass spectroscopy (MS).
- [000512] By performing the exemplary nitrilase reaction on ^{15}N -(R)-HGN (R) (as shown in Figure 17) or ^{15}N -(S)-HGN, one can determine the enantioselectivity of the enzyme by analyzing the amount of each of the two possible labeled versus unlabeled acid products which can be formed.



[000513] The screening experiment may be performed in either direction. The screening experiment can be used for both the ^{15}N -(R)- and (S)-HGN moieties. In fact, to ensure that the label does not effect any artifactual changes, at the onset, both should be investigated.

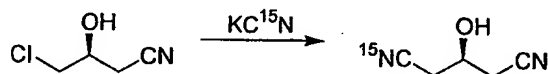


[000514] To equate the observed enantiomeric excess resulting from the nitrilase transformation, the following exemplary formula may be applied:

$$\% \text{ ee} = \{[130] - [129]\} / \{[130] + [129]\},$$
 where each concentration of the light acid (129) and the heavy acid (130) are determined by correlation of the peak area on the mass spectrometer to a standard curve or by direct comparison of the areas of each of the 129 and 130 mass peaks. The actual mass units used to determine the relative amounts of each of the two enantiomers (labeled and unlabelled) are dependent on how the mass spectrometer is tuned.

[000515] In some cases, the % ee observed by mass spectrometry may differ by a factor from that observed by an alternate analytical technique such as liquid chromatography due to background or contaminating peaks resulting from natural isotopic abundance. This does not, however, affect the final outcome of the screening process. Exemplary standard curves for quantification of heavy acid and light acid are shown in Figures 14 A and B.

[000516] The following reaction is a possible synthetic route to prepare, for example, ^{15}N (R)-HGN using chemistry techniques known in the art with commercially available starting materials.



[000517] The amount of each of the two possible stereomeric outcomes can be established by the use of MS in either positive mode, negative mode and from analysis of either of the parental mass or of any fragmentation mass.

Example 23: Stability and activity of exemplary enzymes of the inventionEnzyme stability:

Wild-type enzyme (SEQ ID NOS:209 and 210) was compared to mutant A190H of SEQ ID NOS:209 and 210. In the experiment, each enzyme was incubated at 10 mg/ml in water for 1, 25, 50, 75 and 150 hours at 4°C and at 21°C, on two different substrates: adiponitrile and hydroxyglutaryl nitrile. Both enzymes, in all conditions, were found to retain activity for 150 hours. The wild-type enzyme showed greater activity on adiponitrile, while the mutated (A190H) enzyme showed greater activity on hydroxyglutaryl nitrile, as assessed by the Nitroprusside Bertholet assay (see, e.g., Fawcett, J. K. & Scott, J. (1960); J. Clin. Path., Vol. 13, pg 156).

GSSM™ Variant of SEQ ID NOS:209 and 210	100 mM hydroxyglutaryl nitrile ee%	2.25 mM hydroxyglutaryl nitrile ee%	Time to completion (hours)
A55G	96.5 ± 0.4	Not determined	>160
A55K	94.7 ± 0.2	Not determined	>160
I60E	96.5 ± 0.5	Not determined	>160
N111S	95.8 ± 0.5	96.1 ± 0.9	>160
A190T	96.5 ± 0.2	96.6 ± 0.4	40
A190S	96.8 ± 0.2	95.5 ± 0.7	40
A190H	97.9 ± 0.1	98.1 ± 0.1	15
F191L	97.9 ± 0.1	Not determined	>160
F191T	97.9 ± 0.1	Not determined	>160
F191M	97.9 ± 0.1	Not determined	>160
F191V	97.9 ± 0.1	Not determined	>160
M199E	97.9 ± 0.1	Not determined	160
M199L	97.9 ± 0.1	95.4 ± 0.1	>160
Wild type SEQ ID NOS:209 and 210	94.5 ± 0.1	87.8 ± 0.2	24

GSSM mutants with enhanced enantioselectivity

100 mM reactions were performed with nitrilase expressed from E. coli in whole cell format and were complete with 36 hours. 2.25 M reactions were performed with nitrilase as lyophilized clarified cell lysate. All % ee data reported are the average of three measurements, with standard deviation of the mean. The time for reaction completion was approximated by TLC.

Specifically:

Nitrilase Activity Assay, 100 mM HGN:

Putative nitrilase up-mutants were assayed in triplicate. Each transformant was grown in 5 mL LB (100 µg/mL ampicillin), at 37 °C, 220 rpm for 18 h. The overnight culture was diluted 2-fold and nitrilase expression induced at 37 °C, 220 rpm with 0.1 mM IPTG for 6 h. Cells were harvested by centrifugation, washed in 100 mM pH 7 sodium phosphate buffer and then re-suspended in 1 mL of 100 mM HGN in 100 mM pH 7 sodium phosphate buffer. Reactions were allowed to proceed for at least 36 h at 22 °C with gentle agitation. Reaction progress was monitored by TLC (1:1 EtOAc:Hexanes, R_f=0.5, nitrile; R_f=0.0, acid). Cells and other debris were removed by centrifugation and the treated with one volume methanol prior to lyophilization. The lyophilizate was re-suspended in methanol and treated with TMS-diazomethane (10 equivalents, 2 M solution in hexanes) until gas evolution ceased and yellow color persisted in order to prepare the methyl ester for GC analysis. Selected nitrilase variants producing (R)-(-)-3-hydroxy-4-cyanobutyric acid of 95% ee or greater were then evaluated for performance at 2.25 M HGN.

Nitrilase Activity Assay at 2.25 M 3-HGN:

3-HGN (0.2 g, 1.8 mmol, 3 M) was suspended in sodium phosphate buffer (0.6 mL, pH 7, 100 mM) at 22 °C. Cell lysate (6 mg, normalized for nitrilase content) was added to bring the concentration to 11 mg/ml enzyme and the reaction shaken (100 rpm, 22 °C). Reaction progress was monitored by TLC (1:1 ethyl acetate:hexanes, R_f = 0.32, nitrile; R_f = 0.0, acid). The reaction mixture was treated with one part methanol prior to lyophilization. The lyophilizate was re-suspended in methanol and treated with 10 equivalents of TMS-diazomethane (10 equivalents, 2 M solution in hexanes) to prepare the methyl ester and analyzed by GC.

Description of novel high throughput LC/MS method for screening high numbers of samples:

Ultra High-throughput Primary Chiral Activity Screen:

Distinct members of the GSSM library were arrayed into 384 well plates containing 40 µL of (Luria-Bertani) LB medium (100 µg/mL ampicillin) via an automated colony picker and then incubated at 37 °C, 85% humidity. Nitrilase expression was induced with 0.1 mM IPTG at 37 °C for 24 h. Each plate was replicated and 20% glycerol stocks prepared for archival at -80 °C. To each 384 well plate was added 10 mM 15N-(R)-1 substrate. The plates were incubated at 37 °C, 85% humidity for three days. Cells and other debris were removed by centrifugation and the supernatant was diluted 17,576-fold prior to MS analysis.

LC/MS ionspray was applied for high through-put analysis in the following manner. High-throughput screening was achieved by flow injecting samples from 384-well plates using a CTCPAL autosampler (Leap Technologies, Carrboro, N.C.). An isocratic mixture of 71% acetonitrile, 29% water, with 0.1% formic acid, provided by LC-10ADvp pumps (Shimadzu, Kyoto, Japan) at 2.2 mL/min through an LC-18 cartridge (Supelco, Bellefonte, PA) was used. Samples were applied to an API 4000 TurboIon spray triple-quadrupole mass spectrometer (Applied Biosystems, Foster City, CA). Ion spray and Multiple Reaction Monitoring (MRM) were performed for analytes in the negative ion mode, and each analysis took 60 seconds.

E. coli transformed with wild type enzyme (SEQ ID NOS:209 and 210) was used as a positive activity control and *E. coli* transformed with empty vector was used as the negative activity control. The % ee of the WT enzyme positive control determined by mass spectrometry using either 15N-(R)-1 or 15N-(S)-1 were the same, thus demonstrating the absence of a significant isotope effect.

Temp (°C)	pH	Sodium phosphate buffer conc. (mM)	% ee	Std. Dev.
4	7	100	98.7	0.1 %
19	7	100	98.7	0.1 %
21	7	100	98.6	0.1 %
37	7	100	98.4	0.1 %
21	7	100	98.6	0.1 %
21	6	100	98.6	0.1 %
21	8	100	98.6	0.1 %
21	7	100	98.5	0.1 %
21	7	50	98.6	0.1 %
21	7	25	98.7	0.1 %

Effect of reaction parameters on SEQ ID NOS:209 and 210 with the A190H mutation.

Reactions were performed at 3 M HGN concentration with 150 mg/ml protein (~49 mg/ml enzyme). % ee was determined by GC analysis in triplicate runs.

[000518] While the invention has been described in detail with reference to certain preferred aspects thereof, it will be understood that modifications and variations are within the spirit and scope of that which is described and claimed.

What is claimed is:

1. An isolated or recombinant nucleic acid comprising nucleotides having a sequence at least 50% identical to SEQ ID NO:195, 205, 207, 209, or 237, variants of SEQ ID NO:195, 205, 207, 209, or 237, having one or more mutations: at positions 163-165 AAA, AAG, GGT, GGC, GGA, GGG, CAA, or CAG; at positions 178-180 GAA or GAG; at positions 331-333 TCT, TCC, TCA, TCG, AGT, or AGC; at positions 568-570 CAT, CAC, TCT, TCC, TCA, TCG, AGT, AGC, ACT, ACC, ACA, TCA, TAT, TAC, ATG or ACG; at positions 571-573 TTA, TTG, CTT, CTC, CTA, CTG, GTT, GTC, GTA, GTG, ATG, ACT, ACC, ACA, GAT, GAC, GGT, GGC, GGA, GGG, GAA, GAG, TAT, TAC, or ACG; at positions 595-597 GAA, GAG, TTA, TTG, CTT, CTC, CTA, or CTG; at positions 664-666 TTA, TTG, CTT, CTC, CTA, or CTG; or any combination thereof, fragments thereof, wherein the nucleic acid or fragment encodes a polypeptide having nitrilase activity, or their complements.
2. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid comprises nucleotides having a sequence substantially identical to the SEQ ID NO:195, 205, 207, 209, or 237, or variants of SEQ ID NO:195, 205, 207, 209, or 237, having one or more mutations: at positions 163-165 AAA, AAG, GGT, GGC, GGA, GGG, CAA, or CAG; at positions 178-180 GAA or GAG; at positions 331-333 TCT, TCC, TCA, TCG, AGT, or AGC; at positions 568-570 CAT, CAC, TCT, TCC, TCA, TCG, AGT, AGC, ACT, ACC, ACA, TCA, TAT, TAC, ATG or ACG; at positions 571-573 TTA, TTG, CTT, CTC, CTA, CTG, GTT, GTC, GTA, GTG, ATG, ACT, ACC, ACA, GAT, GAC, GGT, GGC, GGA, GGG, GAA, GAG, TAT, TAC, or ACG; at positions 595-597 GAA, GAG, TTA, TTG, CTT, CTC, CTA, or CTG; at positions 664-666 TTA, TTG, CTT, CTC, CTA, or CTG; or any combination thereof, or their complements.
3. An isolated or recombinant nucleic acid comprising nucleotides having a sequence identical to the SEQ ID NO:195, 205, 207, 209, or 237, fragments having nitrilase activity, or their complements.
4. An isolated or recombinant nucleic acid comprising nucleotides having a sequence identical to a variant of SEQ ID NO:195, 205, 207, 209, or 237, having one or more

mutations: at positions 163-165 AAA, AAG, GGT, GGC, GGA, GGG, CAA, or CAG; at positions 178-180 GAA or GAG; at positions 331-333 TCT, TCC, TCA, TCG, AGT, or AGC; at positions 568-570 CAT, CAC, TCT, TCC, TCA, TCG, AGT, AGC, ACT, ACC, ACA, TCA, TAT, TAC, ATG or ACG; at positions 571-573 TTA, TTG, CTT, CTC, CTA, CTG, GTT, GTC, GTA, GTG, ATG, ACT, ACC, ACA, GAT, GAC, GGT, GGC, GGA, GGG, GAA, GAG, TAT, TAC, or ACG; at positions 595-597 GAA, GAG, TTA, TTG, CTT, CTC, CTA, or CTG; at positions 664-666 TTA, TTG, CTT, CTC, CTA, or CTG; or any combination thereof, fragments having nitrilase activity, or their complements.

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5. An isolated or recombinant nucleic acid that hybridizes to a nucleic acid of SEQ ID NO:195, 205, 207, 209, or 237, or variants of SEQ ID NO:195, 205, 207, 209, or 237, having one or more mutations: at positions 163-165 AAA, AAG, GGT, GGC, GGA, GGG, CAA, or CAG; at positions 178-180 GAA or GAG; at positions 331-333 TCT, TCC, TCA, TCG, AGT, or AGC; at positions 568-570 CAT, CAC, TCT, TCC, TCA, TCG, AGT, AGC, ACT, ACC, ACA, TCA, TAT, TAC, ATG or ACG; at positions 571-573 TTA, TTG, CTT, CTC, CTA, CTG, GTT, GTC, GTA, GTG, ATG, ACT, ACC, ACA, GAT, GAC, GGT, GGC, GGA, GGG, GAA, GAG, TAT, TAC, or ACG; at positions 595-597 GAA, GAG, TTA, TTG, CTT, CTC, CTA, or CTG; at positions 664-666 TTA, TTG, CTT, CTC, CTA, or CTG; or any combination thereof, fragments having nitrilase activity, or their complements.

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7. A nucleic acid probe comprising from about 15 nucleotides to about 50 nucleotides, wherein at least 15 consecutive nucleotides are at least 50% complementary to a nucleic acid target region within a nucleic acid sequence of SEQ ID NO:195, 205, 207, 209, or 237, or variants of SEQ ID NO:195, 205, 207, 209, or 237, having one or more mutations: at positions 163-165 AAA, AAG, GGT, GGC, GGA, GGG, CAA, or CAG; at positions 178-180 GAA or GAG; at positions 331-333 TCT, TCC, TCA, TCG, AGT, or AGC; at positions 568-570 CAT, CAC, TCT, TCC, TCA, TCG, AGT, AGC, ACT, ACC, ACA, TCA, TAT, TAC, ATG or ACG; at positions 571-573 TTA, TTG, CTT,

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CTC, CTA, CTG, GTT, GTC, GTA, GTG, ATG, ACT, ACC, ACA, GAT, GAC, GGT, GGC, GGA, GGG, GAA, GAG, TAT, TAC, or ACG; at positions 595-597 GAA, GAG, TTA, TTG, CTT, CTC, CTA, or CTG; at positions 664-666 TTA, TTG, CTT, CTC, CTA, or CTG; or any combination thereof, or their complements.

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8. A nucleic acid probe comprising at least 15 consecutive nucleotides of a nucleic acid target region within a nucleic acid sequence of SEQ ID NO:195, 205, 207, 209, or 237, or variants of SEQ ID NO:195, 205, 207, 209, or 237, having one or more mutations: at positions 163-165 AAA, AAG, GGT, GGC, GGA, GGG, CAA, or CAG; at positions 178-180 GAA or GAG; at positions 331-333 TCT, TCC, TCA, TCG, AGT, or AGC; at positions 568-570 CAT, CAC, TCT, TCC, TCA, TCG, AGT, AGC, ACT, ACC, ACA, TCA, TAT, TAC, ATG or ACG; at positions 571-573 TTA, TTG, CTT, CTC, CTA, CTG, GTT, GTC, GTA, GTG, ATG, ACT, ACC, ACA, GAT, GAC, GGT, GGC, GGA, GGG, GAA, GAG, TAT, TAC, or ACG; at positions 595-597 GAA, GAG, TTA, TTG, CTT, CTC, CTA, or CTG; at positions 664-666 TTA, TTG, CTT, CTC, CTA, or CTG; or any combination thereof, or their complements.

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9. A nucleic acid vector capable of replication in a host cell, wherein the vector comprises the nucleic acid of any one of claims 1 to 6, 12, or 13.

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10. A host cell comprising the nucleic acid of any one of claims 1 to 6, 12 or 13.

11. A host organism comprising the host cell of claim 10.

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12. An isolated or recombinant nucleic acid encoding a polypeptide comprising amino acids having a sequence at least 50% identical to SEQ ID NO:196, 206, 208, 210 or 238, or variants of SEQ ID NO:196, 206, 208, 210 or 238, having one or more mutations: at residue 55 lysine, glycine, or glutamine; at residue 60 glutamic acid; at residue 111 serine, at residue 190, serine, histidine, tyrosine or threonine; at residue 191, leucine, valine, methionine, aspartic acid, glycine, glutamic acid, tyrosine or threonine; at residue 199 glutamic acid or leucine; at residue 222 leucine; or any combination thereof, fragments encoding polypeptides wherein the polypeptides have nitrilase activity, or its complement.

13. An isolated or recombinant nucleic acid encoding a polypeptide comprising amino acids having a sequence of SEQ ID NO:196, 206, 208, 210 or 238, or variants of SEQ ID NO:196, 206, 208, 210 or 238, having one or more mutations: at residue 55 lysine, glycine, or glutamine; at residue 60 glutamic acid; at residue 111 serine, at residue 190, serine, histidine, tyrosine or threonine; at residue 191, leucine, valine, methionine, aspartic acid, glycine, glutamic acid, tyrosine or threonine; at residue 199 glutamic acid or leucine; at residue 222 leucine; or any combination thereof, fragments encoding a polypeptides having nitrilase activity, or its complement.
14. The isolated or recombinant nucleic acid of any one of claims 1 to 6, 12 or 13, wherein the nucleic acid is affixed to a solid support.
15. The isolated or recombinant nucleic acid of claim 14, wherein the solid support is selected from the group of a gel, a resin, a polymer, a ceramic, a glass, a microelectrode and any combination thereof.
16. An isolated or recombinant polypeptide comprising amino acids having a sequence at least 50% identical to SEQ ID NO:196, 206, 208, 210 or 238, or variants of SEQ ID NO:196, 206, 208, 210 or 238, having one or more mutations: at residue 55 lysine, glycine, or glutamine; at residue 60 glutamic acid; at residue 111 serine, at residue 190, serine, histidine, tyrosine or threonine; at residue 191, leucine, valine, methionine, aspartic acid, glycine, glutamic acid, tyrosine or threonine; at residue 199 glutamic acid or leucine; at residue 222 leucine; or any combination thereof, or fragments thereof, wherein the polypeptide has a nitrilase activity.
17. An isolated or recombinant polypeptide comprising amino acid having SEQ ID NO:196, 206, 208, 210 or 238, or variants of SEQ ID NO:196, 206, 208, 210 or 238, having one or more mutations: at residue 55 lysine, glycine, or glutamine; at residue 60 glutamic acid; at residue 111 serine, at residue 190, serine, histidine, tyrosine or threonine; at residue 191, leucine, valine, methionine, aspartic acid, glycine, glutamic acid, tyrosine or threonine; at residue 199 glutamic acid or leucine; at residue 222

leucine; or any combination thereof, or fragments thereof, wherein the polypeptide has nitrilase activity.

- 5 18. The isolated or recombinant polypeptide of any one of claims 16 or 17, wherein the fragment is at least 20 amino acids in length, and wherein the fragment has nitrilase activity.
- 10 19. A peptidomimetic of the polypeptide of claim 16 or claim 17 or fragments thereof having a nitrilase activity.
- 20 20. A codon-optimized polypeptide of the polypeptide of claim 16 or claim 17, or fragments thereof, having a nitrilase activity, wherein the codon usage is optimized for a particular organism or cell.
- 15 21. The polypeptide of claim 16 or claim 17 or fragments thereof, having a nitrilase activity, or a peptidomimetic thereof having a nitrilase activity, wherein the polypeptide, fragment, or peptidomimetic is affixed to a solid support.
- 20 22. The polypeptide of claim 21, wherein the solid support is selected from the group consisting of a gel, a resin, a polymer, a ceramic, a glass, a microelectrode and any combination thereof.
- 25 23. A purified antibody that specifically binds to the polypeptide of claim 16 or claim 17 or fragments thereof, having a nitrilase activity.
- 30 24. A fragment of the antibody of claim 23, wherein the fragment specifically binds to a polypeptide having a nitrilase activity.
25. An enzyme preparation which comprises at least one of the polypeptides of any one of claims 16 and 17, wherein the preparation is liquid or dry.
26. The enzyme preparation of claim 25, wherein the preparation is affixed to a solid support.

27. A composition comprising at least one nucleic acid of claims 1 to 6, 12, or 13 or comprising at least one polypeptide of claim 16 or claim 17 or fragments thereof, or a peptidomimetic thereof, having nitrilase activity, or any combination thereof.
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28. A method for hydrolyzing a nitrile to a carboxylic acid comprising contacting the molecule with at least one polypeptide of claim 16 or claim 17 or fragments thereof, or a peptidomimetic thereof, having nitrilase activity, under conditions suitable for nitrilase activity.
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29. A method for hydrolyzing a cyanohydrin moiety or an aminonitrile moiety of a molecule, the method comprising contacting the molecule with at least one polypeptide of any one of claim 16 or claim 17 or fragments thereof, or a peptidomimetic thereof, having nitrilase activity, under conditions suitable for nitrilase activity.
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30. A method for making a chiral alpha-hydroxy acid molecule or a chiral amino acid molecule, the method comprising admixing a molecule having a cyanohydrin moiety or an aminonitrile moiety with at least one polypeptide having an amino acid sequence at least claim 16 or claim 17 or fragments thereof, or a peptidomimetic thereof, having enantio-selective nitrilase activity.
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31. A method for making a composition or an intermediate thereof, the method comprising admixing a precursor of the composition or intermediate, wherein the precursor comprises a cyanohydrin moiety or an aminonitrile moiety, with at least one polypeptide of any one of claim 16 or claim 17 or fragments thereof or peptidomimetic thereof having nitrilase activity, hydrolyzing the cyanohydrin or the aminonitrile moiety in the precursor thereby making the composition or the intermediate thereof.
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32. A method for making an (*R*)-ethyl 4-cyano-3-hydroxybutyric acid, the method comprising contacting a hydroxyglutaryl nitrile with at least one polypeptide encoded by a nucleic acid having a sequence of SEQ ID NO:195, 205, 207, 209, OR 237, or a variant of SEQ ID NO:195, 205, 207, 209, or 237, having one or more mutations: at positions 163-165 AAA, AAG, GGT, GGC, GGA, GGG, CAA, or CAG; at positions
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178-180 GAA or GAG; at positions 331-333 TCT, TCC, TCA, TCG, AGT, or AGC; at positions 568-570 CAT, CAC, TCT, TCC, TCA, TCG, AGT, AGC, ACT, ACC, ACA, TCA, TAT, TAC, ATG or ACG; at positions 571-573 TTA, TTG, CTT, CTC, CTA, CTG, GTT, GTC, GTA, GTG, ATG, ACT, ACC, ACA, GAT, GAC, GGT, GGC, GGA, GGG, GAA, GAG, TAT, TAC, or ACG; at positions 595-597 GAA, GAG, TTA, TTG, CTT, CTC, CTA, or CTG; at positions 664-666 TTA, TTG, CTT, CTC, CTA, or CTG; or any combination thereof, or a fragment thereof encoding a polypeptide having nitrilase activity, that selectively produces an (*R*)-enantiomer, so as to make (*R*)-ethyl 4-cyano-3-hydroxybutyric acid.

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33. A method for making an (*S*)-ethyl 4-cyano-3-hydroxybutyric acid, the method comprising contacting a hydroxyglutaryl nitrile with at least one polypeptide having an amino acid sequence of any one of SEQ ID NO:196, 206, 208, 210 or 238, or a variant of SEQ ID NO:196, 206, 208, 210 or 238, having one or more mutations: at residue 55 lysine, glycine, or glutamine; at residue 60 glutamic acid; at residue 111 serine, at residue 190, serine, histidine, tyrosine or threonine; at residue 191, leucine, valine, methionine, aspartic acid, glycine, glutamic acid, tyrosine or threonine; at residue 199 glutamic acid or leucine; at residue 222 leucine; or any combination thereof, or a fragment or peptidomimetic thereof having nitrilase activity that selectively produces an (*S*)-enantiomer, so as to make (*S*)-ethyl 4-cyano-3-hydroxybutyric acid.

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34. A method for making an (*R*)-mandelic acid, the method comprising admixing a mandelonitrile with at least one polypeptide having an amino acid sequence of any one of SEQ ID NO:196, 206, 208, 210 or 238, or a variant of SEQ ID NO:196, 206, 208, 210 or 238, having one or more mutations: at residue 55 lysine, glycine, or glutamine; at residue 60 glutamic acid; at residue 111 serine, at residue 190, serine, histidine, tyrosine or threonine; at residue 191, leucine, valine, methionine, aspartic acid, glycine, glutamic acid, tyrosine or threonine; at residue 199 glutamic acid or leucine; at residue 222 leucine; or any combination thereof, or any fragment or peptidomimetic thereof having nitrilase activity.

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35. A method for making an (*S*)-mandelic acid, the method comprising admixing a mandelonitrile with at least one polypeptide having an amino acid sequence of SEQ ID

NO:196, 206, 208, 210 or 238, or a variant of SEQ ID NO:196, 206, 208, 210 or 238, having one or more mutations: at residue 55 lysine, glycine, or glutamine; at residue 60 glutamic acid; at residue 111 serine, at residue 190, serine, histidine, tyrosine or threonine; at residue 191, leucine, valine, methionine, aspartic acid, glycine, glutamic acid, tyrosine or threonine; at residue 199 glutamic acid or leucine; at residue 222 leucine; or any combination thereof, or any fragment or peptidomimetic thereof having nitrilase activity.

36. A method for making an (*S*)-phenyl lactic acid derivative or an (*R*)-phenyl lactic acid derivative, the method comprising admixing a phenyllactocyanonitrile with at least one polypeptide selected from SEQ ID NO:196, 206, 208, 210 or 238, or a variant of SEQ ID NO:196, 206, 208, 210 or 238, having one or more mutations: at residue 55 lysine, glycine, or glutamine; at residue 60 glutamic acid; at residue 111 serine, at residue 190, serine, histidine, tyrosine or threonine; at residue 191, leucine, valine, methionine, aspartic acid, glycine, glutamic acid, tyrosine or threonine; at residue 199 glutamic acid or leucine; at residue 222 leucine; or any combination thereof, or any fragment or peptidomimetic thereof having nitrilase activity, or any active fragment or peptidomimetic thereof that selectively produces an (*S*)-enantiomer or an (*R*)-enantiomer, thereby producing an (*S*)-phenyl lactic acid derivative or an (*R*)-phenyl lactic acid derivative.

37. A method for making the polypeptide of claim 16 or claim 17 or fragments thereof, the method comprising
(a) introducing a nucleic acid encoding the polypeptide into a host cell under conditions that permit production of the polypeptide by the host cell, and
(b) recovering the polypeptide so produced.

38. A method for generating a nucleic acid variant encoding a polypeptide having nitrilase activity, wherein the variant has an altered biological activity from that which naturally occurs, the method comprising
(a) modifying the nucleic acid of any one of claims 1 to 6, 12, or 13 by
(i) substituting one or more nucleotides for a different nucleotide, wherein the nucleotide comprises a natural or non-natural nucleotide;

- (ii) deleting one or more nucleotides,
- (iii) adding one or more nucleotides, or
- (iv) any combination thereof.

- 5 39. A method for making a polynucleotide from two or more nucleic acids, the method comprising:
- (a) identifying regions of identity and regions of diversity between two or more nucleic acids, wherein at least one of the nucleic acids comprises a nucleic acid of any one of claims 1 to 6, 12, or 13;
- 10 (b) providing a set of oligonucleotides which correspond in sequence to at least two of the two or more nucleic acids; and,
- (c) extending the oligonucleotides with a polymerase, thereby making the polynucleotide.
40. A screening assay for identifying a nitrilase, the assay comprising:
- 15 (a) providing a plurality of nucleic acids or polypeptides comprising at least one of the nucleic acids of any one of claims 1 to 6, 12, or 13, or at least one of the polypeptides of claim 16 or claim 17 or fragments thereof;
- (b) obtaining polypeptide candidates to be tested for nitrilase activity from the plurality;
- (c) testing the candidates for nitrilase activity; and
- 20 (d) identifying those polypeptide candidates which are nitrilases.
41. A kit comprising (a) the nucleic acid of any one of claims 1 to 6, 12, or 13, or a fragment thereof encoding a polypeptide having nitrilase activity, or (b) the polypeptide of any one of claim 16 or claim 17 or fragments thereof, or a peptidomimetic thereof
- 25 having nitrilase activity, or a combination thereof; and (c) a buffer.
42. A method for modifying a molecule comprising:
- (a) mixing a polypeptide of any one of claim 16 or claim 17 or fragments thereof, or peptidomimetic thereof having nitrilase activity, with a starting molecule to produce a
- 30 reaction mixture;
- (b) reacting the starting molecule with the polypeptide to produce the modified molecule.

43. A method for identifying a modified compound comprising:

(a) admixing a polypeptide of any one of claim 16 or claim 17 or fragments thereof, or peptidomimetic thereof having nitrilase activity, with a starting compound to produce a reaction mixture and thereafter a library of modified starting compounds;

5 (b) testing the library to determine whether a modified starting compound is present within the library which exhibits a desired activity;

(c) identifying the modified compound exhibiting the desired activity.

44. A computer readable medium having stored thereon at least one nucleotide sequence
10 selected from the group consisting of: SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179,
15 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349,
20 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383 385, or variants thereof, and/or at least one amino acid sequence selected from the group consisting of: SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118,
25 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288,
30 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384 and 386, and variants thereof.

45. A computer system comprising a processor and a data storage device, wherein the data storage device has stored thereon at least one nucleotide sequence selected from the group consisting of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, and variants thereof and/or at least one amino acid sequence selected from the group consisting of: SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, and variants thereof.

46. A method for identifying a feature in a sequence which comprises:

- (a) inputting the sequence into a computer;
- (b) running a sequence feature identification program on the computer so as to identify a feature within the sequence; and
- (c) identifying the feature in the sequence,

wherein the sequence comprises SEQ ID NOS:1-386, variants, or any combination thereof.

47. An assay for identifying a functional fragment of a polypeptide which comprises:

- 5 (a) obtaining a fragment of at least one polypeptide of claim 16 or claim 17;
- (b) contacting at least one fragment from step (a) with a substrate having a cyanohydrin moiety or an aminonitrile moiety under reaction conditions suitable for nitrilase activity;
- (c) measuring the amount of reaction product produced by each at least one fragment
- 10 from step (b); and
- (d) identifying the at least one fragment which is capable of producing a nitrilase reaction product; thereby identifying a functional fragment of the polypeptide.

48. An assay for identifying a functional variant of a polypeptide which comprises:

- 15 (a) obtaining at least one variant of at least one polypeptide of claim 16 or claim 17;
- (b) contacting at least one variant from step (a) with a substrate having a cyanohydrin moiety or an aminonitrile moiety under reaction conditions suitable for nitrilase activity;
- (c) measuring the amount of reaction product produced by each at least one variant from step (b); and
- 20 (d) identifying the at least one variant which is capable of producing a nitrilase reaction product; thereby identifying a functional variant of the polypeptide.

49. An assay for screening enantioselective transformation comprising:

- (a) labeling one of two prochiral or enantiotopic moieties in a molecule;
- (b) modifying at least one of the two moieties by selective catalyst to produce
- 25 products; and
- (c) determining the resultant products by mass spectroscopy.

50. The assay of claim 49, wherein the label is heavier or lighter isotope.

30 51. The assay of claim 49, wherein the selective catalyst is an enzyme.

52. The assay of claim 49, wherein the use of mass spectroscopy is by a positive mode or a negative mode.

53. The assay of claim 49, wherein the analysis is of either a parental mass or a fragmentation mass.
- 5 54. The assay of claim 49, wherein the assay can be used to monitor or determine % enantiomeric excess or % diastomeric excess.
- 10 55. An isolated or recombinant polypeptide having a nitrilase activity comprising a sequence as set forth in SEQ ID NO:196, 206, 208, 210 or 238 and having one or more mutations selected from the group consisting of a mutation at residue 55 lysine, residue 55 glycine, residue 55 glutamine, residue 60 glutamic acid, residue 111 serine, residue 190, residue 190 serine, residue 190 histidine, residue 190 tyrosine, residue 190 threonine, residue 191 leucine, residue 191 valine, residue 191 methionine, residue 191 aspartic acid, residue 191 glycine, residue 191 glutamic acid, residue 191 tyrosine, residue 191 threonine, residue 199 glutamic acid, residue 199 leucine, residue 222 leucine, and any combination thereof.
- 15 56. An isolated or recombinant polypeptide having a nitrilase activity comprising a sequence as set forth in SEQ ID NO:196, 206, 208, 210 or 238 and having a mutation at residue 190 or equivalent, wherein alanine is replaced with a hydrogen-binding amino acid or peptidomimetic residue.
- 20 57. An isolated or recombinant polypeptide having a nitrilase activity comprising a sequence as set forth in SEQ ID NO:196, 206, 208, 210 or 238 and having a mutation at residue 190 or equivalent, wherein alanine is replaced with a hydrophobic amino acid or peptidomimetic residue.
- 25 58. An isolated or recombinant nitrilase having the equivalent of one or more mutations at residue 55 lysine, glycine, or glutamine; at residue 60 glutamic acid; at residue 111 serine, at residue 190, serine, histidine, tyrosine or threonine; at residue 191, leucine, valine, methionine, aspartic acid, glycine, glutamic acid, tyrosine or threonine; at residue 199 glutamic acid or leucine; at residue 222 leucine of SEQ ID NO:196, 206, 208, 210 or 238.
- 30

59. An amplification primer pair for amplifying a nucleic acid encoding a polypeptide having a nitrilase activity, wherein the primer pair is capable of amplifying a nucleic acid comprising a sequence as set forth in claim 1, or a subsequence thereof.
- 5
60. The amplification primer pair of claim 59, wherein a member of the amplification primer sequence pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of the sequence, or, about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more consecutive bases of the sequence.
- 10
61. A nitrilase-encoding nucleic acid generated by amplification of a polynucleotide using an amplification primer pair as set forth in claim 59.
62. The nitrilase-encoding nucleic acid of claim 61, wherein the amplification is by
- 15 polymerase chain reaction (PCR).
63. The nitrilase-encoding nucleic acid of claim 62, wherein the nucleic acid generated by amplification of a gene library.
- 20
64. The nitrilase-encoding nucleic acid of claim 63, wherein the gene library is an environmental library.
65. An isolated or recombinant nitrilase encoded by a nitrilase-encoding nucleic acid as set forth in claim 61.

Figure 1

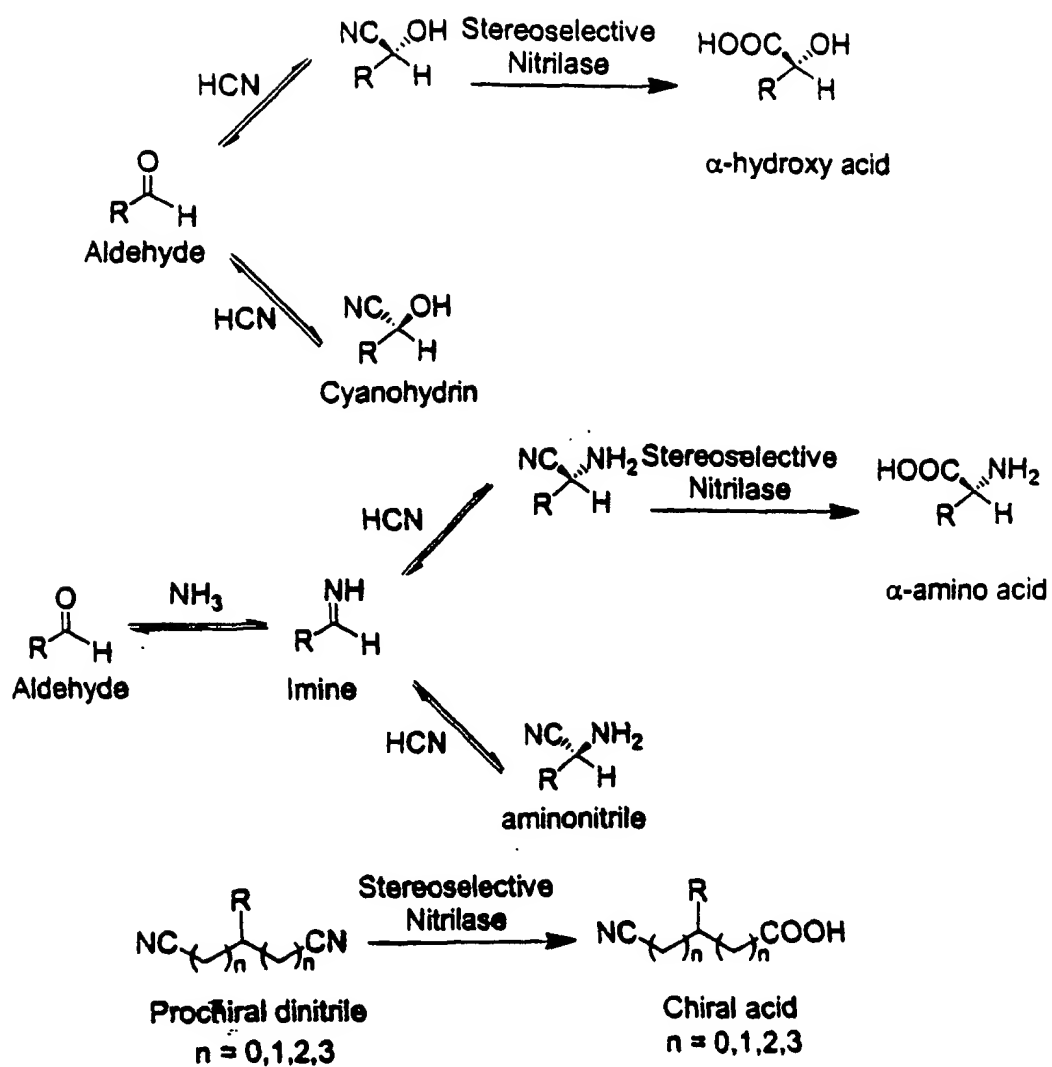


Figure 2

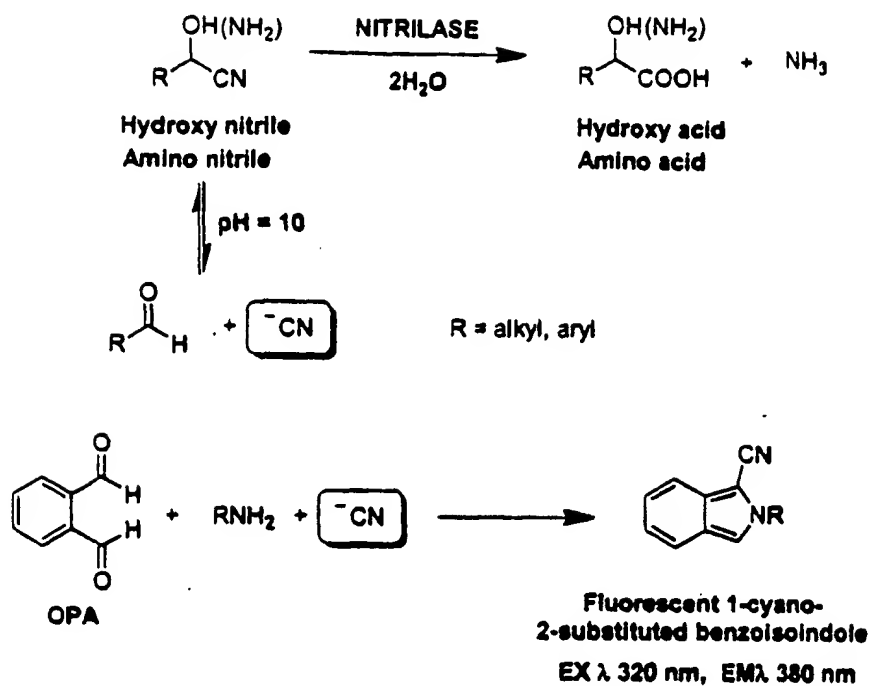


Figure 3

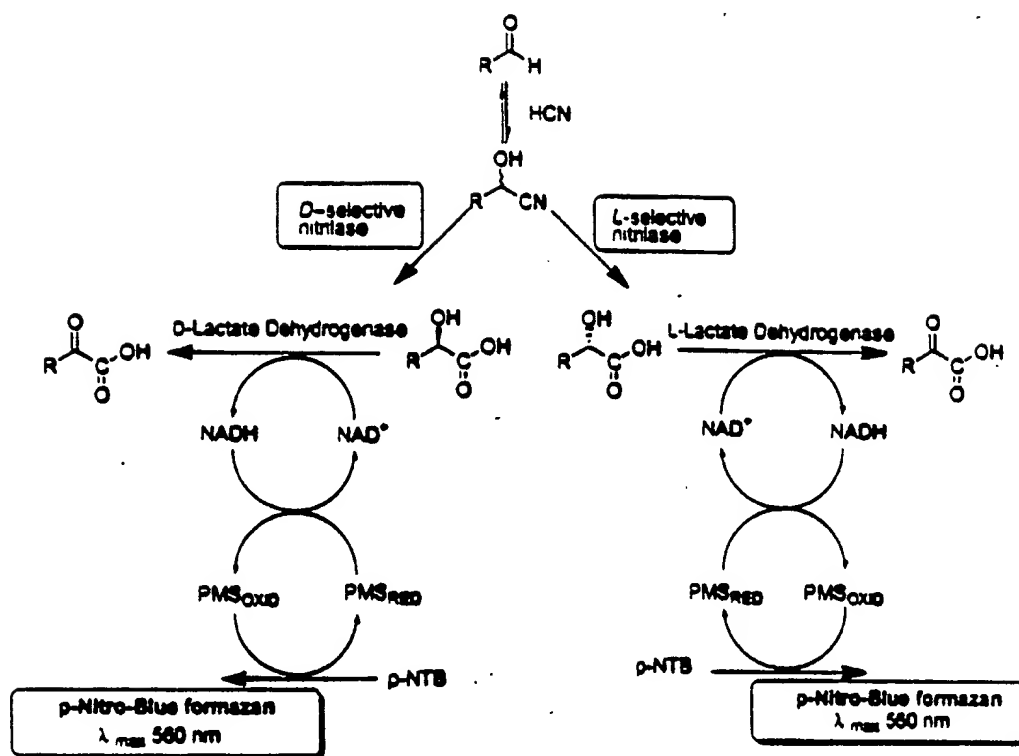


Figure 4

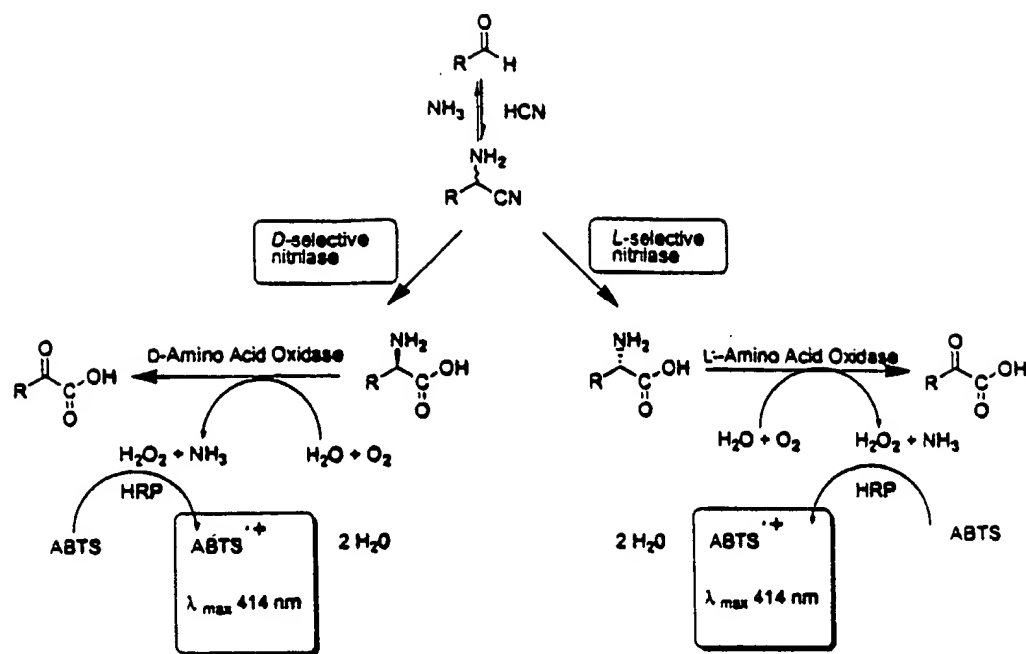


Figure 5
NITRILASE SCREENING PARADIGM

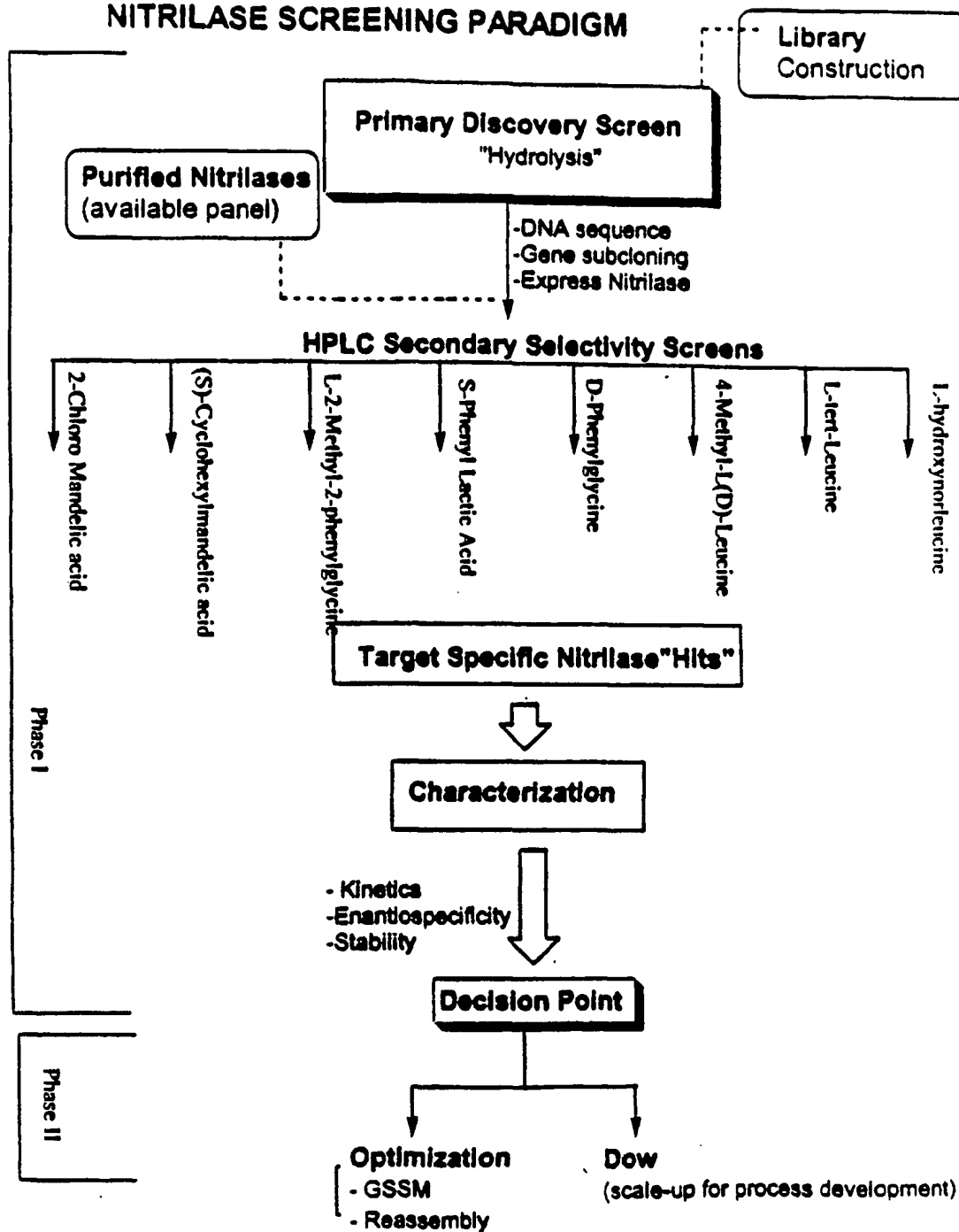


Figure 6A

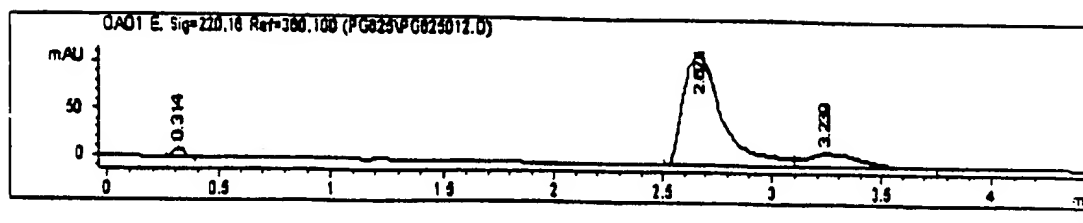


Figure 6B

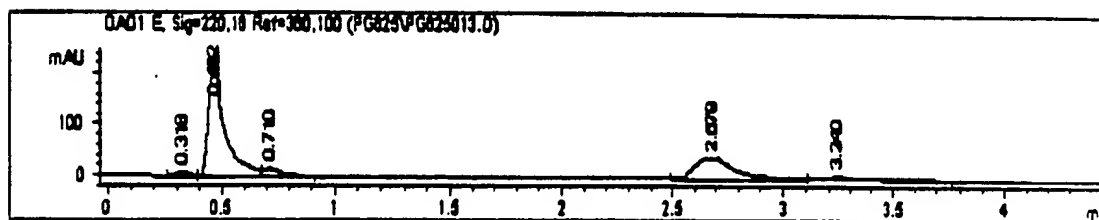
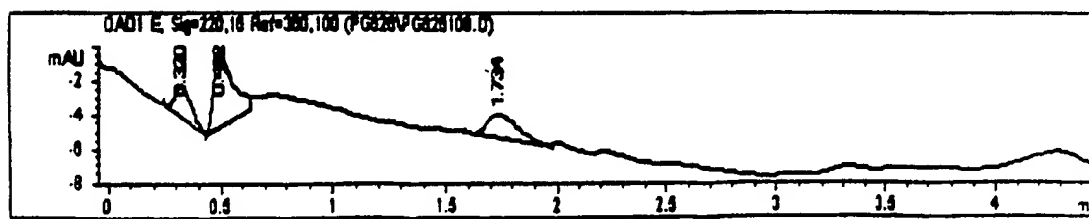
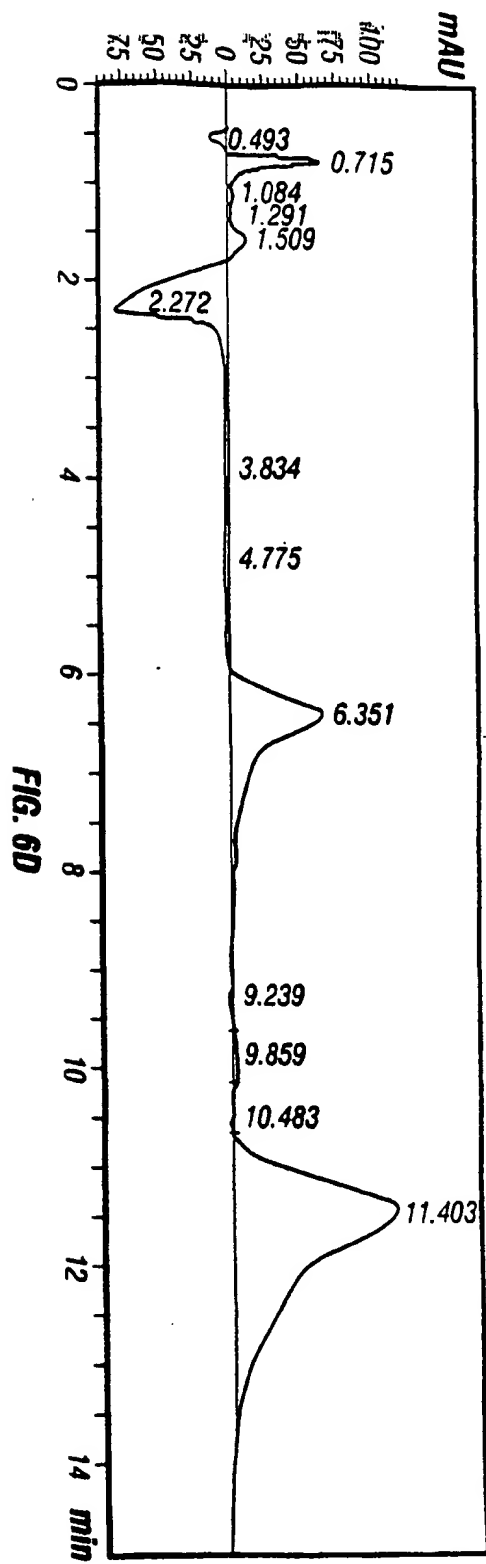
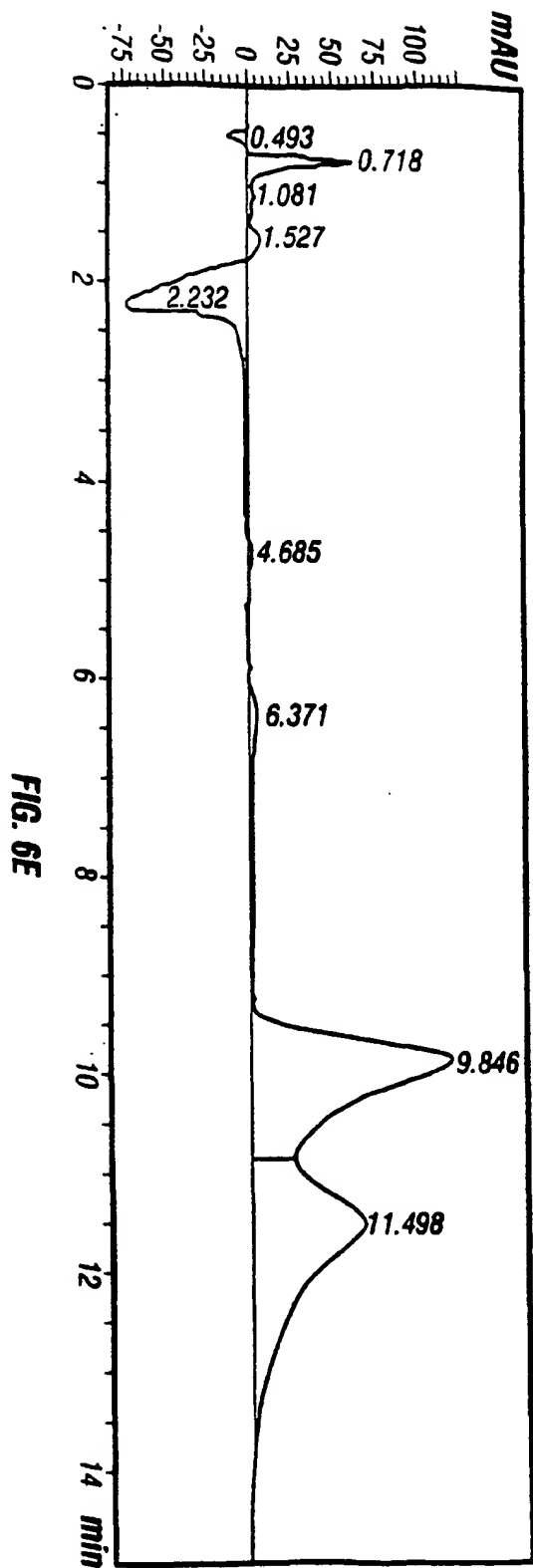


Figure 6C





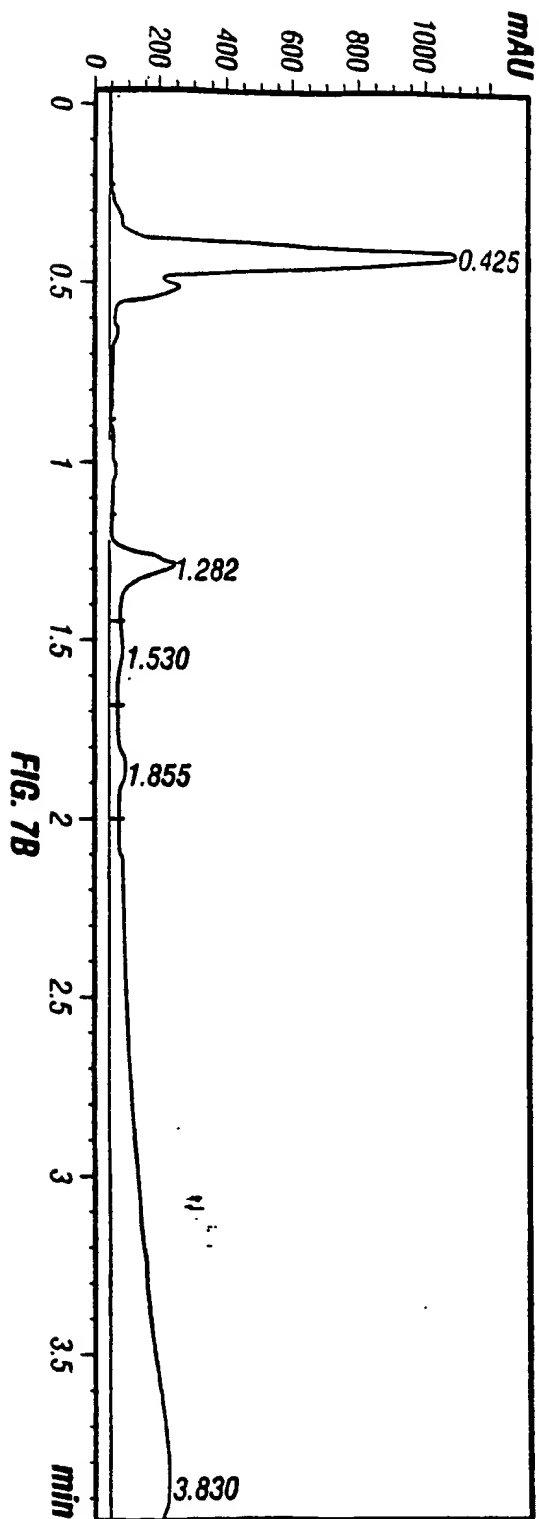


FIG. 7B

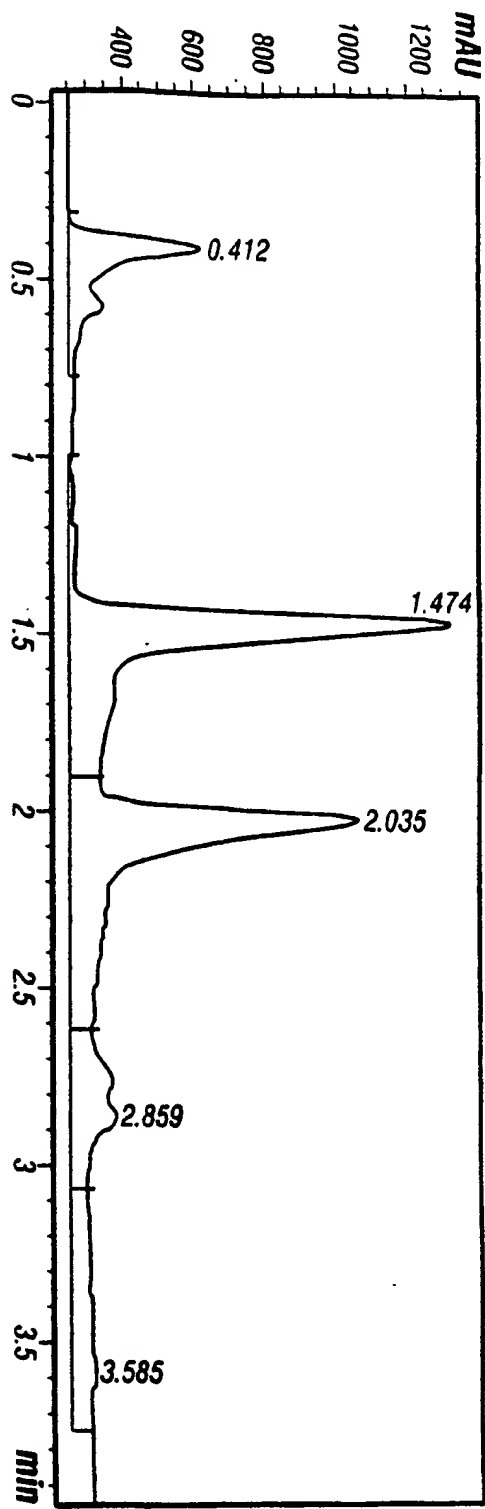
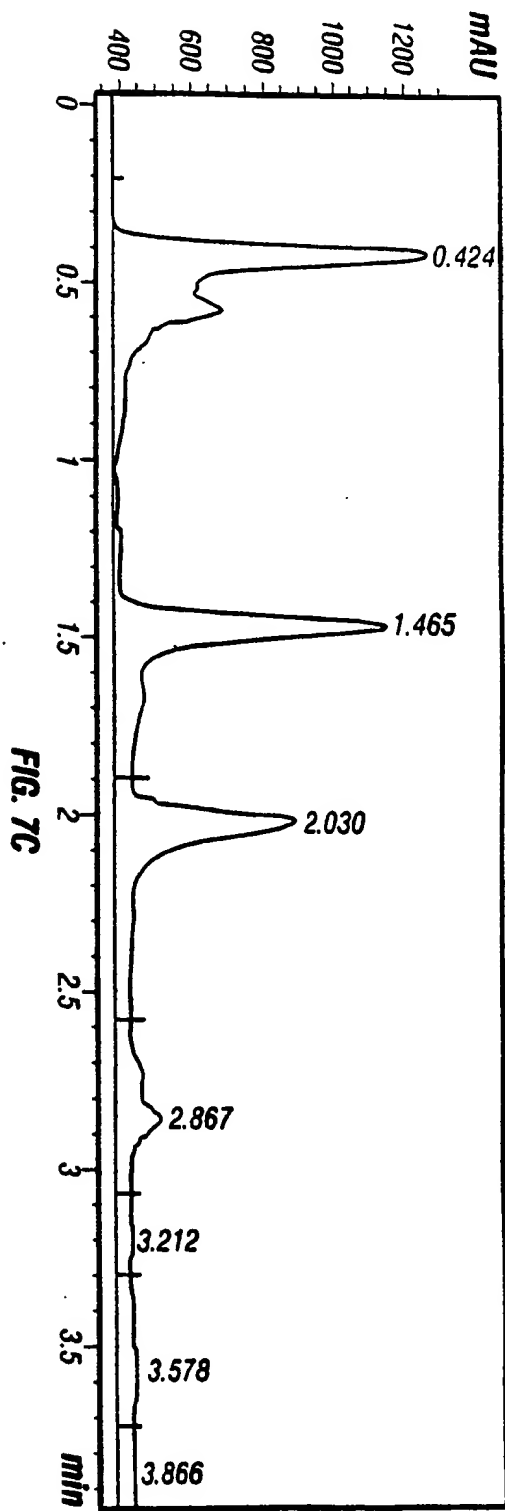
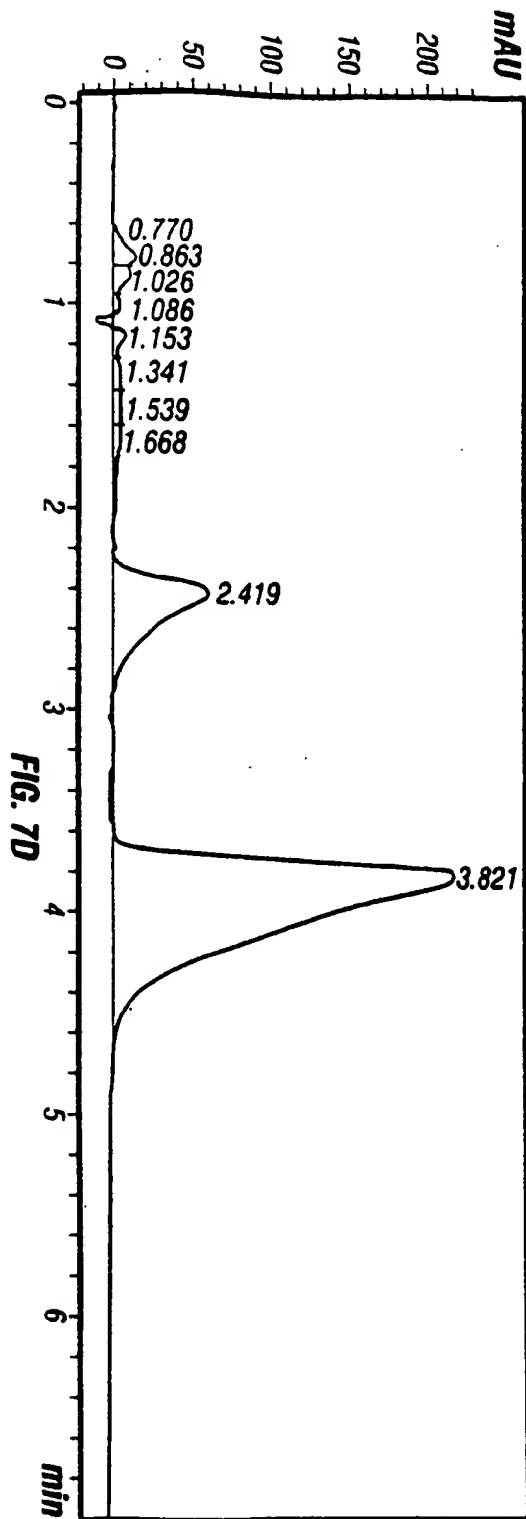
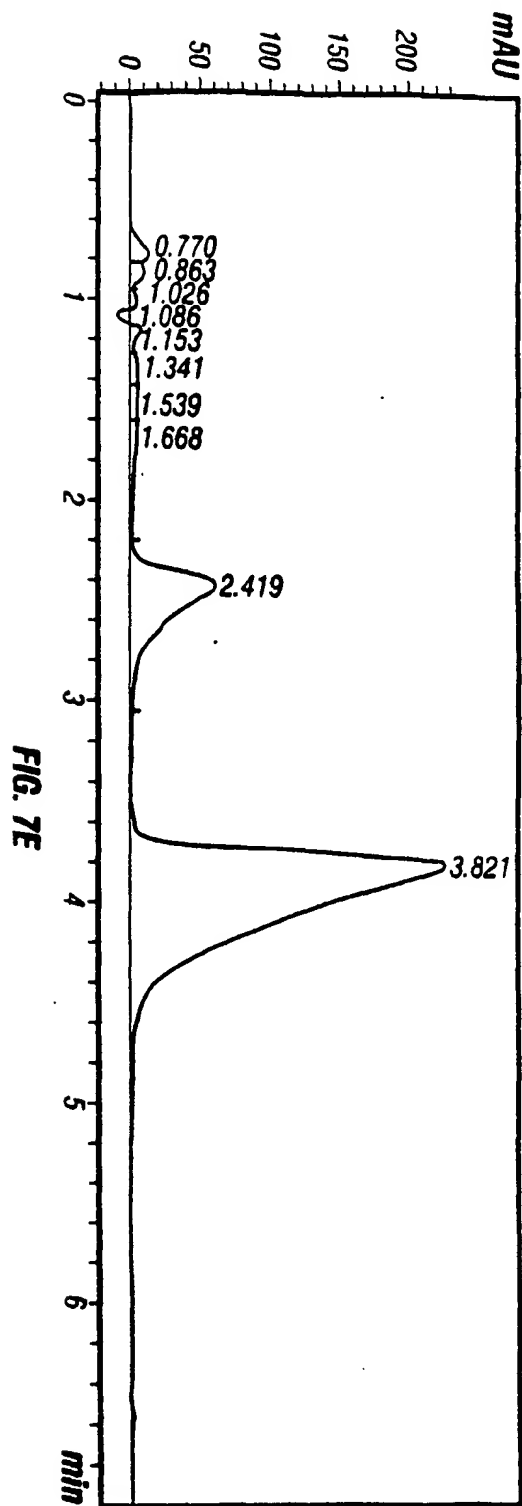
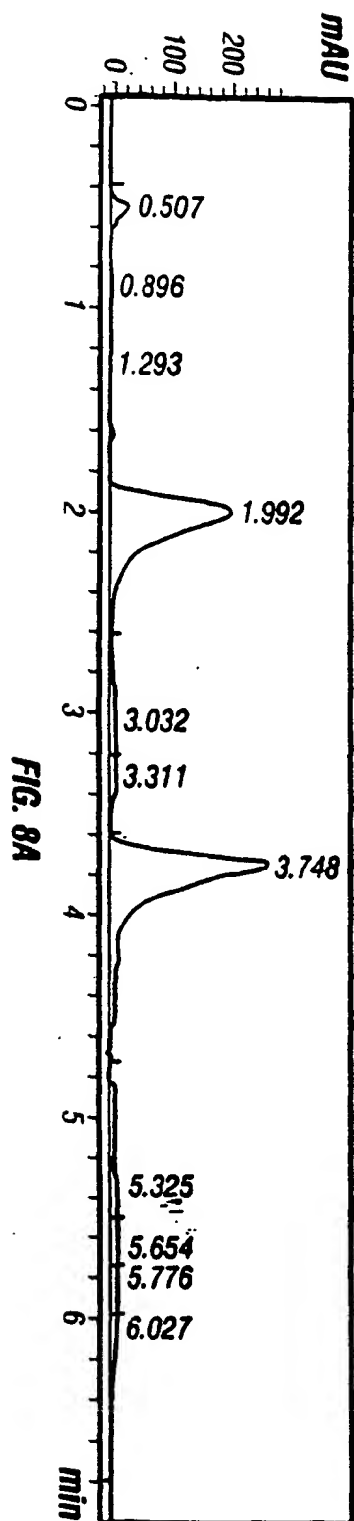
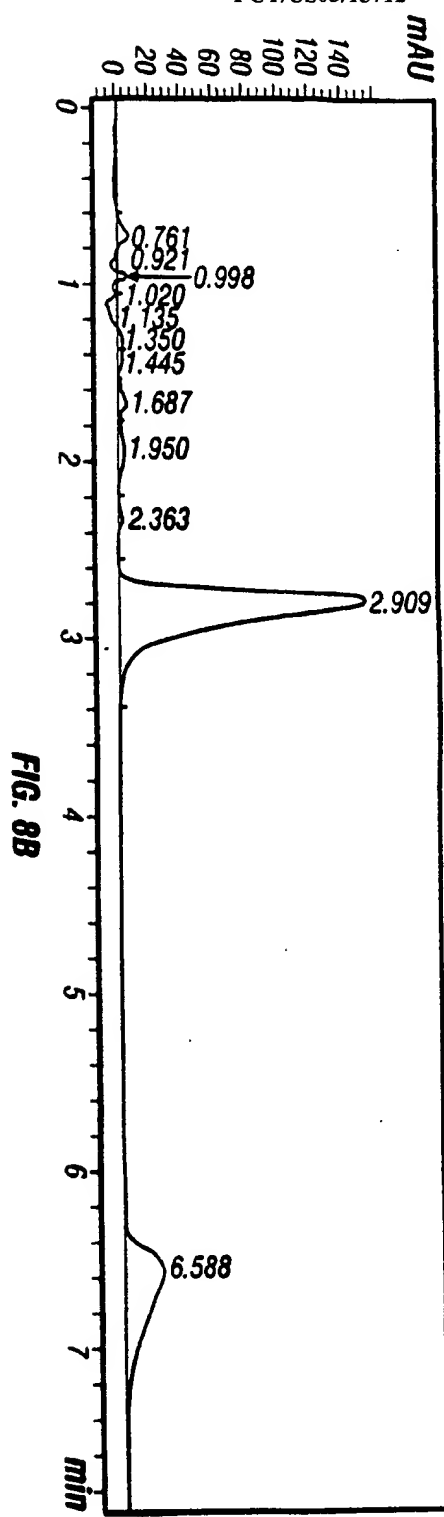
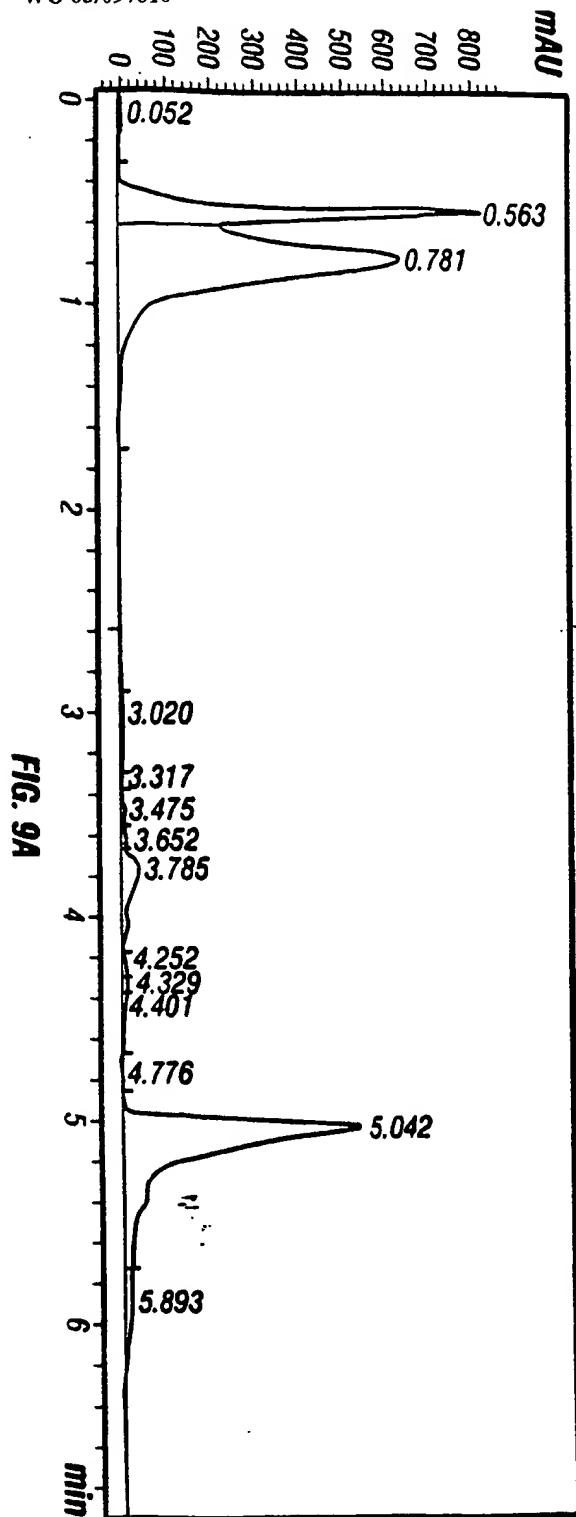


FIG. 7A







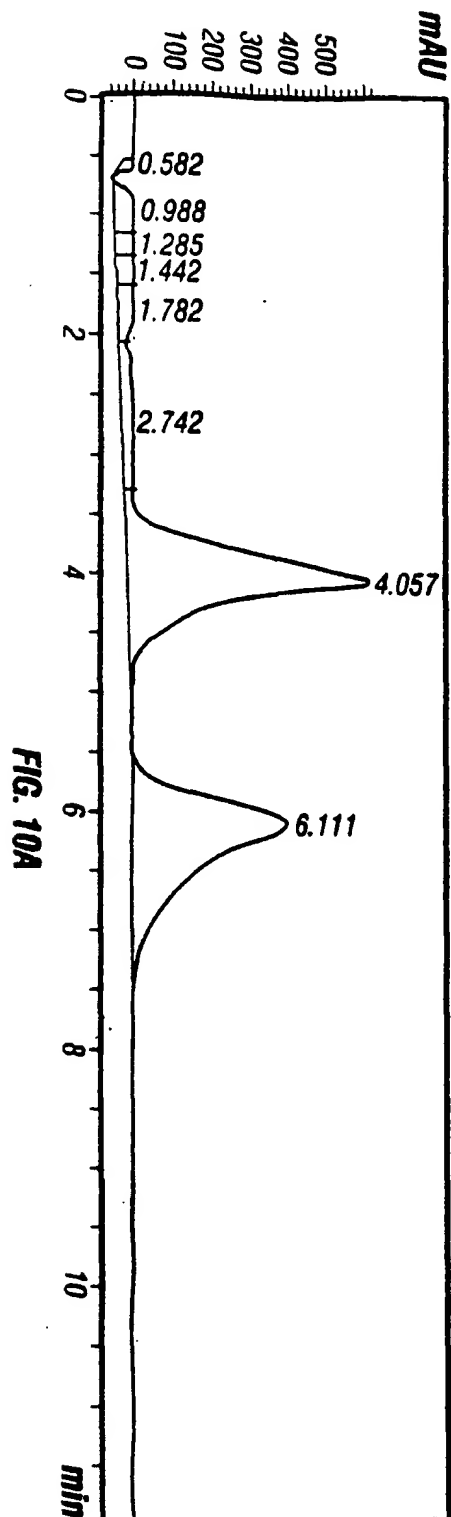
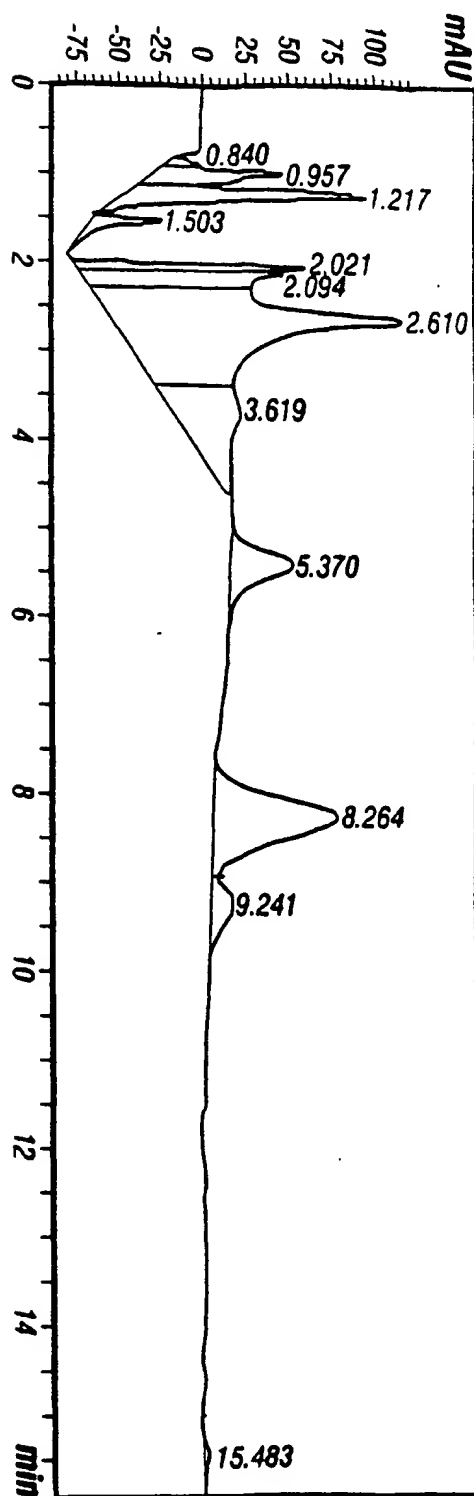
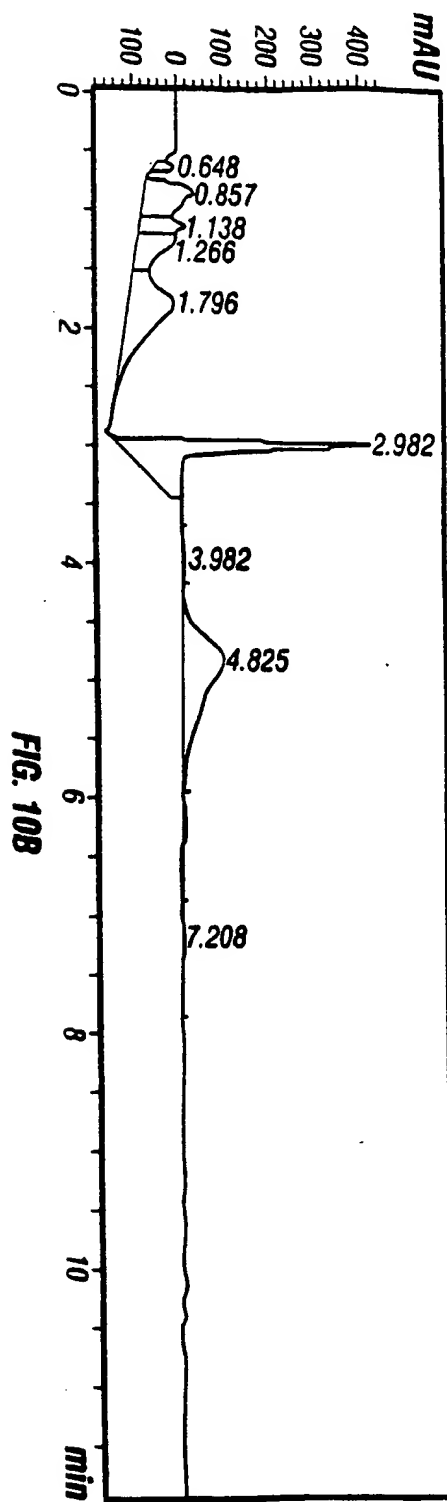
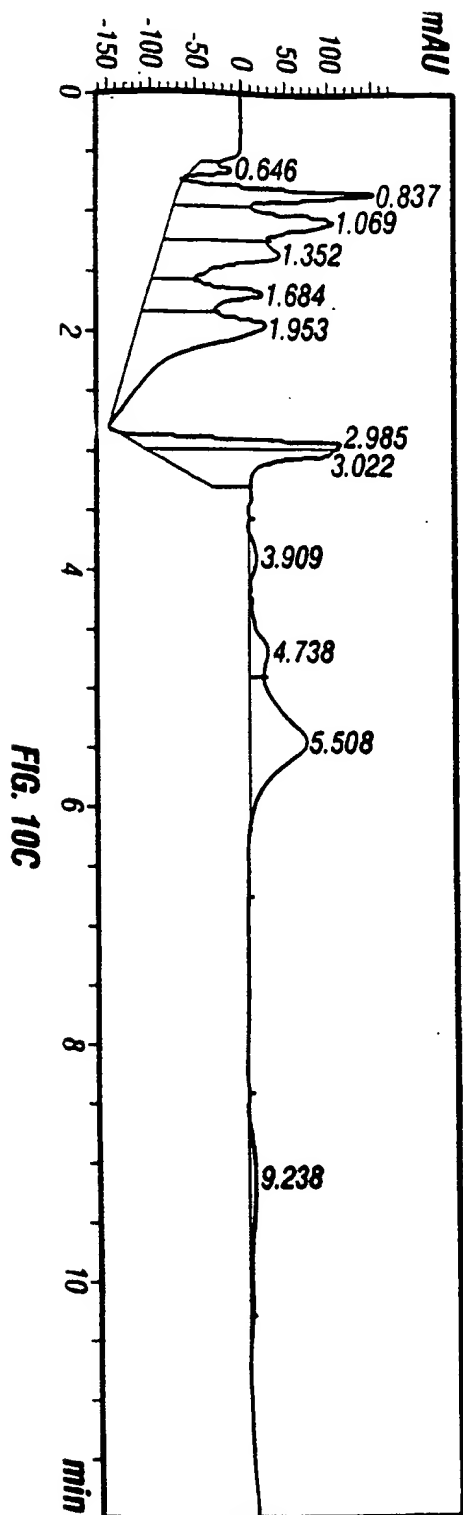
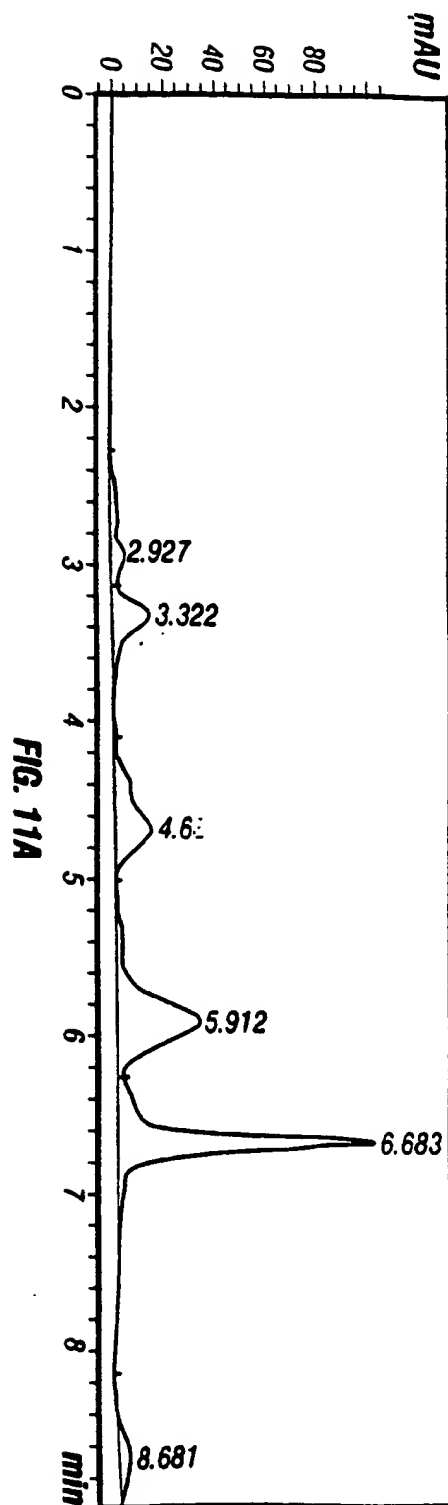
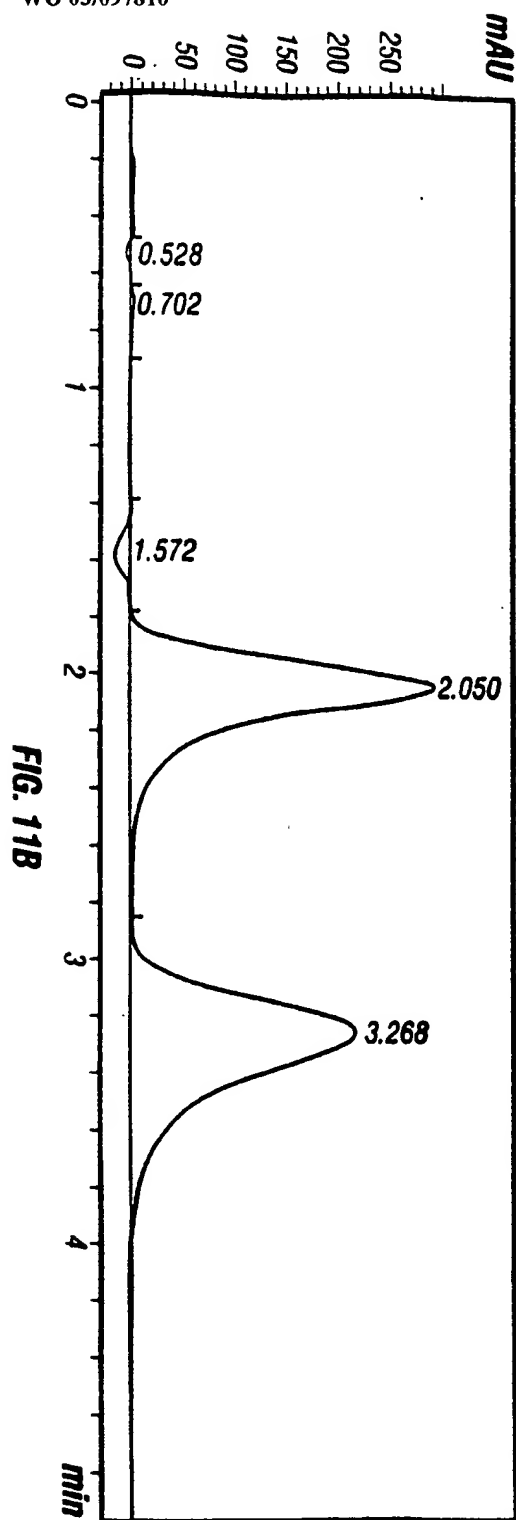
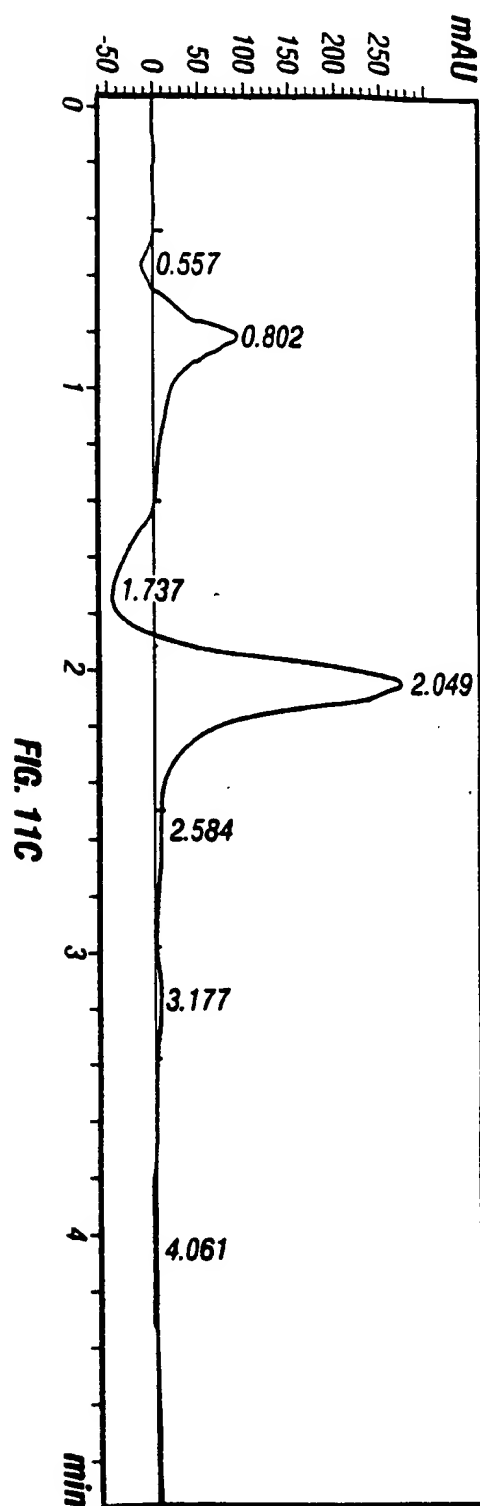
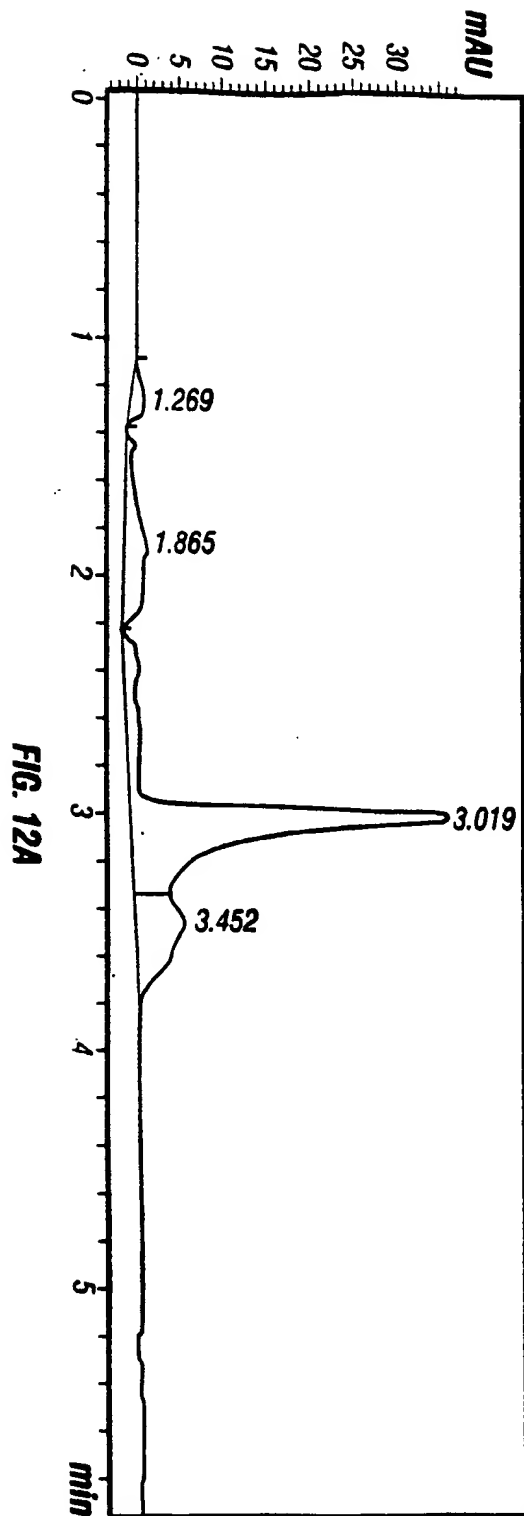


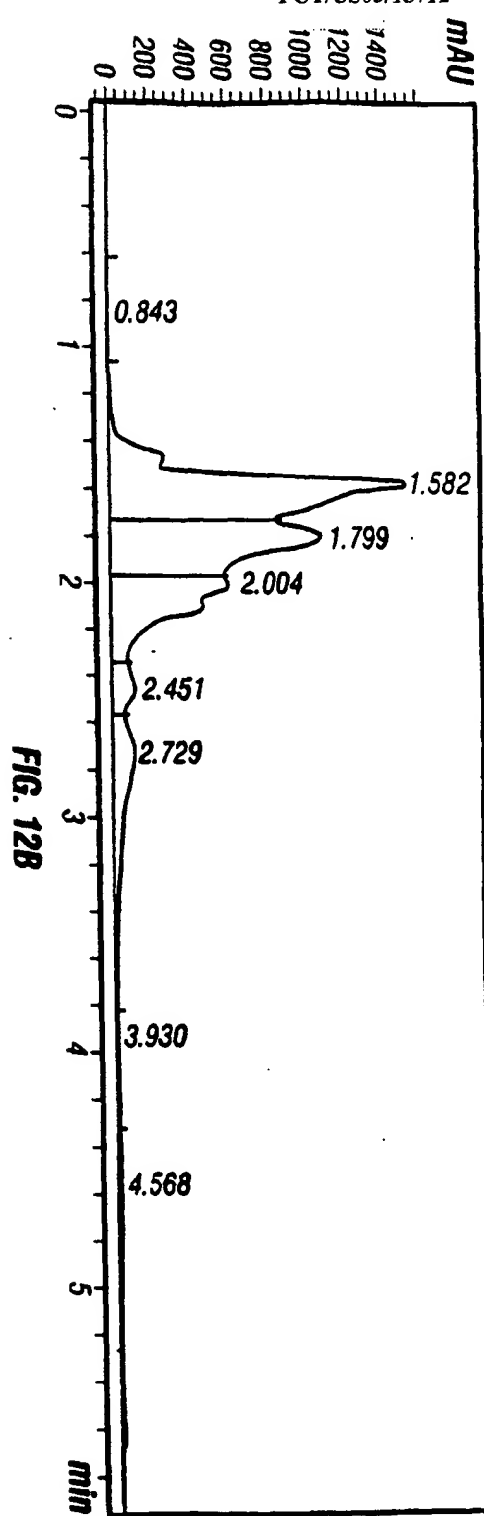
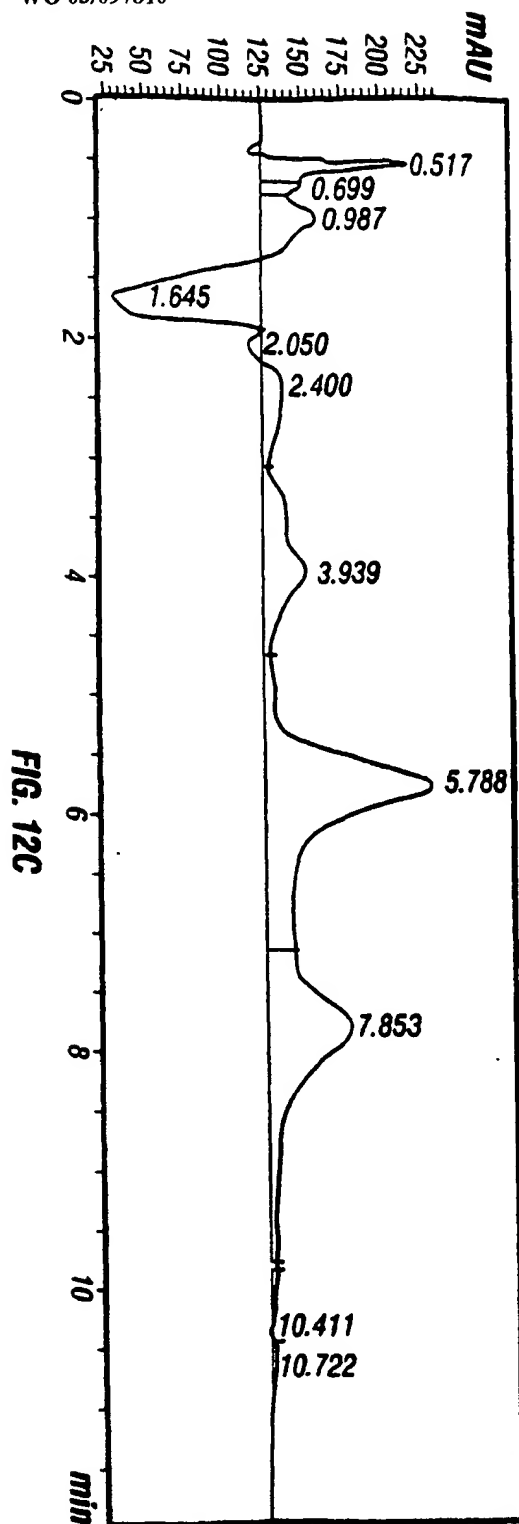
FIG. 9B











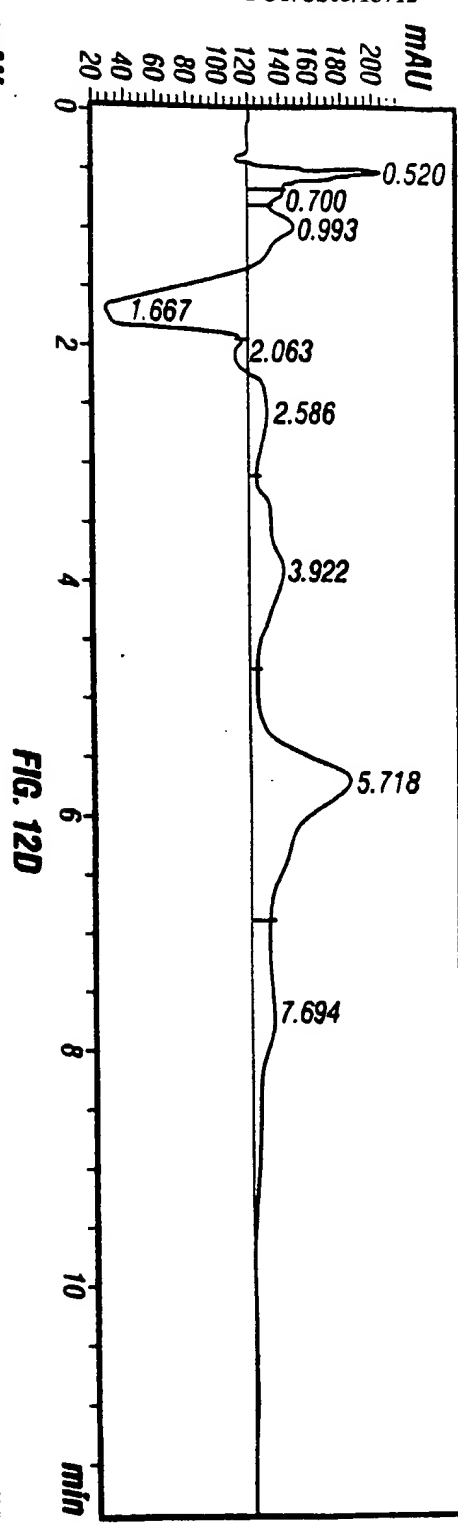
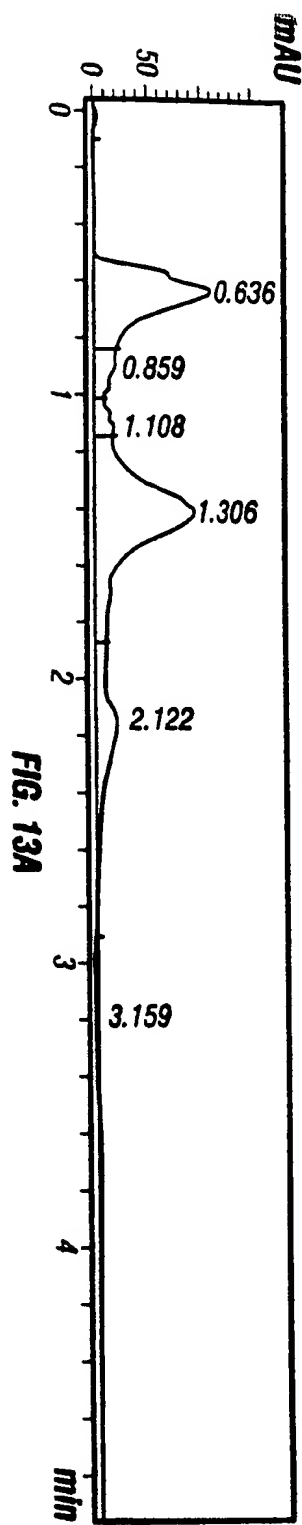
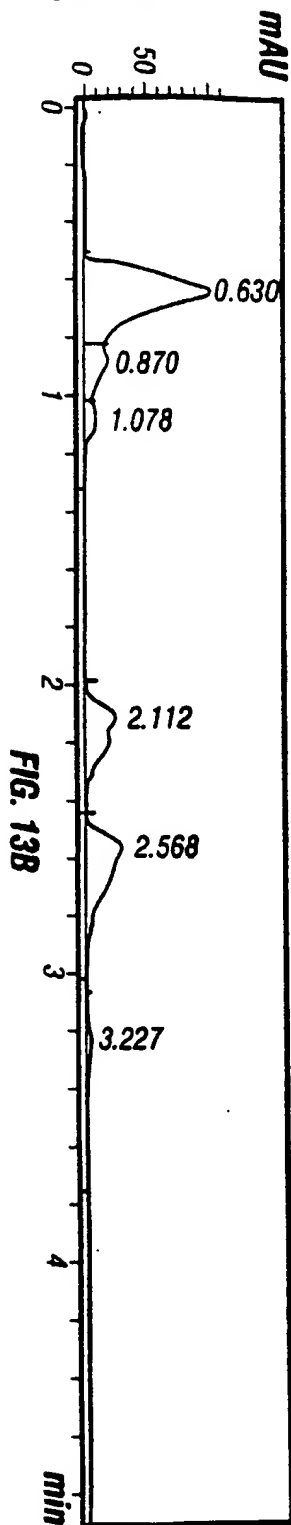


FIGURE 14A

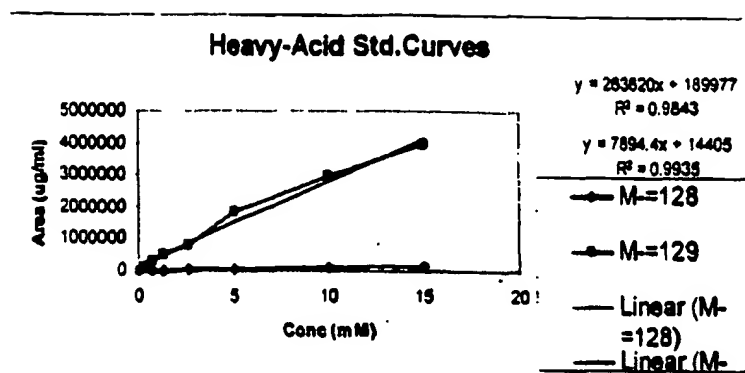


FIGURE 14B

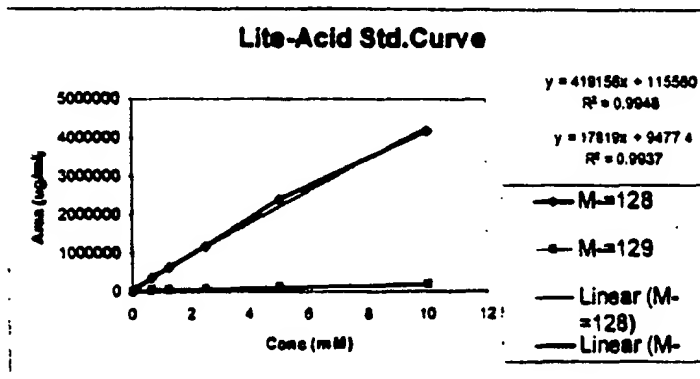


Figure 15

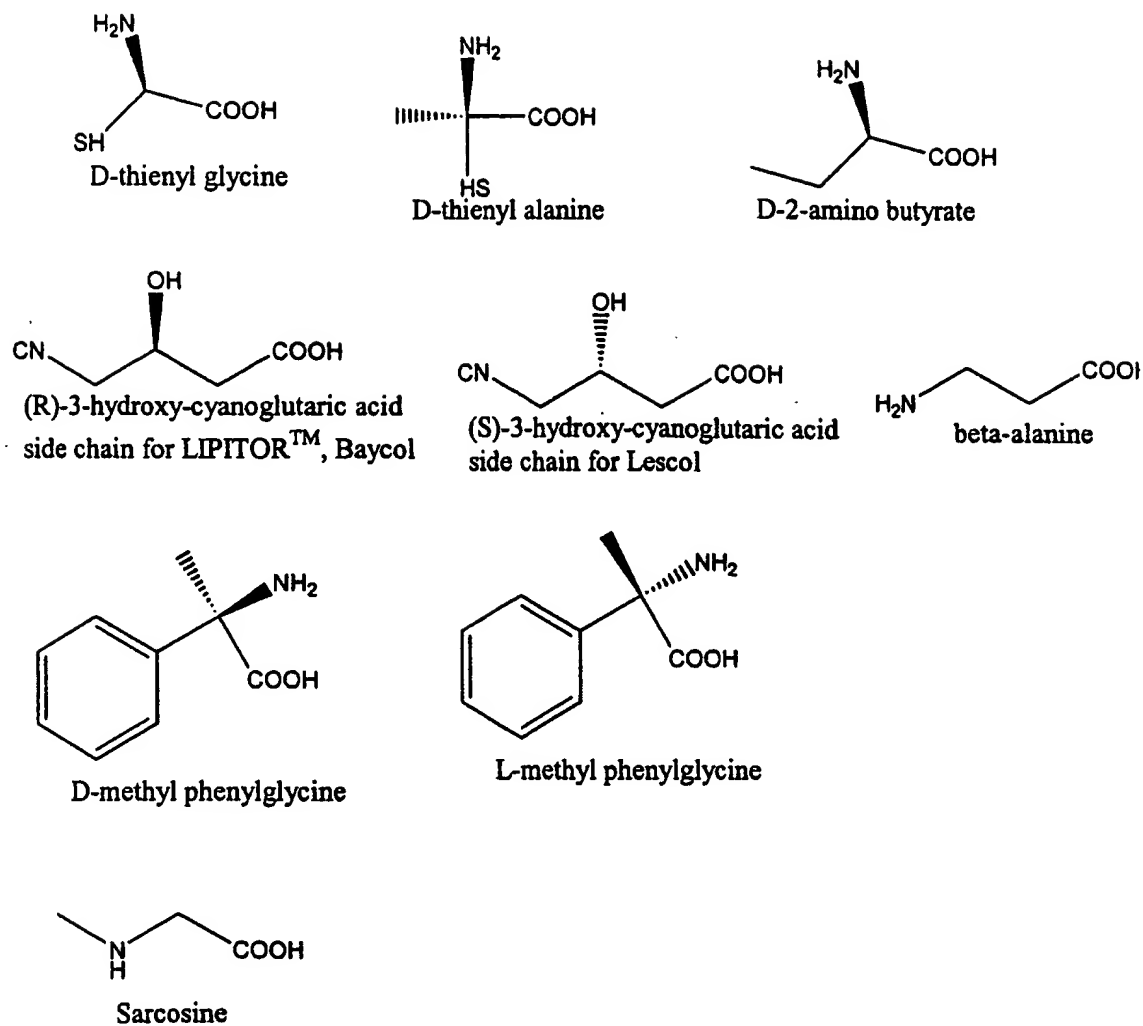


Figure 15

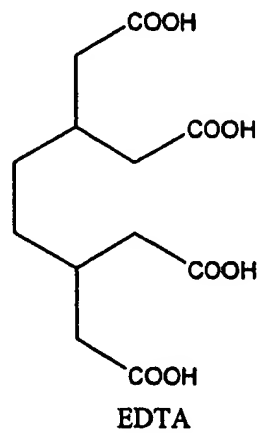
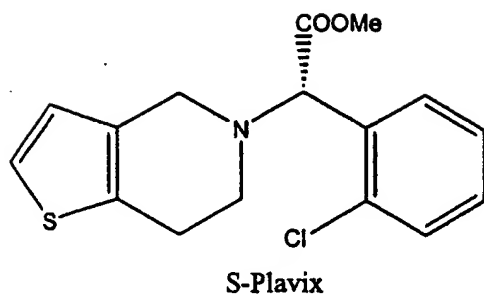
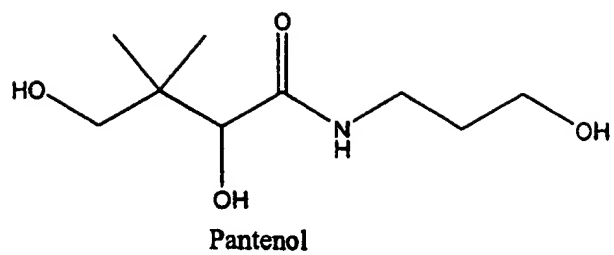
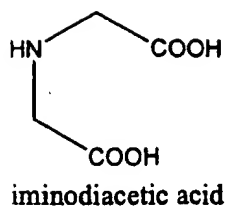


Figure 15

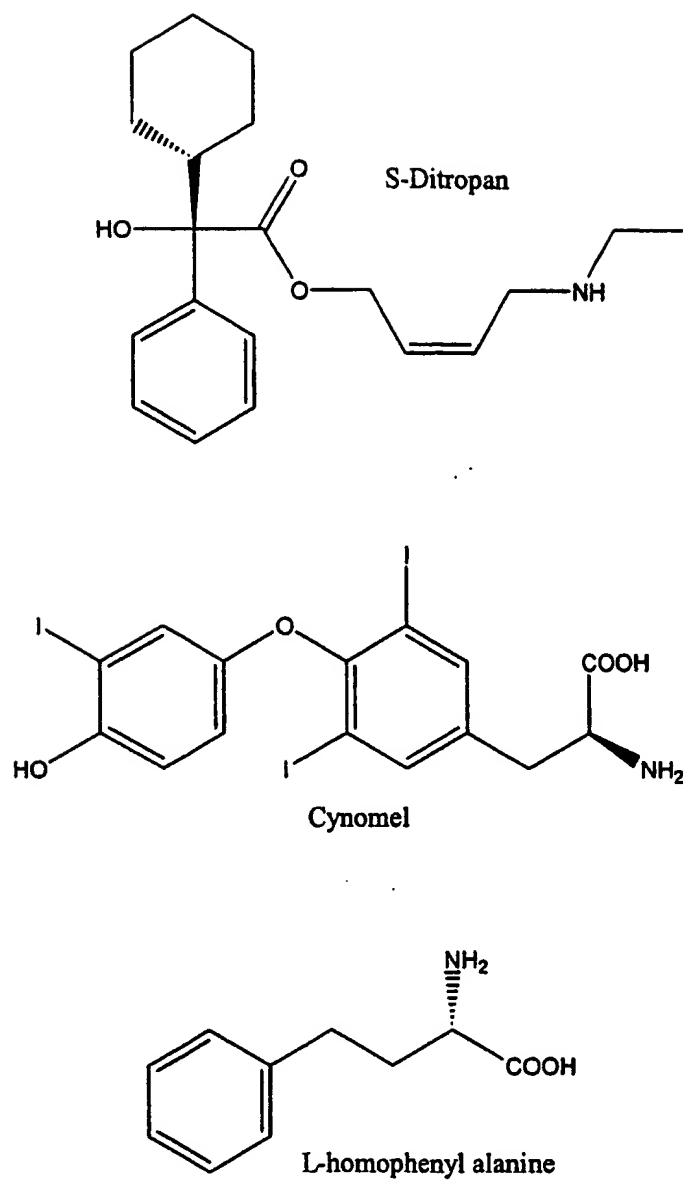


Figure 15

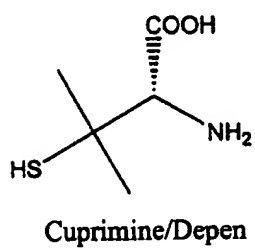
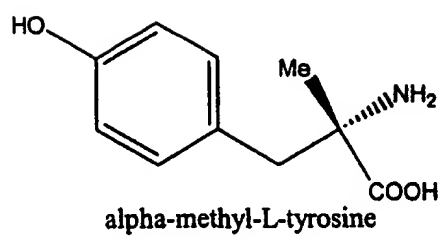
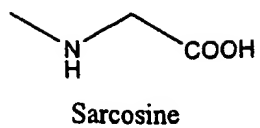


Figure 15

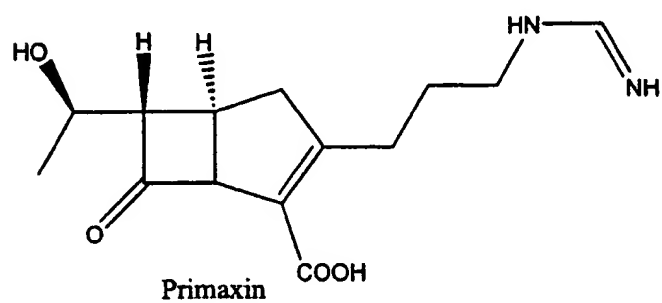
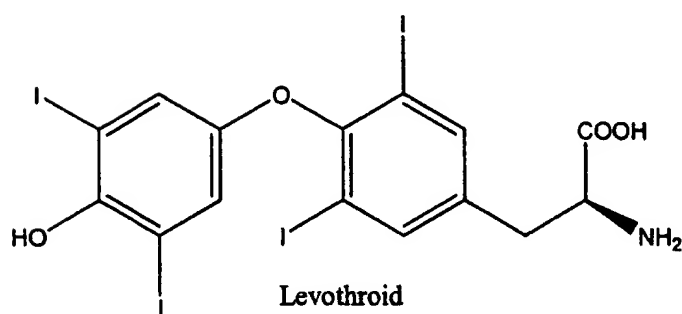
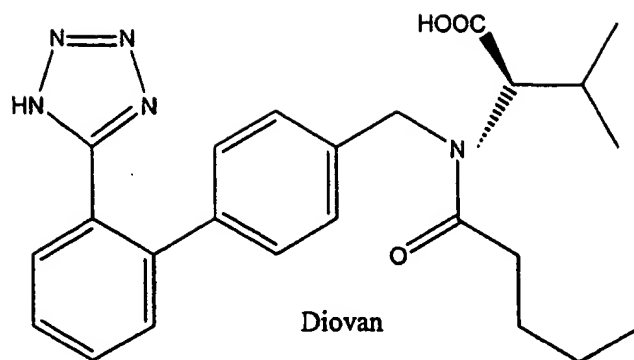


Figure 15

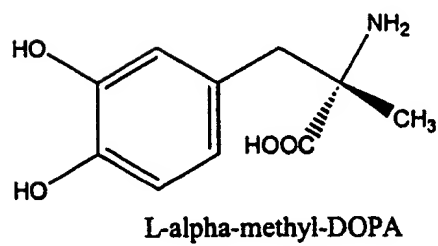
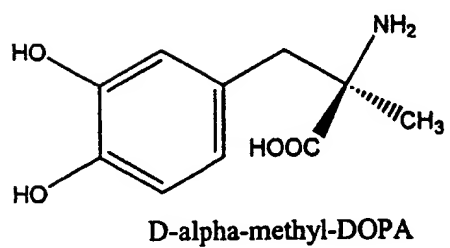
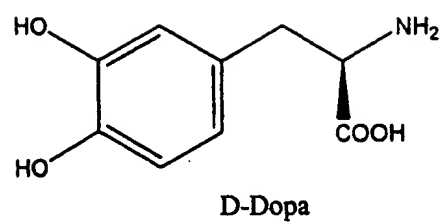
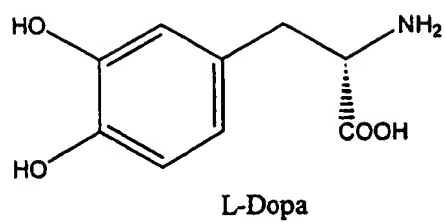
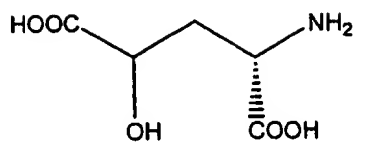
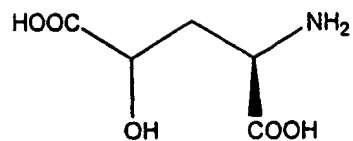


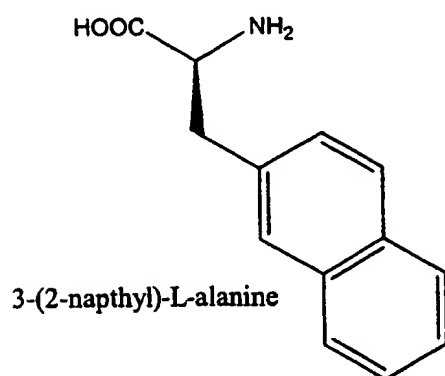
Figure 15



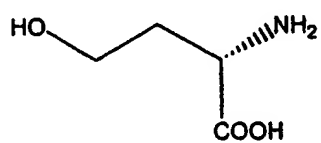
L-gamma-hydroxy glutamate



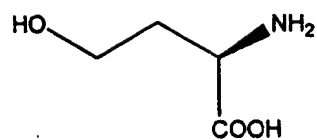
D-gamma-hydroxy glutamate



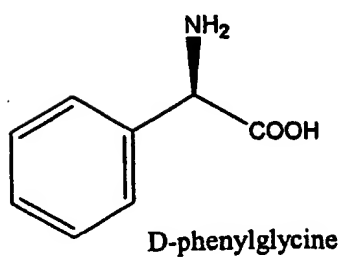
3-(2-naphthyl)-L-alanine



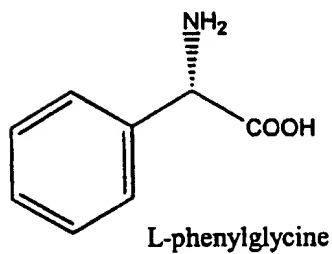
L-homoserine



D-homoserine



D-phenylglycine



L-phenylglycine

Figure 15

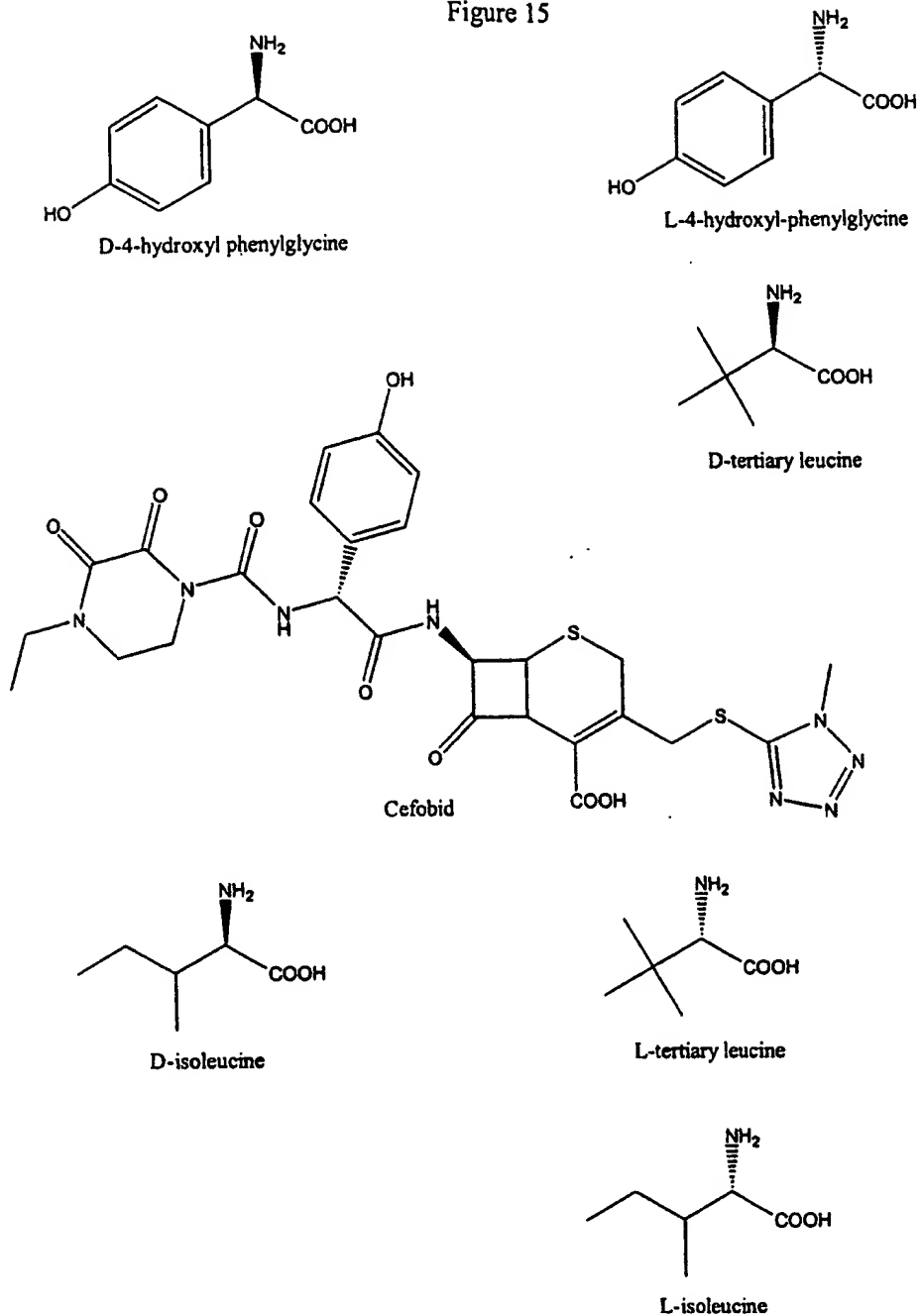
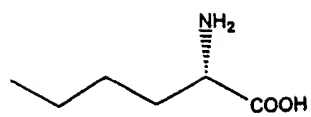
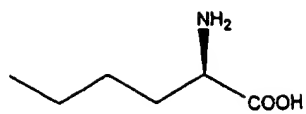


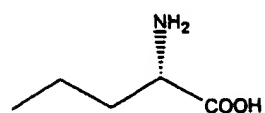
Figure 15



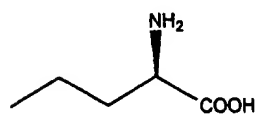
L-norleucine



D-norleucine



L-norvaline



D-norvaline

Figure 15

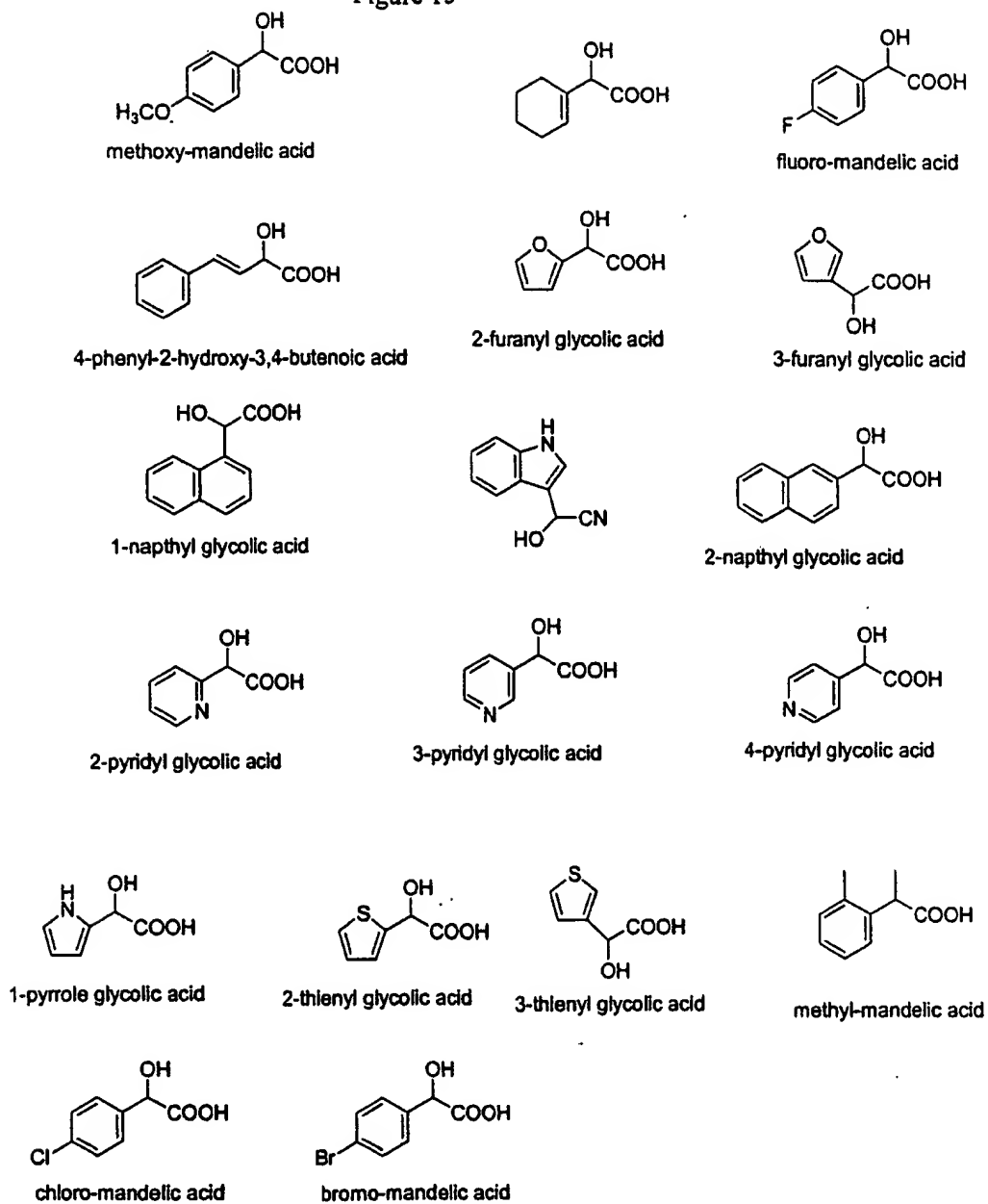


Figure 15

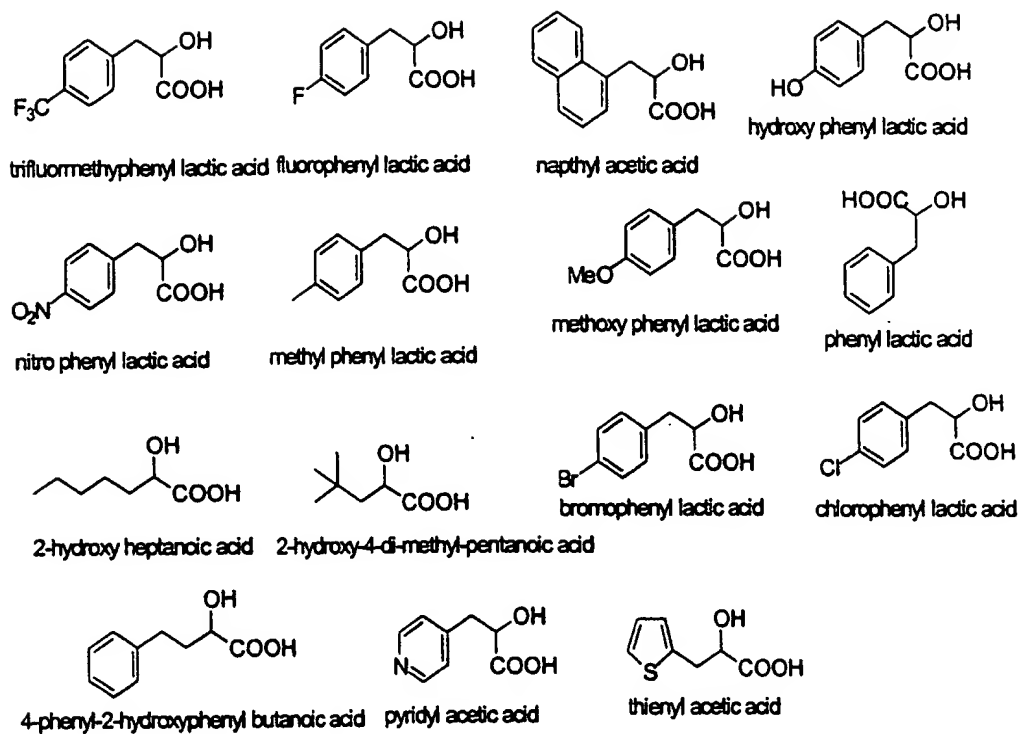


Figure 15

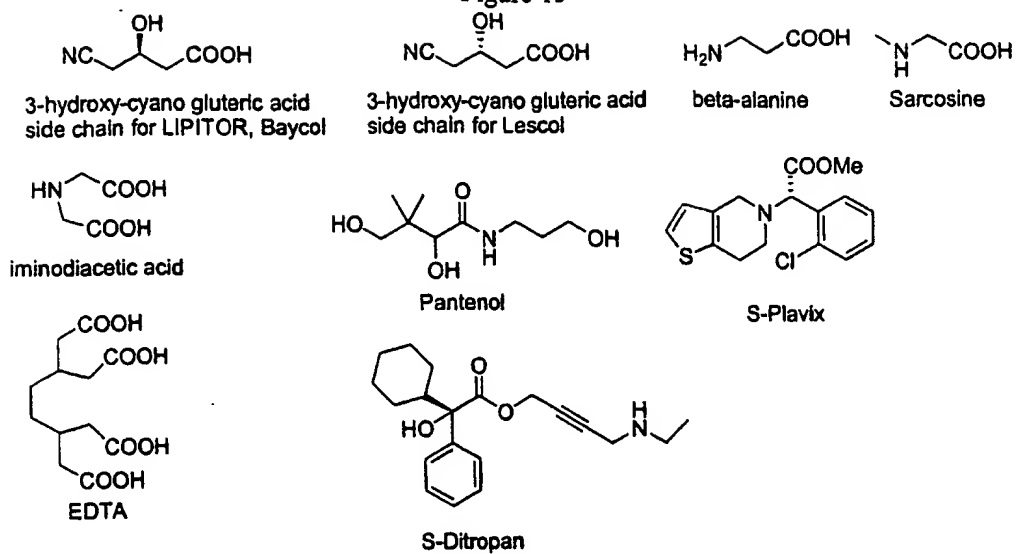
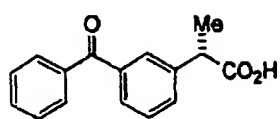
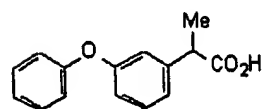


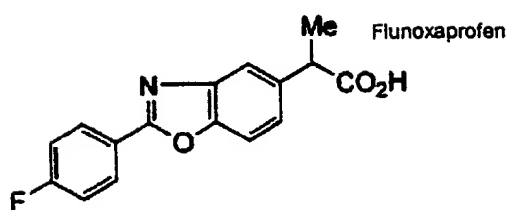
Figure 15



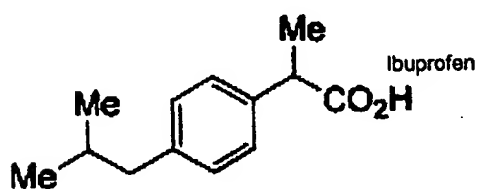
Dexketoprofen



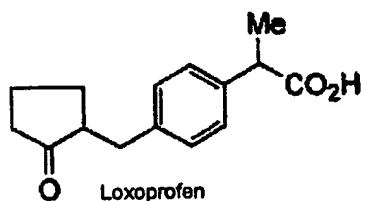
Fenoprofen



Flunoxaprofen

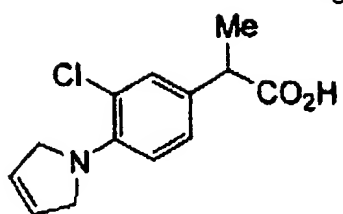


Ibuprofen

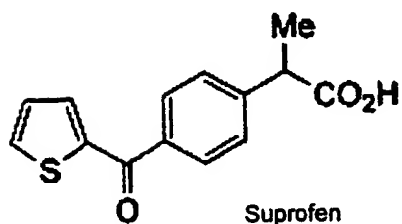


Loxoprofen

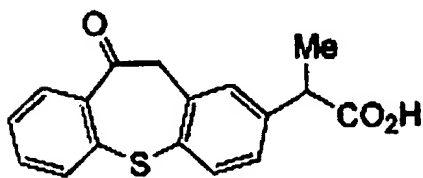
Figure 15



Pirprofen

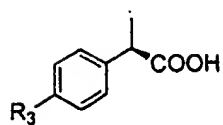


Suprofen

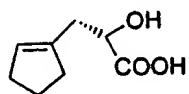


Zaltoprofen

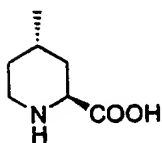
Figure 15



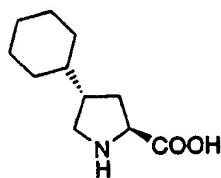
alpha-methyl benzyl cyanide derivatives



intermediate for Trocade

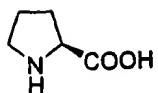


3-methyl-2-carboxy-piperidine

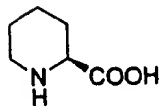


Fospril

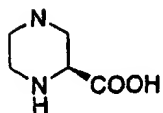
Figure 15



2-carboxy-cyclobutyl amine



2-carboxy-piperidine



2-carboxy-piperazine

Figure 16

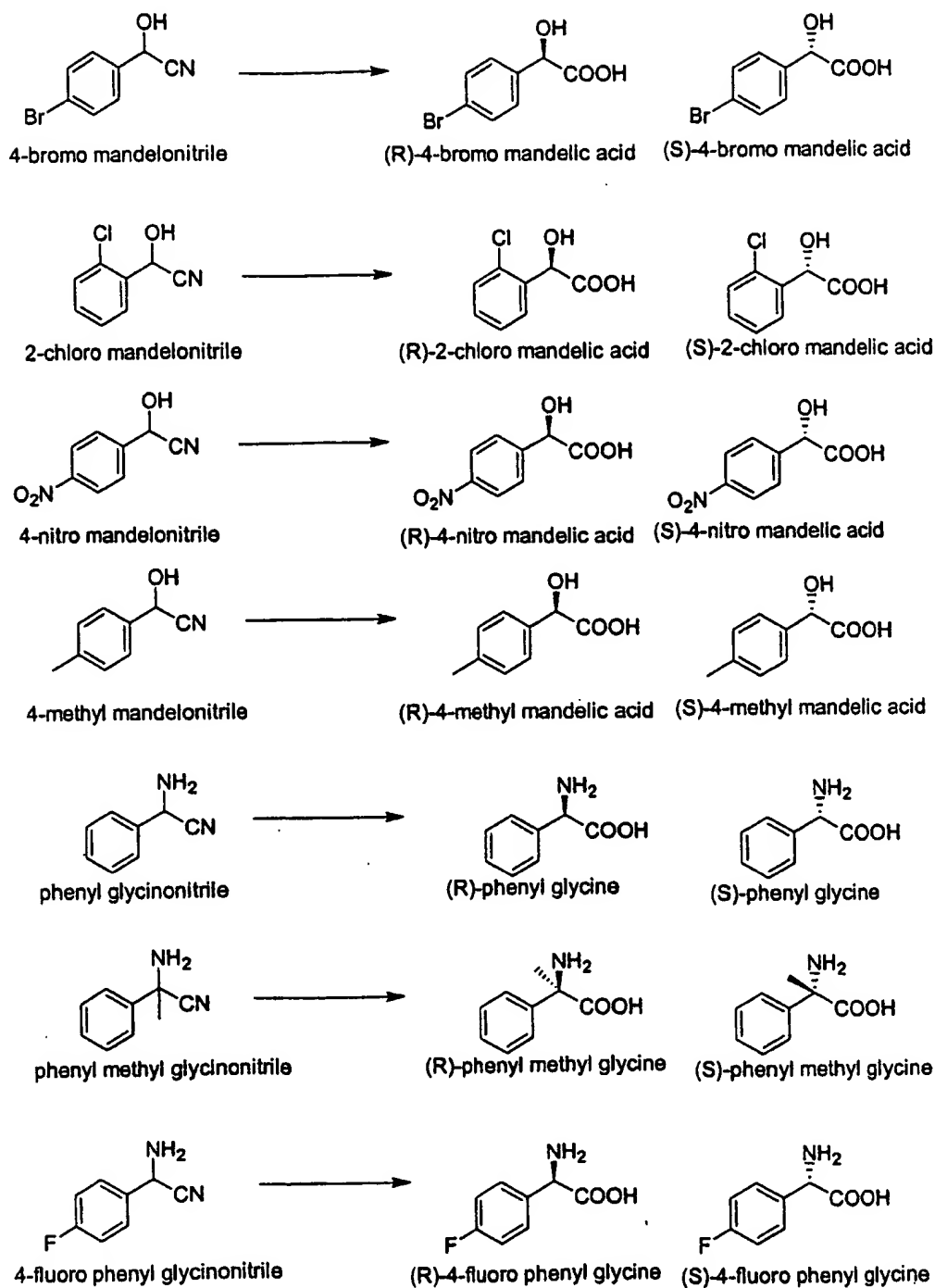


Figure 16

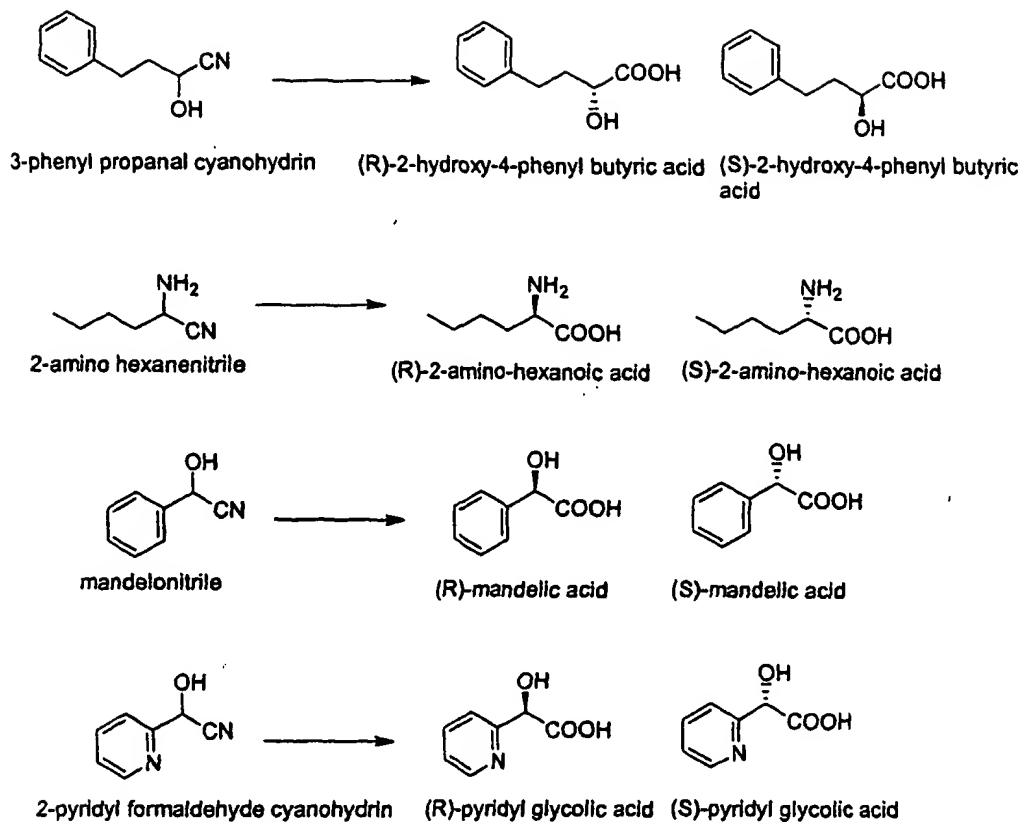


Figure 16

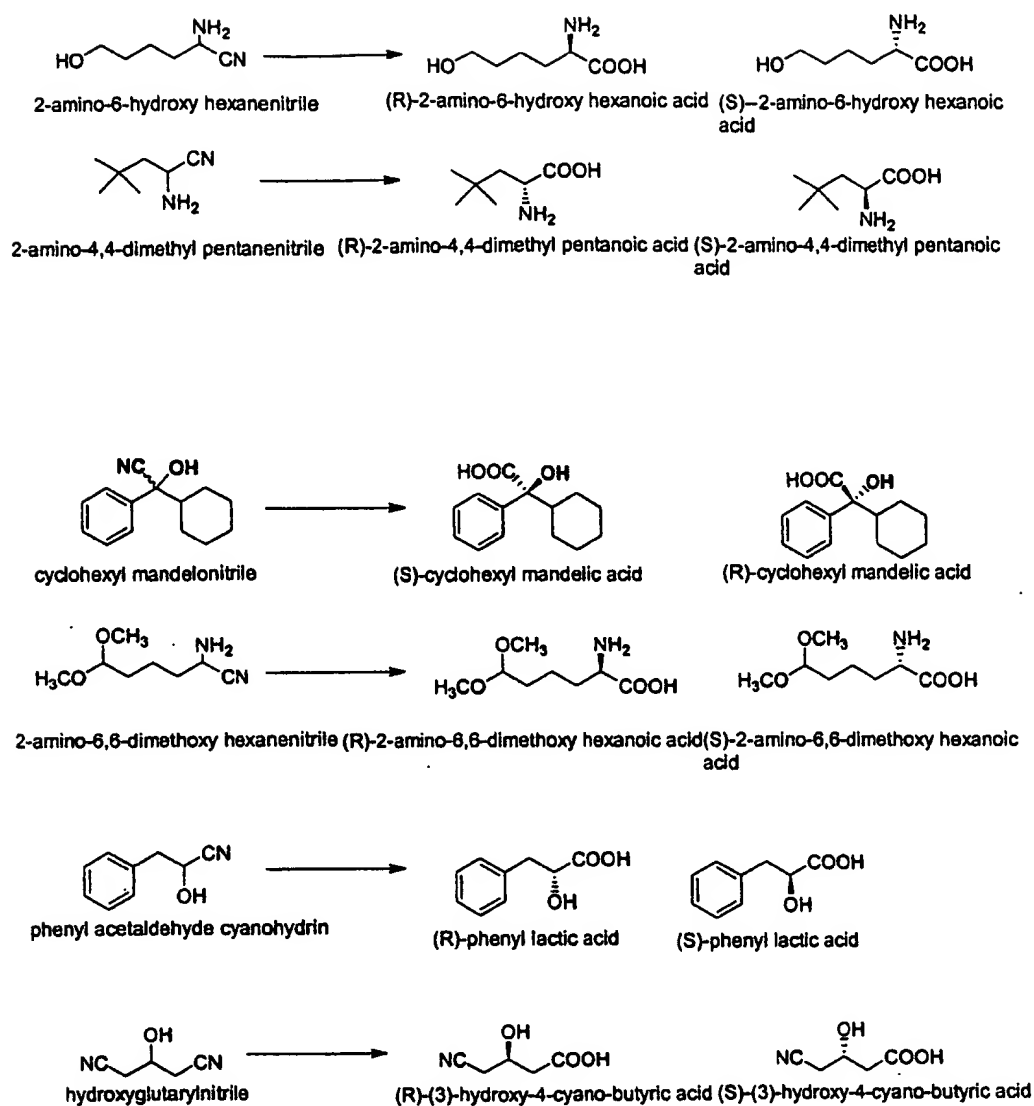


Figure 16

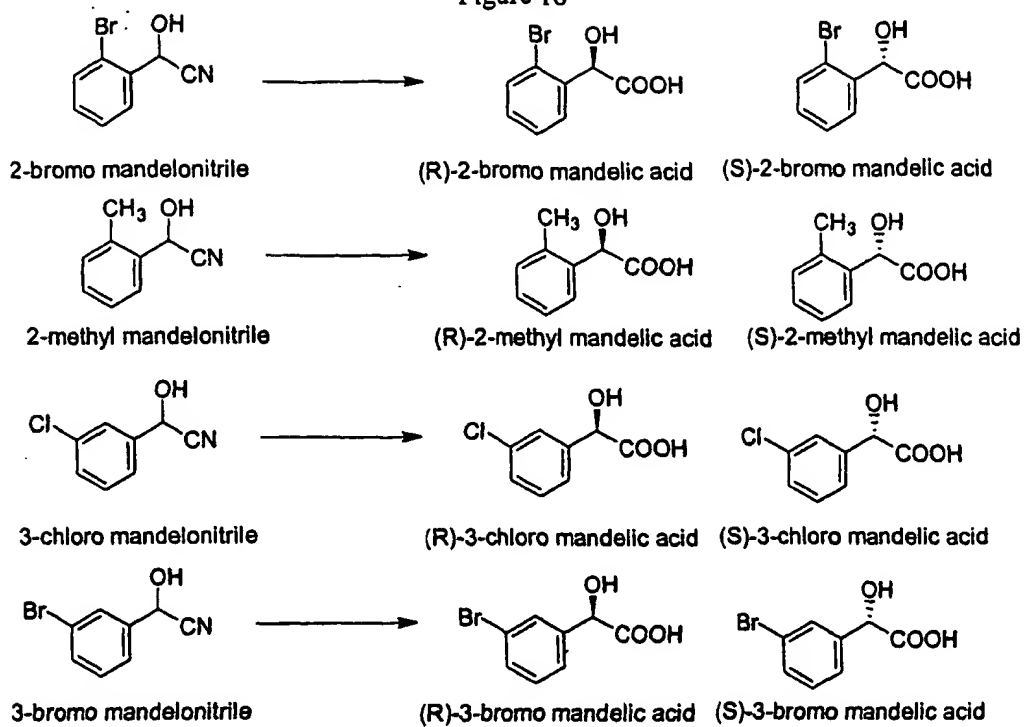


Figure 16

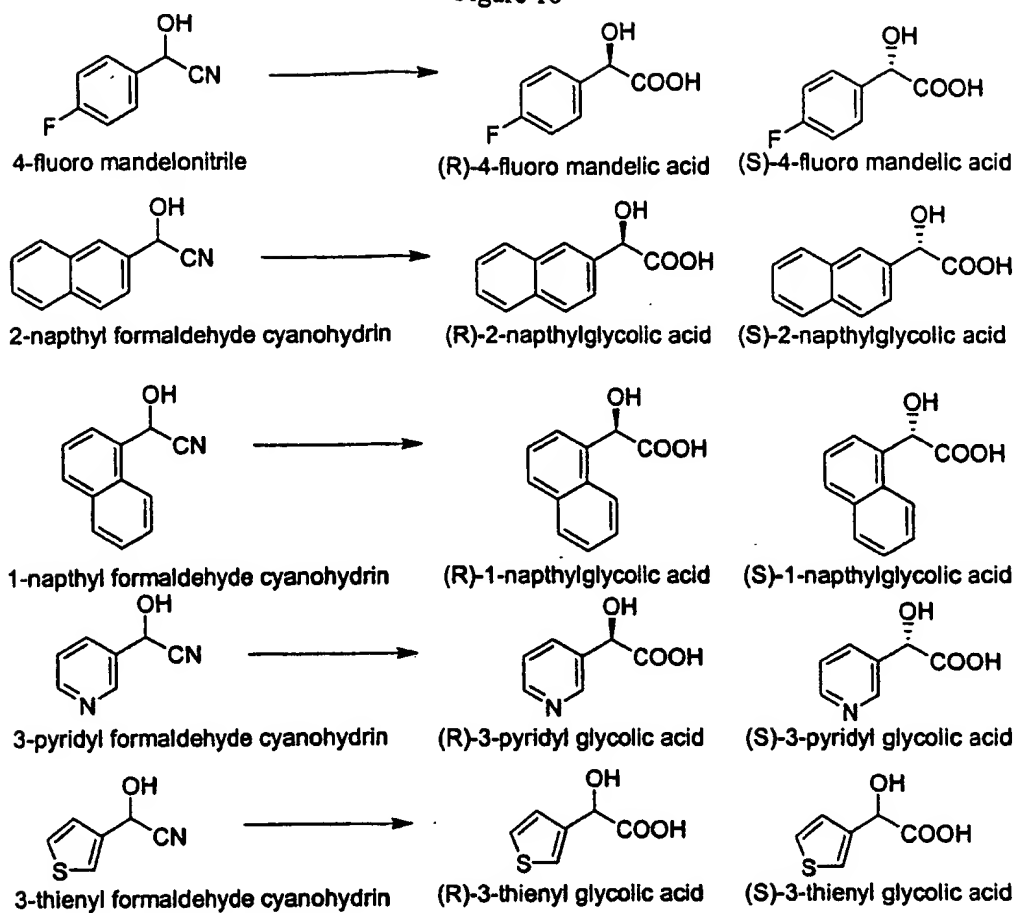


Figure 16

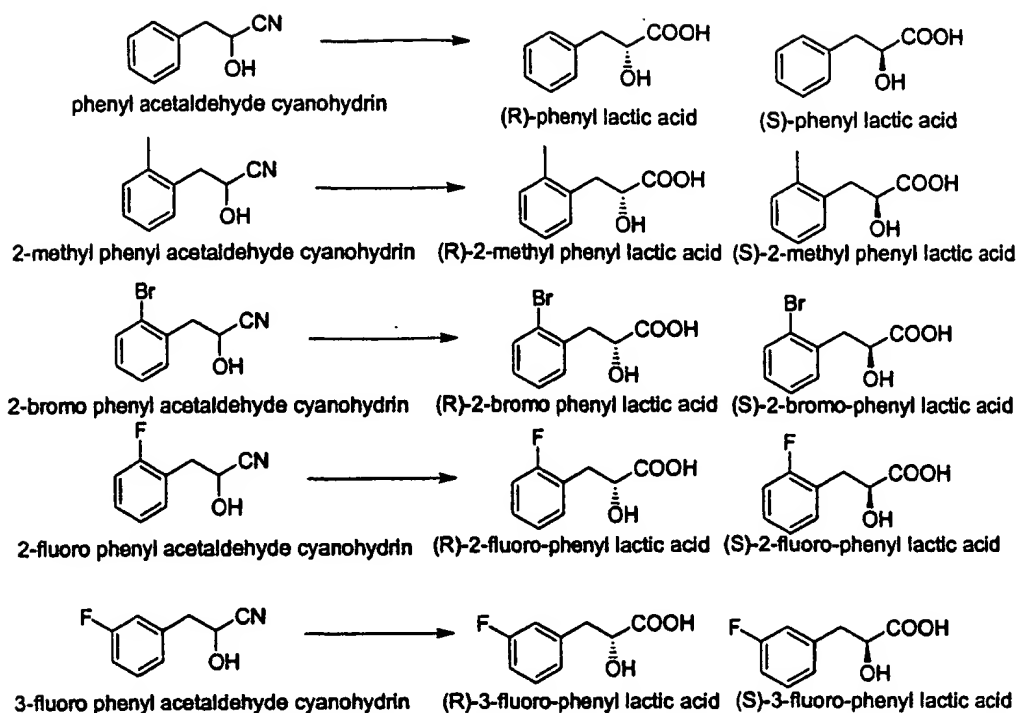


Figure 16

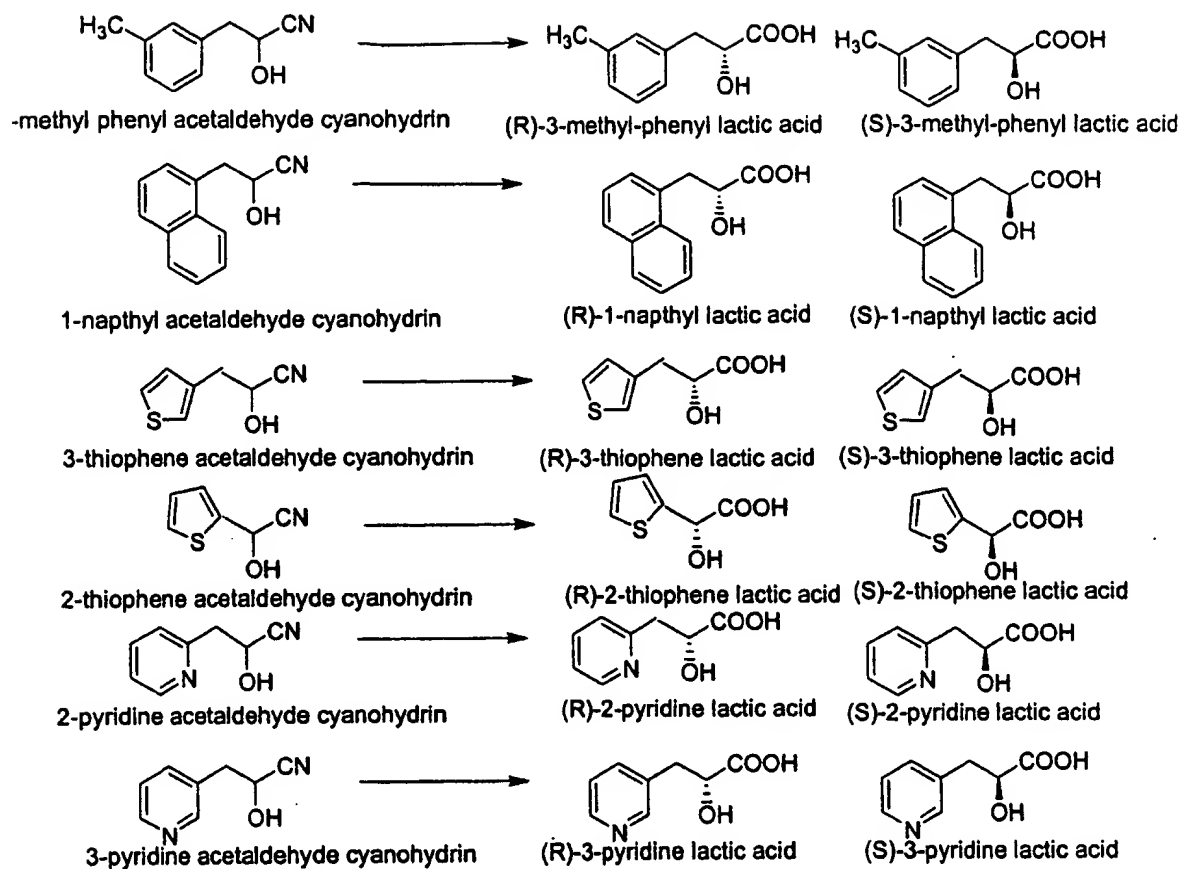
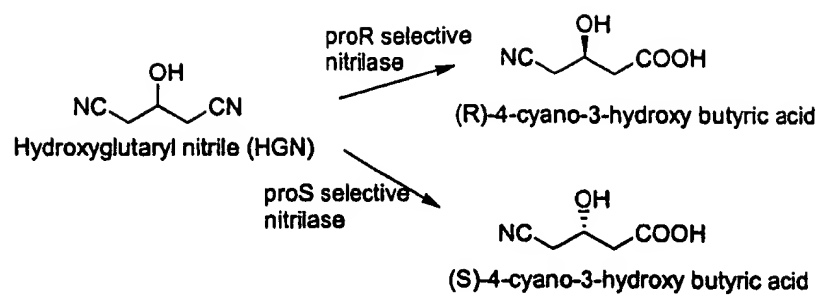


Figure 17



SEQUENCE LISTING

<110> DIVERSA CORPORATION

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<130> Docket No. 09010-120WO4

<140> Unknown

<141> 2003-05-15

<150> US 10/241,742

<151> 2002-09-09

<150> US 10/146,772

<151> 2002-05-15

<150> US 60/309,006

<151> 2001-07-30

<150> US 60/351,336

<151> 2002-01-22

<150> US 60/300,189

<151> 2001-06-21

<150> US 09/751,299

<151> 2000-12-28

<150> US 60/254,414

<151> 2000-12-07

<150> US 60/173,609

<151> 1999-12-29

<160> 386

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<210> 1

<211> 939

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

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attgctttgc cggagttctt caatacgggc gttagtggga acaaaaaaat tgccttggct	180
attcagacgc ctgacggcaa ggctgcgatg ttcttacgcg acttttctgc aagacatcat	240
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atgtgttatg ccaacggcgc tctcgtgggc aaacatgaca aagacctacc cacgatgtgg	360
gaaaatgctt tttatgaagg tggggattcc agcgatattg gggtgctggg aacatttgaa	420
aatacgcgcg ttgggtgcagc cgtctgttgg gagttcatgc ggacgatgac tgcccggcgt	480
cttcgcaatc aggtggatgt catcatgggt ggttctgtct ggtggagcat accgaccaat	540
ttccccgggt ttgtgcaaaa gctgtgggaa cctggaaata gccgcaacgc gcttgcgtgcc	600

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atacaggata atgcgcgtct cattggcgtg cgggttggtc atgccgctca ttgcgggtgaa 660
attgagtgtc cgaatgccagg attgccgata gggttacagg gggttcttga gggtaacgcg 720
gccattgtga atgcagaagg tcaggtgctt gcgcacgcgg gtgctggcga gggcgaagga 780
attgtttgcg cggagatttt accggtagcc aaatcaaaca ggtcggaaat tcccaatcgt 840
tactgggtgc gctgcagagg ctttctacct atttttgcct ggcatcagca acgttggttg 900
ggaaggcatt ggtatttgcg caatgtgcgc aggacttaa 939

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<210> 2

<211> 312

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

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20     25     30
Ala Val Asn Glu Gly Ala Arg Trp Ile Ala Leu Pro Glu Phe Phe Asn
35     40     45
Thr Gly Val Ser Trp Asn Lys Ile Ala Leu Ala Ile Gln Thr Pro
50     55     60
Asp Gly Lys Ala Ala Met Phe Leu Arg Asp Phe Ser Ala Arg His His
65     70     75     80
Val Leu Ile Gly Gly Ser Phe Leu Cys Arg Leu Pro Asp Gly Ser Val
85     90     95
Arg Asn Arg Tyr Met Cys Tyr Ala Asn Gly Ala Leu Val Gly Lys His
100    105    110
Asp Lys Asp Leu Pro Thr Met Trp Glu Asn Ala Phe Tyr Glu Gly Gly
115    120    125
Asp Ser Ser Asp Ile Gly Val Leu Gly Thr Phe Glu Asn Thr Arg Val
130    135    140
Gly Ala Ala Val Cys Trp Glu Phe Met Arg Thr Met Thr Ala Arg Arg
145    150    155    160
Leu Arg Asn Gln Val Asp Val Ile Met Gly Gly Ser Cys Trp Trp Ser
165    170    175
Ile Pro Thr Asn Phe Pro Gly Phe Val Gln Lys Leu Trp Glu Pro Gly
180    185    190
Asn Ser Arg Asn Ala Leu Ala Ala Ile Gln Asp Asn Ala Arg Leu Ile
195    200    205
Gly Val Pro Val Val His Ala Ala His Cys Gly Glu Ile Glu Cys Pro
210    215    220
Met Pro Gly Leu Pro Ile Gly Tyr Arg Gly Phe Phe Glu Gly Asn Ala
225    230    235    240
Ala Ile Val Asn Ala Glu Gly Gln Val Leu Ala His Arg Gly Ala Gly
245    250    255
Glu Gly Glu Gly Ile Val Cys Ala Glu Ile Leu Pro Val Ala Lys Ser
260    265    270
Asn Arg Ser Glu Ile Pro Asn Arg Tyr Trp Leu Arg Cys Arg Gly Phe
275    280    285
Leu Pro Ile Phe Ala Trp His Gln Gln Arg Trp Leu Gly Arg His Trp
290    295    300
Tyr Leu Arg Asn Val Arg Arg Thr
305    310

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<210> 3

<211> 981

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 3

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gtggtctttc cggaggcgtt tgtgcccggg taccactgtt gggctctggt cattccggca      180
gggcattcgc aaccactgcg ggagttatac gccgaactgg tggggaacgc cgtggcggta      240
ccgggcatg ccaccgatcg gctttgcgcg gcagccagag aagccggcgt ggtagtggcg      300
atcgcatca atgaagtga cagcgaagcc agcggcacga cgatttaca tacgctgctg      360
tacatcgag cggacggcgc gattctgggc aaacaccgca aagtaatgcc gacgggcgga      420
gagcgcctgg tctgggcgct tggcgatggg agcgacctgg aggtctacga cctgccttc      480
ggccgattgg gtggcctggt gtgctgggag aactacatgc ccctggccc gtacgcgatg      540
tcggcatggg gaaccgagat ctacgtggct ccaactggg atcgcggaga accgtggctg      600
tcacaaatgc ggcataatgc gaaagaagg cgatgctac tagtgggatg ctgcagtgc      660
atgaaaattg acgatgtacc cgaccggctg gcgttcaaag ggaagtatct gtcgacggcc      720
gagggctggc tcaaccccg cgatagcgta atcgctcgatc cggacggcaa gctgatcgcg      780
ggcccgcaa gcgagcagga gacgattctg tatgccgatg ccgaccggtc taagatcacc      840
gggccaggt ggcaattgga tgtggccggc cactacgcgc ggccggatat cttcgaactg      900
atcgtgcacc gcgaacctaa gcgattttg acgatagctc cgcgacgaa ggaggagcgg      960
gagcctgggc cggaggcctg a                                     981

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<210> 4

<211> 326

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 4

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Leu Asp Arg Gly Ala Thr Val Ala Lys Ala Cys Arg Leu Ile Ala Glu
20     25     30
Ala Ala Ala Ala Gly Ala Ser Leu Val Val Phe Pro Glu Ala Phe Val
35     40     45
Pro Gly Tyr Pro Leu Trp Val Trp Phe Ile Pro Ala Gly His Ser Gln
50     55     60
Pro Leu Arg Glu Leu Tyr Ala Glu Leu Val Gly Asn Ala Val Ala Val
65     70     75     80
Pro Gly Asp Ala Thr Asp Arg Leu Cys Ala Ala Arg Glu Ala Gly
85     90     95
Val Val Val Ala Ile Gly Ile Asn Glu Val Asn Ser Glu Ala Ser Gly
100    105    110
Thr Thr Ile Tyr Asn Thr Leu Leu Tyr Ile Gly Ala Asp Gly Ala Ile
115    120    125
Leu Gly Lys His Arg Lys Val Met Pro Thr Gly Gly Glu Arg Leu Val
130    135    140
Trp Ala Leu Gly Asp Gly Ser Asp Leu Glu Val Tyr Asp Leu Pro Phe
145    150    155    160
Gly Arg Leu Gly Gly Leu Leu Cys Trp Glu Asn Tyr Met Pro Leu Ala
165    170    175
Arg Tyr Ala Met Ser Ala Trp Gly Thr Glu Ile Tyr Val Ala Pro Thr
180    185    190
Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Met Arg His Ile Ala Lys
195    200    205

```

Glu Gly Arg Cys Tyr Val Val Gly Cys Cys Ser Cys Met Lys Ile Asp
 210 215 220
 Asp Val Pro Asp Arg Leu Ala Phe Lys Gly Lys Tyr Leu Ser Thr Ala
 225 230 235 240
 Glu Gly Trp Leu Asn Pro Gly Asp Ser Val Ile Val Asp Pro Asp Gly
 245 250 255
 Lys Leu Ile Ala Gly Pro Ala Ser Glu Gln Glu Thr Ile Leu Tyr Ala
 260 265 270
 Asp Ala Asp Arg Ser Lys Ile Thr Gly Pro Arg Trp Gln Leu Asp Val
 275 280 285
 Ala Gly His Tyr Ala Arg Pro Asp Ile Phe Glu Leu Ile Val His Arg
 290 295 300
 Glu Pro Lys Arg Phe Leu Thr Ile Ala Pro Arg Thr Lys Glu Glu Arg
 305 310 315 320
 Glu Pro Gly Pro Glu Ala
 325

<210> 5

<211> 1005

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

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gcgaagctca	ttgcgttccc	ggaaacctgg	attcccggct	atccgtggca	catctgggtc	180
ggcacgcggg	cgtgggcgat	cagccgcggc	ttcgtgcagc	gctacttcga	caattcactg	240
gcctacgaca	gcccgcaggc	ccagcgcatc	gcggacgccc	cgaagaagaa	caagatcacc	300
gtggtgctcg	gcctgtcggg	gcgcgagggt	ggcagccttt	atatctcgca	gtggctgatt	360
gggccgggacg	gcgagaccat	tgccaagcgc	cgaaaactgc	gccccaccca	cgtcgagcgc	420
accgtgttcg	gcgatggcga	cggcagccac	atcgcggtgc	acgagcgtgc	tgacatcggc	480
cgcctcggcg	cgctgtgctg	ctgggagcac	atccagccgc	tgaccaaata	cgccatgtat	540
gcccagaacg	agcaggtgca	cgtcgcggcc	tgccgagct	tctcgatgta	cgagccgttc	600
gcccacgcgc	tcggctggga	agtcaacaat	gcggcgagca	agatctacgc	cgtcgaaggc	660
tcgtgtttcg	tgctcggcgc	atgcgcggtg	atctcgagg	cgatggtcga	cgaaatgtgc	720
gacaccgagg	acaagcgggc	gctggtccat	gccggcggcg	gccacgcggt	gatcttcggg	780
ccggacggca	gatcgctggc	ggacaagatt	ccggagaccc	aggaaggcct	gctctatgcc	840
gacatcgacc	tcggcgcaat	tggcgtggcc	aagaacgcgg	ccgatccggc	ggggcactac	900
tcgcgcccgg	acgtgacgcg	gctcctgttc	aacaacaagc	cggcgcggcg	ggtcgagtat	960
ttctcgctgc	cggtcgacgc	ggtcgagacg	ccgcgcgagc	cctga		1005

<210> 6

<211> 334

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

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Pro Glu Trp Leu Asp Leu Asp Arg Thr Val Asp Lys Thr Ile Ala Leu	
20 25 30	
Ile Glu Glu Ala Ala Gly Ala Gly Ala Lys Leu Ile Ala Phe Pro Glu	
35 40 45	

Thr Trp Ile Pro Gly Tyr Pro Trp His Ile Trp Val Gly Thr Pro Ala
 50 55 60
 Trp Ala Ile Ser Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
 65 70 75 80
 Ala Tyr Asp Ser Pro Gln Ala Gln Arg Ile Ala Asp Ala Ala Lys Lys
 85 90 95
 Asn Lys Ile Thr Val Val Leu Gly Leu Ser Glu Arg Glu Gly Gly Ser
 100 105 110
 Leu Tyr Ile Ser Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
 115 120 125
 Lys Arg Arg Lys Leu Arg Pro Thr His Val Glu Arg Thr Val Phe Gly
 130 135 140
 Asp Gly Asp Gly Ser His Ile Ala Val His Glu Arg Ala Asp Ile Gly
 145 150 155 160
 Arg Leu Gly Ala Leu Cys Cys Trp Glu His Ile Gln Pro Leu Thr Lys
 165 170 175
 Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ala Trp Pro
 180 185 190
 Ser Phe Ser Met Tyr Glu Pro Phe Ala His Ala Leu Gly Trp Glu Val
 195 200 205
 Asn Asn Ala Ala Ser Lys Ile Tyr Ala Val Glu Gly Ser Cys Phe Val
 210 215 220
 Leu Gly Ala Cys Ala Val Ile Ser Gln Ala Met Val Asp Glu Met Cys
 225 230 235 240
 Asp Thr Glu Asp Lys Arg Ala Leu Val His Ala Gly Gly Gly His Ala
 245 250 255
 Val Ile Phe Gly Pro Asp Gly Arg Ser Leu Ala Asp Lys Ile Pro Glu
 260 265 270
 Thr Gln Glu Gly Leu Leu Tyr Ala Asp Ile Asp Leu Gly Ala Ile Gly
 275 280 285
 Val Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
 290 295 300
 Val Thr Arg Leu Leu Phe Asn Asn Lys Pro Ala Arg Arg Val Glu Tyr
 305 310 315 320
 Phe Ser Leu Pro Val Asp Ala Val Glu Thr Pro Pro Gln Pro
 325 330

<210> 7

<211> 999

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 7

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 ggcgcacgctc tgatcgtgtt tcctgaagcg ttcattccca cctatcccga ttgggtctgg 180
 accattccac ctggggagat gcggtgctt ggcgaactct acacagagtt gcttgccaat 240
 gcggtcacga tccccagtaa tgcaacggat aggctctgcc aggtgcgaa acgagctgct 300
 gcgtatgtgg tcatgggaat gaacgaacgc aatatcgagg cgagtggaag gagtctctat 360
 aacaccctgt tatacatcga tgctcagggc cagatcatgg gcaaacaccg caagttgata 420
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 aacctctggc tctctactct gcggcatatc gctaaggagg gaggcgtcta tgttcttggt 660
 ttagtagtatg tcatgcgcaa gaatgacatt cccgatcact ttgctttcaa agagcagttt 720
 tatgctactg tggacgaatg gatcaacgtt ggtgacagcg ccattgtcca tcccaggggg 780
 aactttcttg cgggaccggg gcgccacaaa gaagagattc tctatgcaga acttgatcca 840

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cgccaatcgt gcgggtccggg atggatgctc gatgtggctg ggcactatgc acgccctgat      900
gtgtttgaat tgattgtcca cacagagatg cgacccatga tgaagcaaga agaggttagga      960
ggagaaaata catctgaggg aggtgtacga ttcttgtaa      999

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<210> 8
 <211> 332
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

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20     25     30
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35     40     45
Glu Ala Phe Ile Pro Thr Tyr Pro Asp Trp Val Trp Thr Ile Pro Pro
50     55     60
Gly Glu Met Arg Leu Leu Gly Glu Leu Tyr Thr Glu Leu Leu Ala Asn
65     70     75     80
Ala Val Thr Ile Pro Ser Asn Ala Thr Asp Arg Leu Cys Gln Ala Ala
85     90     95
Lys Arg Ala Ala Ala Tyr Val Val Met Gly Met Asn Glu Arg Asn Ile
100    105    110
Glu Ala Ser Gly Arg Ser Leu Tyr Asn Thr Leu Leu Tyr Ile Asp Ala
115    120    125
Gln Gly Gln Ile Met Gly Lys His Arg Lys Leu Ile Pro Thr Ala Gly
130    135    140
Glu Arg Leu Ile Trp Ala Gln Gly Asp Gly Ser Thr Phe Gln Val Tyr
145    150    155    160
Asp Thr Pro Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn Tyr
165    170    175
Met Pro Leu Ala Arg Tyr Ala Met Tyr Ala Trp Gly Thr Gln Ile Tyr
180    185    190
Val Ala Pro Thr Trp Asp Arg Gly Asn Leu Trp Leu Ser Thr Leu Arg
195    200    205
His Ile Ala Lys Glu Gly Gly Val Tyr Val Leu Gly Cys Ser Met Val
210    215    220
Met Arg Lys Asn Asp Ile Pro Asp His Phe Ala Phe Lys Glu Gln Phe
225    230    235    240
Tyr Ala Thr Val Asp Glu Trp Ile Asn Val Gly Asp Ser Ala Ile Val
245    250    255
His Pro Glu Gly Asn Phe Leu Ala Gly Pro Val Arg His Lys Glu Glu
260    265    270
Ile Leu Tyr Ala Glu Leu Asp Pro Arg Gln Ser Cys Gly Pro Gly Trp
275    280    285
Met Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Glu Leu
290    295    300
Ile Val His Thr Glu Met Arg Pro Met Met Lys Gln Glu Glu Val Gly
305    310    315    320
Gly Glu Asn Thr Ser Glu Gly Gly Val Arg Phe Leu
325    330

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<210> 9
 <211> 945
 <212> DNA
 <213> Unknown

<220>

<223> Obtained from an environmental sample

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gtgtttccgg	aggcctacat	ccccggctac	ccggactgga	tctggcgctc	gcgcccctac	180
ccggacgtca	agctggccgc	cgagctgcac	gaacggctgc	tcgccaacgc	ggtggatctc	240
tccaccgacg	tgctggcgcc	ggtgctggcg	gcggcggcgc	gtcacgggct	caccgtggtc	300
atgtgcgtgc	aggagcgcg	cgccggattc	agccgcgcca	cactttacaa	caccgcgtg	360
gtcatcgacg	ccgccggcaa	gatcgcgaa	cggcaccgca	agctcatgcc	caccaacccc	420
gagcgaatgg	tgtggggatt	cggtgacgcc	tcggggctgc	gggtggtag	cacgcccgtc	480
gggcgggtgg	gcacgctcct	gtgctgggag	agctacatgc	ccctggcgcg	ctgcgcgtc	540
tacgccgagg	gggtcgagat	ctacgtgacc	ccgacctggg	actacggcga	aggctggcgc	600
gccagcatgc	agcacatcgc	ccgcgagggg	cgctgctggg	tggtgaccgc	ttgcatgtgc	660
gtgcaggcgc	gcgacgtgcc	ggccgacttc	cccgggcgcg	cccagctcta	ccccgacgag	720
gaggagtgg	tgaacccggg	cgattcgctg	gtggtcgacc	ccggcggcaa	gatcgtggcc	780
ggtccgatgt	cgcgcgagaa	ggggatcttg	tacgcggaga	tcgatccgga	tcgctggcgc	840
ggggcgcaac	gctcggtcga	cgctgtgggc	cactactcgc	gtcccgcgtg	gttccggctg	900
gaggtcgatc	ggacaccggc	ggcgccggtg	agcttcaaaa	aatga		945

<210> 10

<211> 314

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 10

Met	Ala	Ala	His	Lys	Ile	Ala	Val	Val	Gln	Ala	Pro	Ser	Val	Leu	Leu
1			5						10				15		
Asp	Arg	Glu	Gly	Ser	Val	Ala	Arg	Ala	Val	Thr	Leu	Leu	Asp	Glu	Ala
		20					25					30			
Ala	Ala	Ala	Gly	Ala	Arg	Leu	Val	Phe	Pro	Glu	Ala	Tyr	Ile	Pro	
		35				40					45				
Gly	Tyr	Pro	Asp	Trp	Ile	Trp	Arg	Leu	Arg	Pro	Tyr	Pro	Asp	Val	Lys
	50				55					60					
Leu	Ala	Ala	Glu	Leu	His	Glu	Arg	Leu	Leu	Ala	Asn	Ala	Val	Asp	Leu
65				70					75				80		
Ser	Thr	Asp	Val	Leu	Ala	Pro	Val	Leu	Ala	Ala	Ala	Ala	Arg	His	Gly
			85					90					95		
Leu	Thr	Val	Val	Met	Cys	Val	Gln	Glu	Arg	Asp	Ala	Gly	Phe	Ser	Arg
		100						105				110			
Ala	Thr	Leu	Tyr	Asn	Thr	Ala	Leu	Val	Ile	Asp	Ala	Ala	Gly	Lys	Ile
		115				120						125			
Ala	Asn	Arg	His	Arg	Lys	Leu	Met	Pro	Thr	Asn	Pro	Glu	Arg	Met	Val
	130					135					140				
Trp	Gly	Phe	Gly	Asp	Ala	Ser	Gly	Leu	Arg	Val	Val	Ser	Thr	Pro	Val
145					150				155					160	
Gly	Arg	Val	Gly	Thr	Leu	Leu	Cys	Trp	Glu	Ser	Tyr	Met	Pro	Leu	Ala
			165					170					175		
Arg	Cys	Ala	Leu	Tyr	Ala	Glu	Gly	Val	Glu	Ile	Tyr	Val	Thr	Pro	Thr
		180					185					190			
Trp	Asp	Tyr	Gly	Glu	Gly	Trp	Arg	Ala	Ser	Met	Gln	His	Ile	Ala	Arg
	195					200					205				
Glu	Gly	Arg	Cys	Trp	Val	Val	Thr	Ala	Cys	Met	Cys	Val	Gln	Ala	Arg
	210					215					220				


```

Asp Val Pro Ala Asp Phe Pro Gly Arg Ala Gln Leu Tyr Pro Asp Glu
225                230                235                240
Glu Glu Trp Leu Asn Pro Gly Asp Ser Leu Val Val Asp Pro Gly Gly
                245                250                255
Lys Ile Val Ala Gly Pro Met Ser Arg Glu Lys Gly Ile Leu Tyr Ala
                260                265                270
Glu Ile Asp Pro Asp Arg Val Ala Gly Ala His Arg Ser Phe Asp Val
                275                280                285
Val Gly His Tyr Ser Arg Pro Asp Val Phe Arg Leu Glu Val Asp Arg
                290                295                300
Thr Pro Ala Ala Pro Val Ser Phe Lys Lys
305                310

```

<210> 11
 <211> 966
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

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<400> 11
atgactggat cttatcctaa agacacactg atcgttgggc tagctcaaat cgctcctgtc      60
tggctggatc gggcggggac actgtcaaag atactggctc aagtccatgc ggcaaatcaa      120
gcggttggtc atctcgtagc atttggcgaa gggctgcttc ctggatatcc gttttggatt      180
gagcgaacaa atggcgcgct gttcaactcg actgtacaaa aggaaatcca cgcgcattat      240
atggatcagg cggtgcagat cgaagccggt catctcgatc cgctttgtgc aacagccaag      300
aaatttggaa tcaccgttgt actcggatgc atcgaacgcc cactcgatcg gggcggtcac      360
agcttgtatg caagtctggt atatattgat tccgagggca gcattcaatc cgtgcatcgc      420
aaactaatgc caacctacga agaacgactt acctggctcg caggcgatgg gcacggttta      480
cgagtgcata ccttaggtgc gtttacggtg ggtggtctca actgttggga aaattggatg      540
cccttggcgc gcgcagcgat gtatggtcag ggtgaagatt tacatgttgc gatctggcca      600
ggcggttctc atctcacgca ggatattacc cgctttattg cgctcgaatc acgttcgtac      660
gtattatctg tctccggtct gatgcgcgca accgatattc caaaagatac tccccatctt      720
gcctccatcc tagctaaagg tgaagagatt cttgcgaatg gtggttcttg tattgcagggt      780
cctgacggca agtgggtcgt tgggcctctt gtaggagaag agaagttaat tgtcgcaacc      840
attgatcact gccgcgtgcg cgaagaacgt cagaatttcg atccttccgg gcattacagc      900
cggccccgatg tactgcaatt aaaaatcaac agggaacgcc agagcacaat ttcatttagc      960
gagtag

```

<210> 12
 <211> 321
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 12
Met Thr Gly Ser Tyr Pro Lys Asp Thr Leu Ile Val Gly Leu Ala Gln
1          5          10          15
Ile Ala Pro Val Trp Leu Asp Arg Ala Gly Thr Leu Ser Lys Ile Leu
20          25          30
Ala Gln Val His Ala Ala Asn Gln Ala Gly Cys His Leu Val Ala Phe
35          40          45
Gly Glu Gly Leu Leu Pro Gly Tyr Pro Phe Trp Ile Glu Arg Thr Asn
50          55          60
Gly Ala Leu Phe Asn Ser Thr Val Gln Lys Glu Ile His Ala His Tyr
65          70          75          80

```

Met Asp Gln Ala Val Gln Ile Glu Ala Gly His Leu Asp Pro Leu Cys
 85 90 95
 Ala Thr Ala Lys Phe Gly Ile Thr Val Val Leu Gly Cys Ile Glu
 100 105 110
 Arg Pro Leu Asp Arg Gly Gly His Ser Leu Tyr Ala Ser Leu Val Tyr
 115 120 125
 Ile Asp Ser Glu Gly Ser Ile Gln Ser Val His Arg Lys Leu Met Pro
 130 135 140
 Thr Tyr Glu Glu Arg Leu Thr Trp Ser Ser Gly Asp Gly His Gly Leu
 145 150 155 160
 Arg Val His Thr Leu Gly Ala Phe Thr Val Gly Gly Leu Asn Cys Trp
 165 170 175
 Glu Asn Trp Met Pro Leu Ala Arg Ala Ala Met Tyr Gly Gln Gly Glu
 180 185 190
 Asp Leu His Val Ala Ile Trp Pro Gly Gly Ser His Leu Thr Gln Asp
 195 200 205
 Ile Thr Arg Phe Ile Ala Leu Glu Ser Arg Ser Tyr Val Leu Ser Val
 210 215 220
 Ser Gly Leu Met Arg Ala Thr Asp Phe Pro Lys Asp Thr Pro His Leu
 225 230 235 240
 Ala Ser Ile Leu Ala Lys Gly Glu Glu Ile Leu Ala Asn Gly Gly Ser
 245 250 255
 Cys Ile Ala Gly Pro Asp Gly Lys Trp Val Val Gly Pro Leu Val Gly
 260 265 270
 Glu Glu Lys Leu Ile Val Ala Thr Ile Asp His Cys Arg Val Arg Glu
 275 280 285
 Glu Arg Gln Asn Phe Asp Pro Ser Gly His Tyr Ser Arg Pro Asp Val
 290 295 300
 Leu Gln Leu Lys Ile Asn Arg Glu Arg Gln Ser Thr Ile Ser Phe Ser
 305 310 315 320
 Glu

<210> 13

<211> 1014

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 13

atgggcattc	aacatccgaa	atataagggt	gcggtggtgc	aggcggcgcc	ggcctggctc	60
gatctcgatg	cgtcgatcgc	caaatcgatc	gcgttgatcg	aggaggcggc	tgccaatggc	120
gccaaactga	tcgccttccc	ggaggcggtc	atccctggct	atccctggta	tatctggctg	180
gactcgccgg	cctgggcatg	cggccgcggt	tttgtgcagc	gctatttcga	caactcgctg	240
gcctatgaca	gccccgagcg	cgagaagctg	cggctggcgg	tgaagaaggc	cggcctcacc	300
gccgtgatcg	gcctctccga	gcgcgagggc	ggcagccttt	atctcgcgca	atggctgatc	360
gggcccgatg	gcgagaccat	cgcaaagcgc	cgcaagctgc	ggccgaccga	tgccgagcgc	420
accgtctatg	gcgaaggcga	tggcagcgat	ctgcggtgct	atgaccgccc	cggcatcggc	480
cggctcggcg	cgctgtgctg	ctgggagcat	ctgcagccgc	tgtcgaaaata	cgcgatgtat	540
gcccagaacg	agcaggttca	tgtcgcggcc	tggccgagct	tctcgtctta	cgacccgttc	600
gcgcgcggcg	tcggctggga	ggtcaacaat	gcggcctcac	gcgtctatgc	ggtggaaggc	660
tcgtgcttcg	tgctggcgcc	ctgcgcgacg	gtgtcgaaag	cgatgatcga	cgagctctgc	720
gaccgcgacg	acaagcacgg	gctgctgcat	gtcggcgggg	gacacgccgc	gatctatggg	780
ccggacggct	cttcgattgc	ggagaaattg	ccgccggagc	aggaggccct	gctctatgcc	840
gacatcgatc	tcggcgccat	cgggattgcc	aagaacgccg	ccgatccggc	cggacattac	900
tcgcggcccg	acgtgacgcg	gctgttgctc	aacaagaagc	cgtcgaaagc	tgtcgagcat	960
ttttcgctgc	cggtcgacaa	tgtcgagccg	gagatcgacg	ccgccgccag	ctga	1014

<210> 14

<211> 337
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 14
 Met Gly Ile Gln His Pro Lys Tyr Lys Val Ala Val Val Gln Ala Ala
 1 5 10 15
 Pro Ala Trp Leu Asp Leu Asp Ala Ser Ile Ala Lys Ser Ile Ala Leu
 20 25 30
 Ile Glu Glu Ala Ala Ala Asn Gly Ala Lys Leu Ile Ala Phe Pro Glu
 35 40 45
 Ala Phe Ile Pro Gly Tyr Pro Trp Tyr Ile Trp Leu Asp Ser Pro Ala
 50 55 60
 Trp Ala Ile Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
 65 70 75 80
 Ala Tyr Asp Ser Pro Gln Ala Glu Lys Leu Arg Leu Ala Val Lys Lys
 85 90 95
 Ala Gly Leu Thr Ala Val Ile Gly Leu Ser Glu Arg Glu Gly Gly Ser
 100 105 110
 Leu Tyr Leu Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
 115 120 125
 Lys Arg Arg Lys Leu Arg Pro Thr His Ala Glu Arg Thr Val Tyr Gly
 130 135 140
 Glu Gly Asp Gly Ser Asp Leu Ala Val His Asp Arg Pro Gly Ile Gly
 145 150 155 160
 Arg Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys
 165 170 175
 Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ala Trp Pro
 180 185 190
 Ser Phe Ser Leu Tyr Asp Pro Phe Ala Pro Ala Leu Gly Trp Glu Val
 195 200 205
 Asn Asn Ala Ala Ser Arg Val Tyr Ala Val Glu Gly Ser Cys Phe Val
 210 215 220
 Leu Ala Pro Cys Ala Thr Val Ser Lys Ala Met Ile Asp Glu Leu Cys
 225 230 235 240
 Asp Arg Asp Asp Lys His Gly Leu Leu His Val Gly Gly Gly His Ala
 245 250 255
 Ala Ile Tyr Gly Pro Asp Gly Ser Ser Ile Ala Glu Lys Leu Pro Pro
 260 265 270
 Glu Gln Glu Gly Leu Leu Tyr Ala Asp Ile Asp Leu Gly Ala Ile Gly
 275 280 285
 Ile Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
 290 295 300
 Val Thr Arg Leu Leu Leu Asn Lys Lys Pro Ser Lys Arg Val Glu His
 305 310 315 320
 Phe Ser Leu Pro Val Asp Asn Val Glu Pro Glu Ile Asp Ala Ala Ala
 325 330 335
 Ser

<210> 15
 <211> 1047
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 15
atgccaaacat caaaacaatt tagagtcgct gcagttcaag ccgccccggt atttcttgac      60
ctggagggcg caataagcaa aggcattctcc ctcataggag aggccgcttc caatggagcc      120
aagctcattg ccttcccggg aacgtggatt cccggctacc cctgggtgat ctggctggac      180
tcaccgcgtt ggggcatgcg ctttgtccag cgctattttg acaactcgct catgctgggt      240
agtgcagcaag ccaagcgcgt gaaccaggct gccgccaata acaagattta cgtggtgatg      300
ggttatagcg aacgcagtg ggcagcctc tacatgggccc aatccattat caacgacaag      360
gggtgaaacga tttttaccgg ccgcaaactc aagccaactc atgtcgagcg taccgtgttt      420
ggggaggggag acggcagcca tctttgcgta atggataccg agattggccg cgtcggcgcg      480
atgtgctggt gggaacattt gcagccgctc agcaaataag caatgtattc tcaggatgaa      540
caaattcaca ttgcctcctg gccgagcttt tcgttatatc ggggggcagc ctatgcactc      600
ggccccgaac tgaacaacgc cgccagccaa atgtatgcag ccgaaggcca gtgctttgtc      660
cttgcctcctt gcgccaccgt ctcaaaggag atgatcgaaa tgctgataga tgatcccagg      720
aaagagccgc ttctgctgga aggtggcggg ttcacatga tttacggccc cgatgggcga      780
cctctggcta aaccgttgcc tgaaaacgag gaagggctgc tatatgccga tattgacctg      840
gtcactcgcc tactattcaa ttccgcgccc gccaatcgcg tcgagtatat caaccagcg      900
tcaggcccaa ccgaatcctt aaaagatatg ggaaagatgc aaatggaggc cgaacagcaa      960
aaggcgcccc tgcgagagat gatctaa      1020
                                     1047

```

<210> 16

<211> 348

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 16

```

Met Pro Thr Ser Lys Gln Phe Arg Val Ala Ala Val Gln Ala Ala Pro
 1              5              10              15
Val Phe Leu Asp Leu Glu Gly Ala Ile Ser Lys Gly Ile Ser Leu Ile
 20              25              30
Glu Glu Ala Ala Ser Asn Gly Ala Lys Leu Ile Ala Phe Pro Glu Thr
 35              40              45
Trp Ile Pro Gly Tyr Pro Trp Trp Ile Trp Leu Asp Ser Pro Ala Trp
 50              55              60
Gly Met Arg Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu Met Leu Gly
 65              70              75              80
Ser Glu Gln Ala Lys Arg Met Asn Gln Ala Ala Ala Asn Asn Lys Ile
 85              90              95
Tyr Val Val Met Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Met
100              105              110
Gly Gln Ser Ile Ile Asn Asp Lys Gly Glu Thr Ile Phe Thr Arg Arg
115              120              125
Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly Asp
130              135              140
Gly Ser His Leu Cys Val Met Asp Thr Glu Ile Gly Arg Val Gly Ala
145              150              155              160
Met Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr Ala Met Tyr
165              170              175
Ser Gln Asp Glu Gln Ile His Ile Ala Ser Trp Pro Ser Phe Ser Leu
180              185              190
Tyr Arg Gly Ala Ala Tyr Ala Leu Gly Pro Glu Leu Asn Asn Ala Ala
195              200              205
Ser Gln Met Tyr Ala Ala Glu Gly Gln Cys Phe Val Leu Ala Pro Cys
210              215              220
Ala Thr Val Ser Lys Glu Met Ile Glu Met Leu Ile Asp Asp Pro Arg
225              230              235              240
Lys Glu Pro Leu Leu Leu Glu Gly Gly Gly Phe Thr Met Ile Tyr Gly
245              250              255

```

```

Pro Asp Gly Arg Pro Leu Ala Lys Pro Leu Pro Glu Asn Glu Glu Gly
      260      265      270
Leu Leu Tyr Ala Asp Ile Asp Leu Gly Met Ile Ser Met Ala Lys Ala
      275      280      285
Ala Ala Asp Pro Ala Gly His Tyr Ala Arg Pro Asp Val Thr Arg Leu
      290      295      300
Leu Phe Asn Ser Ala Pro Ala Asn Arg Val Glu Tyr Ile Asn Pro Ala
305      310      315      320
Ser Gly Pro Thr Glu Ser Leu Lys Asp Met Gly Lys Met Gln Met Glu
      325      330      335
Ala Glu Gln Gln Lys Ala Ala Leu Arg Glu Met Ile
      340      345

```

<210> 17
 <211> 993
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 17
atgagagttg ttaaagccgc agctgtccaa ctgagtcctc tcctctatag ccgcgagggg 60
acgggtcgaga aggtcgtgcg gaagatccat gaacttgccg aagagggagt cgagttcgtc 120
acctttcctg agaccgtggt gccttattac ccgtactttt cgttcgttca gacgcccttg 180
cagcaaatct tcggaacaga gtatctgagg ctgctcgacc aggcagtcac cgtgccatcc 240
gccgccaccg acgcgatcgg cgaggtgcc aggttcgctg gagttgttgt ctcgatcggc 300
gtcaacgagc gagacggggg aactctgtac aacactcagc ttctcttcga tgccgacgga 360
agcttaatc agcggcgccg caagatcacg cccaccatt acgagcgcat gatctggggc 420
caggggtgacg gctcaggtct gcgggcccgt gatagcaagg ccggccgcat tggtcagctg 480
gcatgctggg agcacaacaa tccactggcg cgctacgcgc tgatagccga cggcgagcag 540
atccattcgg ccatgtatcc gggctccatg ttccgcgact cgtttgccaa aaagaccgaa 600
atcaatatcc ggcagcatgc gctggagtct gcgtgcttcg tcgtgaacgc aacggcctgg 660
ctggacggcg atcaacaggc gcaaactcatg aaggacaccg gctgcagcat cggcccgatc 720
tccggcggtt gcttcaccac tatcgtggcg ccggacgggt ccctgatcgg cgagcccctc 780
cgctcgggtg agggcggtgt catcgccgac ctgacttca cgtaaatcga caggcgtaag 840
caggtgatgg actcgcgagg ccactacagc cggccggagt tgctcagcct cttaatagac 900
cgcaccccta ccgcgcactt tcacgaacgc gcttcgcacc ccacgacagg agctgagcaa 960
ggctccgagg atgtgttcga ggctaacatt taa 993

```

<210> 18
 <211> 330
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 18
Met Arg Val Val Lys Ala Ala Ala Val Gln Leu Ser Pro Val Leu Tyr
1      5      10      15
Ser Arg Glu Gly Thr Val Glu Lys Val Val Arg Lys Ile His Glu Leu
20     25     30
Ala Glu Glu Gly Val Glu Phe Val Thr Phe Pro Glu Thr Val Val Pro
35     40     45
Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Thr Pro Leu Gln Gln Ile Phe
50     55     60
Gly Thr Glu Tyr Leu Arg Leu Leu Asp Gln Ala Val Thr Val Pro Ser
65     70     75     80
Ala Ala Thr Asp Ala Ile Gly Glu Ala Ala Arg Phe Ala Gly Val Val
85     90     95

```

Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn Thr
 100 105 110
 Gln Leu Leu Phe Asp Ala Asp Gly Ser Leu Ile Gln Arg Arg Arg Lys
 115 120 125
 Ile Thr Pro Thr His Tyr Glu Arg Met Ile Trp Gly Gln Gly Asp Gly
 130 135 140
 Ser Gly Leu Arg Ala Val Asp Ser Lys Ala Gly Arg Ile Gly Gln Leu
 145 150 155 160
 Ala Cys Trp Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Leu Ile Ala
 165 170 175
 Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Met Phe Gly
 180 185 190
 Asp Ser Phe Ala Lys Lys Thr Glu Ile Asn Ile Arg Gln His Ala Leu
 195 200 205
 Glu Ser Ala Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Gly Asp
 210 215 220
 Gln Gln Ala Gln Ile Met Lys Asp Thr Gly Cys Ser Ile Gly Pro Ile
 225 230 235 240
 Ser Gly Gly Cys Phe Thr Thr Ile Val Ala Pro Asp Gly Ser Leu Ile
 245 250 255
 Gly Glu Pro Leu Arg Ser Gly Glu Gly Val Val Ile Ala Asp Leu Asp
 260 265 270
 Phe Thr Leu Ile Asp Arg Arg Lys Gln Val Met Asp Ser Arg Gly His
 275 280 285
 Tyr Ser Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro Thr
 290 295 300
 Ala His Phe His Glu Arg Ala Ser His Pro Thr Thr Gly Ala Glu Gln
 305 310 315 320
 Gly Ser Glu Asp Val Phe Glu Ala Asn Ile
 325 330

<210> 19

<211> 1050

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 19

atggaaagca acttccttgc cgcagcagtg caagcagaac cggtttactt caatgctttt 60
 cagacggccg aaaagggccg gtcattgatt gacgatgccg gtcggcaggg ggctcgctta 120
 gtgacatttc ccgaaacgtg gctgcccggt taccgctact ggatctggct tggcgcccc 180
 gcctggggaa tgcattcattt catcctaaag taccatcaaa actcgccggt tgcaggagga 240
 ccagaggaac agatcctttg tcaggcggcc cgccgcaacg ggatttttgt cgtcatggga 300
 ctacagcgaga aaatcggggc aagcctctac atggcgagtg ggttcattcag tccagacggc 360
 aaagtggctg ctgcccagc caaattgaag cctactcacg tcgaacgttc ggtcttcggg 420
 gaaggggatg gttccgacat tgtcgttctt gataacccc ttggaaaggc cgggggcctt 480
 tgctgctggg agcacatgca gccactttcg aagtacgcca tgtactcgca aggcgagcag 540
 atccatgctg cttcttggcc gagtggttagc gtctatcgcg ataaaaattha cgttctgggg 600
 ccggagctga acggtgccgc caatcagatg tatgcggcag aaggctcagt tttcgtcctg 660
 gcacccctgg caacggtttc acaagcggtt atcgatcttt ttgacgacac gcccgacaag 720
 gccgcgctca tgaaaattgg tgggtgtttt tcccagatct atgggcccaga cgggtgcccc 780
 ctggcgaagc cgttgccgga ggacgtcgaa ggattggtga ccgctgagat tgacttcaat 840
 gccatcacgc gcgtgaaagc agcggcgagc cccgtagggc actatagccg gcccgatgta 900
 ttccgcctgt tgttcaatcg tacgcgcaaa gaacgcgtgg tttctgtcaa cacgtttgtg 960
 ccaggtgtca cccagcgaac cgccaagaat gggctcggcg acgaattggt cggtcacccg 1020
 gagaacgctg tcgcccgggc tgcagagtaa 1050

<210> 20

<211> 349

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 20

```

Met Glu Ser Asn Phe Leu Ala Ala Ala Val Gln Ala Glu Pro Val Tyr
 1          5          10          15
Phe Asn Ala Phe Gln Thr Ala Glu Lys Ala Ala Ser Leu Ile Asp Asp
 20          25          30
Ala Gly Arg Gln Gly Ala Arg Leu Val Thr Phe Pro Glu Thr Trp Leu
 35          40          45
Pro Gly Tyr Pro Tyr Trp Ile Trp Leu Gly Ala Pro Ala Trp Gly Met
 50          55          60
His His Phe Ile Leu Lys Tyr His Gln Asn Ser Pro Val Ala Gly Gly
 65          70          75          80
Pro Glu Glu Gln Ile Leu Cys Gln Ala Ala Arg Arg Asn Gly Ile Phe
 85          90          95
Val Val Met Gly Leu Ser Glu Lys Ile Gly Ala Ser Leu Tyr Met Ala
100          105          110
Gln Trp Phe Ile Ser Pro Asp Gly Lys Val Val Ala Arg Arg Arg Lys
115          120          125
Leu Lys Pro Thr His Val Glu Arg Ser Val Phe Gly Glu Gly Asp Gly
130          135          140
Ser Asp Ile Val Val Leu Asp Thr Pro Leu Gly Lys Val Gly Gly Leu
145          150          155          160
Cys Cys Trp Glu His Met Gln Pro Leu Ser Lys Tyr Ala Met Tyr Ser
165          170          175
Gln Gly Glu Gln Ile His Ala Ala Ser Trp Pro Ser Val Ser Val Tyr
180          185          190
Arg Asp Lys Ile Tyr Val Leu Gly Pro Glu Leu Asn Gly Ala Ala Asn
195          200          205
Gln Met Tyr Ala Ala Glu Gly Gln Cys Phe Val Leu Ala Ser Trp Ala
210          215          220
Thr Val Ser Gln Ala Ala Ile Asp Leu Phe Cys Asp Thr Pro Asp Lys
225          230          235          240
Ala Ala Leu Met Lys Ile Gly Gly Gly Phe Ser Gln Ile Tyr Gly Pro
245          250          255
Asp Gly Cys Pro Leu Ala Lys Pro Leu Pro Glu Asp Val Glu Gly Leu
260          265          270
Val Thr Ala Glu Ile Asp Phe Asn Ala Ile Thr Arg Val Lys Ala Ala
275          280          285
Ala Asp Pro Val Gly His Tyr Ser Arg Pro Asp Val Phe Arg Leu Leu
290          295          300
Phe Asn Arg Thr Arg Gln Glu Arg Val Val Ser Val Asn Thr Phe Val
305          310          315          320
Pro Gly Val Thr Gln Arg Thr Ala Lys Asn Gly Ser Ala Asp Glu Leu
325          330          335
Val Gly His Pro Glu Asn Ala Val Ala Arg Ala Ala Glu
340          345

```

<210> 21

<211> 1065

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 21

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atggcactag aacatccgaa gtacgtggcg gccgtgggtc aggccgcgcc cgaattcctg      60
aatctagaca gagggatcga aaagacgatc gcattgatcg acgaagcggg acagaaaggg      120
gcggccctga ttgcatttcc ggaaacctgg ctgccgggct atccgtttca tgtctggctc      180
ggctctcccg catgggcgct tggtccagga ttctccagc gctatttca caactcgatg      240
acgtacgata gtcctcaggc cgctgcactg agggacgctg ccgcgcgcaa cgggatcacg      300
gtggtattgg gcttgtcgga gcgatgcggc ggacgcctct atatcgcgca atggatcatc      360
ggccccgatg gcgcgacggt cgccacgcgc cgcaaattgc ggccgactca tatcgagcgc      420
accgttttcg gcgatggcga cggcagcgat ctggcagtac acgatctcaa catcgccgcg      480
cttggcgcac tgtgtctgtg ggagcacatt cagccgctga ccaagtacgc gatgtatgcg      540
cagcacgaac aggtgcacgt cgcgccctgg ccgagcttct ccatgtatga attcgcgccc      600
gcgctcggtc acgaggtgaa caacgcagtc agccgcgtct atgccgttga gggatcgtgc      660
ttcgtgctcg cgccgtgcgc ggtcatcagc gagcaaatgg tcgacatggt gtgcgacacg      720
gcagacaagc gcgcgatgat acgtgccggc ggccgggcacg cagtggcggt cgggcccggac      780
ggcgaagctc tggtcgagaa actgccggaa aatgaggaag gcttgcgtgt ggtcgatata      840
gatctcggtc gcattctcgt tgcgaaggct gcggccgacc ccgtcggtea ctacgcgcgc      900
cccgatgtct tgcggctctg gttcgacaag caaccgcggc ggtgcgtcga acatgccggc      960
gagaacgacg cgtcgcgcag gtcgcacggg tcgtccgggt cacaatcgcc ggccgaggat      1020
ggccggcgca acgacatggt agaccgtcag gaaaacgtcg attga                      1065

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<210> 22
 <211> 354
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 22
Met Ala Leu Glu His Pro Lys Tyr Val Ala Ala Val Val Gln Ala Ala
  1          5          10          15
Pro Glu Phe Leu Asn Leu Asp Arg Gly Ile Glu Lys Thr Ile Ala Leu
  20          25          30
Ile Asp Glu Ala Gly Gln Lys Gly Ala Ala Leu Ile Ala Phe Pro Glu
  35          40          45
Thr Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Pro Pro Ala
  50          55          60
Trp Ala Leu Gly Ser Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Met
  65          70          75          80
Thr Tyr Asp Ser Pro Gln Ala Ala Ala Leu Arg Asp Ala Ala Ala Arg
  85          90          95
Asn Gly Ile Thr Val Val Leu Gly Leu Ser Glu Arg Cys Gly Gly Ser
  100          105          110
Leu Tyr Ile Ala Gln Trp Ile Ile Gly Pro Asp Gly Ala Thr Val Ala
  115          120          125
Thr Arg Arg Lys Leu Arg Pro Thr His Ile Glu Arg Thr Val Phe Gly
  130          135          140
Asp Gly Asp Gly Ser Asp Leu Ala Val His Asp Leu Asn Ile Gly Arg
  145          150          155          160
Leu Gly Ala Leu Cys Cys Trp Glu His Ile Gln Pro Leu Thr Lys Tyr
  165          170          175
Ala Met Tyr Ala Gln His Glu Gln Val His Val Ala Ala Trp Pro Ser
  180          185          190
Phe Ser Met Tyr Glu Phe Ala Pro Ala Leu Gly His Glu Val Asn Asn
  195          200          205
Ala Val Ser Arg Val Tyr Ala Val Glu Gly Ser Cys Phe Val Leu Ala
  210          215          220
Pro Cys Ala Val Ile Ser Glu Gln Met Val Asp Met Leu Cys Asp Thr
  225          230          235          240
Ala Asp Lys Arg Ala Met Ile Arg Ala Gly Gly Gly His Ala Val Ala
  245          250          255
Phe Gly Pro Asp Gly Glu Ala Leu Val Glu Lys Leu Pro Glu Asn Glu

```


260 265 270
 Glu Gly Leu Leu Val Asp Ile Asp Leu Gly Arg Ile Ser Leu Ala
 275 280 285
 Lys Ala Ala Ala Asp Pro Val Gly His Tyr Ala Arg Pro Asp Val Leu
 290 295 300
 Arg Leu Trp Phe Asp Lys Gln Pro Arg Arg Cys Val Glu His Ala Gly
 305 310 315 320
 Glu Asn Asp Ala Ser Arg Arg Ser His Gly Ser Ser Gly Ser Gln Ser
 325 330 335
 Pro Ala Gln Asp Gly Pro Ala Asn Asp Met Val Asp Arg Gln Glu Asn
 340 345 350
 Val Asp

<210> 23

<211> 1005

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 23

atgaccgtta tcaaagcagc cgccattcaa atcagccccg tgctctacag ccgggcccggg 60
 acagtcgaga aagttgttag gaaggttaga gagctcgggg ccaaagggtgt ccgattcgct 120
 acctttcccg aaaccatcat accgtactac ccgtacttct cggtcgttca gtcggcggttc 180
 gacatgaagc ttgggagtga acatcagcgg ctgctcgcacg aatcagtcac aattccttcg 240
 tccgagacgg acgcatcgc ccaggccgcc aaggaagcgg gcattggtgt gtccgtcggg 300
 gtcaatgagc gcgatgggcg atccatctac aacactcaac ttctgttcga cgctgatggc 360
 acgctcatte agcgtaggcg aaagatcacc ccgacctatc acgagcgcg gatttggggt 420
 caaggcgatg gatccggcct acgcgcggtc gatagcgcgg tgggcccggat cggccagctt 480
 gcctgctggg agcactacct tcccctggcg cggtacgccc tcatcgcgga cggagagcaa 540
 atccactcgg caatgtatcc aggtcgttc gctggtccgc tatttgccga gcagatagag 600
 gttagtatcc gccagcacgc gcttgagtca gcctgcttcg tcgtcaacgc gaccggatgg 660
 cttagcgcgg agcagcaagc tcaaatagtg aaggataccg gatgcgtcgt tggaccaatc 720
 tccggtggct gctttacggc gattgttgat ccggagggtc ggatcatggg ggcgccactc 780
 aaggcagggt agggggaggt catcgagat ctcgattttg cgcagattga ttccgcaag 840
 cgtgtgatgg atacgcgagg gcaactacagc cgccccgaac ttctaagcct cacgatcgac 900
 cgcatgcagc accatcacat gactgagcga ggccgccgat accgtgtaga ccacgcaaag 960
 ccaacggtca ccgcagagca gtcggccgct gagccggcgg aatga 1005

<210> 24

<211> 334

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 24

Met Thr Val Ile Lys Ala Ala Ala Ile Gln Ile Ser Pro Val Leu Tyr
 1 5 10 15
 Ser Arg Ala Gly Thr Val Glu Lys Val Val Arg Lys Val Arg Glu Leu
 20 25 30
 Gly Ala Lys Gly Val Arg Phe Ala Thr Phe Pro Glu Thr Ile Ile Pro
 35 40 45
 Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Ser Ala Phe Asp Met Lys Leu
 50 55 60
 Gly Ser Glu His Gln Arg Leu Leu Asp Glu Ser Val Thr Ile Pro Ser
 65 70 75 80
 Ser Glu Thr Asp Ala Ile Ala Gln Ala Ala Lys Glu Ala Gly Met Val

```
<210> 26
<211> 312
<212> PRT
```

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 26

```

Val Ser Ser Thr Ile Lys Val Ala Ile Ile Gln Ala Ala Pro Ala Tyr
 1           5           10           15
Tyr Asp Leu Gln Ala Ser Leu Ala Lys Ala Ala Ser Leu Ile Arg Glu
      20           25           30
Ala Ala Arg Gly Gly Ala Gln Phe Val Ala Phe Gly Glu Thr Trp Leu
      35           40           45
Pro Gly Tyr Pro Met Trp Leu Asp Trp Cys Pro Gly Ala Ile Ile Trp
      50           55           60
Asp Asn Pro Ala Thr Lys Thr Val Phe Ala Arg Leu His Glu Asn Ser
      65           70           75           80
Val Ala Val Pro Gly Arg Glu Thr Ala Phe Leu Ala Asp Leu Ala Met
      85           90           95
Ser Leu Ser Ile Val Leu Cys Ile Gly Val Asn Glu Lys Val Met Asn
      100          105          110
Gly Pro Gly His Gly Thr Leu Tyr Asn Thr Leu Leu Thr Phe Asp Ala
      115          120          125
Thr Gly Glu Ile Ile Asn His His Arg Lys Leu Met Pro Thr Tyr Gly
      130          135          140
Glu Arg Leu Val Trp Gly Pro Gly Asp Ala Val Gly Val Gln Ala Val
      145          150          155          160
Asp Ser Thr Val Gly Arg Ile Gly Gly Leu Ile Cys Trp Glu His Trp
      165          170          175
Met Pro Leu Pro Arg Gln Leu Met His Asn Ser Gly Glu Gln Ile His
      180          185          190
Val Cys Ala Trp Pro Gly Val His Glu Met His Gln Ile Ala Ser Arg
      195          200          205
His Tyr Ala Phe Glu Gly Arg Cys Phe Val Leu Ala Ala Gly Leu Ile
      210          215          220
Met Pro Ala Phe Asp Leu Pro Ser Glu Leu Glu Phe Pro Pro Glu Leu
      225          230          235          240
Ala Asp Lys Arg Asp Tyr Leu Leu Met Asn Gly Gly Ser Ala Ile Ile
      245          250          255
Lys Pro Asn Gly Lys Tyr Leu Ala Gly Pro Val Tyr Asp Glu Glu Thr
      260          265          270
Ile Leu Cys Ala Asp Leu Asp Leu Thr Glu Asn Ile Lys Glu Gln Met
      275          280          285
Thr Leu Asp Val Thr Gly His Tyr Ala Arg Ala Glu Leu Phe Asp Leu
      290          295          300
Asn Val Val Arg Arg Arg Asn Ala
      305          310

```

<210> 27

<211> 1056

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 27

```

atgccaaccc ccagcgatca tttcaaaatc gccgctgttc aggcctcgcc cgtgtttctg      60
gaccgggagg ccactgtgga aaaggcctgc cggttgatcg ccgaagccgc aaagcagggc      120
gcccgctca tcgtctttcc ggaatctttc atcccgacct acccgattg ggtgtgggccc      180
gttcccccgg gaagggaaag aatcctgaac cagctgtatt ctgaattcct ggccaatgcc      240
gtcgtgtttc ccggcgccgc gaccgaacaa cttgccccagg ctgcacgaat ggccggcgcc      300

```

```

tatgtgatta tgggcgtcac cgaagagac acctcggcca gcggggccag cctctacaac 360
accctgctct acttcagccc cgaagcatc ctaatgggca aacaccggaa gctgggtccc 420
acggggggcg aacggctggt ctgggcctac ggagacggca gcacgctgga ggtctacgac 480
actccgctgg gaaagatcgg cgggctgata tgctgggaga actacatgcc cctggccccg 540
tacacgatgt acgcctgggg caccagatt tacatcgccg ccacctggga ccgcggggaa 600
ccgtggctct ccaccctgcg gcatatcgcc aaggaaggaa gggctctacgt catcgggtgc 660
tgcacgcccc tgcgccagg ggatatcccg gaccggttcg agtacaaggg aaaattttat 720
tccgggtccc gggagtggat caatgagggc gacagcgcca tcgtgaaccc ggacggggaa 780
ttcatcgccg ggcgggtgcg gatgaaggag gagatcctgt atgccgagat agaccccccg 840
cagatcgccg gccccaagt gatgctcgat gtggccggtc attacgcccg gccggatata 900
ttcgaagctca tcgtccaccg gaatccccc cccgatgatca aaatcgccga agacaggggc 960
acgggggatcg cctcaagttt gattcgcccc cgcctaacc ttcccccatc aagggggagg 1020
aaatcgccaa gaagcaaacg caagcccaaa aaatga 1056

```

<210> 28

<211> 351

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 28

```

Met Pro Thr Pro Ser Asp His Phe Lys Ile Ala Ala Val Gln Ala Ser
1          5          10          15
Pro Val Phe Leu Asp Arg Glu Ala Thr Val Glu Lys Ala Cys Arg Leu
20          25          30
Ile Ala Glu Ala Ala Lys Gln Gly Ala Arg Leu Ile Val Phe Pro Glu
35          40          45
Ser Phe Ile Pro Thr Tyr Pro Asp Trp Val Trp Ala Val Pro Pro Gly
50          55          60
Arg Glu Arg Ile Leu Asn Gln Leu Tyr Ser Glu Phe Leu Ala Asn Ala
65          70          75          80
Val Asp Val Pro Gly Ala Ala Thr Glu Gln Leu Ala Gln Ala Ala Arg
85          90          95
Met Ala Gly Ala Tyr Val Ile Met Gly Val Thr Glu Arg Asp Thr Ser
100          105          110
Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Phe Ser Pro Glu
115          120          125
Gly Ile Leu Met Gly Lys His Arg Lys Leu Val Pro Thr Gly Gly Glu
130          135          140
Arg Leu Val Trp Ala Tyr Gly Asp Gly Ser Thr Leu Glu Val Tyr Asp
145          150          155          160
Thr Pro Leu Gly Lys Ile Gly Gly Leu Ile Cys Trp Glu Asn Tyr Met
165          170          175
Pro Leu Ala Arg Tyr Thr Met Tyr Ala Trp Gly Thr Gln Ile Tyr Ile
180          185          190
Ala Ala Thr Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Leu Arg His
195          200          205
Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys Ile Ala Leu
210          215          220
Arg Gln Gly Asp Ile Pro Asp Arg Phe Glu Tyr Lys Gly Lys Phe Tyr
225          230          235          240
Ser Gly Ser Arg Glu Trp Ile Asn Glu Gly Asp Ser Ala Ile Val Asn
245          250          255
Pro Asp Gly Glu Phe Ile Ala Gly Pro Val Arg Met Lys Glu Glu Ile
260          265          270
Leu Tyr Ala Glu Ile Asp Pro Arg Gln Met Arg Gly Pro Lys Trp Met
275          280          285
Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Ile Phe Glu Leu Ile
290          295          300

```

Val His Arg Asn Pro His Pro Met Ile Lys Ile Ala Glu Asp Arg Gly
 305 310 315 320
 Thr Gly Ile Ala Ser Ser Leu Ile Arg Pro Arg Pro Asn Leu Pro Pro
 325 330 335
 Ser Arg Gly Arg Lys Ser Ala Arg Ser Lys Arg Lys Pro Lys Lys
 340 345 350

<210> 29

<211> 1017

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 29

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atgggcatcg aacatacgaa atacaaggtg gcggtgggtc aggcggcgcc ggcctggctc 60
gacctcgagg cctcgatcgg caagtccatc ggcctaata aggaggccgc ggacaagggc 120
gccaaagctga tcgcctttcc ggaggccttc atccccggtt acccctggta tatctggatg 180
gactcgccgg cctgggcgat cggccgcggc ttcgtccagc gctatttcga caattcgctc 240
tcctacgaca gtccccaggc cgagcggctg cgtgatgccg tgcgccaggc caagctcacc 300
gccgtgatcg gcctgtccga acgcgacggc ggcagcctt acctggcgca atggttgatc 360
gggcccgcag gcgaaaccat tgccaagcgc cgcaagctgc ggccgaccca tgccgagcgc 420
accgtctatg gcgaagcgga cggcagcgat ctggccgtac atgcccgcc cgacatcggt 480
cgcttgggcg cgctgtgctg ctgggagcat cttcagccgt tgcgaagta cgcaatgtac 540
gccagaacg agcaggtcca cgtcgctgcc tggccgagct tctcgctcta cgatcccttc 600
gccccggcgc tcggcgccga ggtcaacaac gctgcctcgc gctctatgc ggtggagggc 660
tcctgtctcg tgctcgcgcc ttgcgcgacg gtgtcgagg ccatgatcga cgaactctgc 720
gatcgcccg ataagcatgc gctgctgcat gccggcgagg gctttgccgc gatctacggc 780
cccgacggca gccagatcgg cgagaagctg gcgccggatc aggagggtct gctgatcgcc 840
gagattgac tgggcgccat cgggtgttgc aagaacgcgg cagatcccgc cggtcattat 900
tcacggccgg atgtgacgcg gttgctgctc aacaagaagc ggtaccagcg cgtcgagcaa 960
tttgccttgc ccgccgacat ggtcgagccc gcggacatag gcgcggcgcc gagctga 1017

```

<210> 30

<211> 338

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 30

```

Met Gly Ile Glu His Thr Lys Tyr Lys Val Ala Val Val Gln Ala Ala
1 5 10 15
Pro Ala Trp Leu Asp Leu Glu Ala Ser Ile Gly Lys Ser Ile Gly Leu
20 25 30
Ile Lys Glu Ala Ala Asp Lys Gly Ala Lys Leu Ile Ala Phe Pro Glu
35 40 45
Ala Phe Ile Pro Gly Tyr Pro Trp Tyr Ile Trp Met Asp Ser Pro Ala
50 55 60
Trp Ala Ile Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
65 70 75 80
Ser Tyr Asp Ser Pro Gln Ala Glu Arg Leu Arg Asp Ala Val Arg Gln
85 90 95
Ala Lys Leu Thr Ala Val Ile Gly Leu Ser Glu Arg Asp Gly Gly Ser
100 105 110
Leu Tyr Leu Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
115 120 125
Lys Arg Arg Lys Leu Arg Pro Thr His Ala Glu Arg Thr Val Tyr Gly
130 135 140

```

Glu Gly Asp Gly Ser Asp Leu Ala Val His Ala Arg Pro Asp Ile Gly
 145 150 155 160
 Arg Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys
 165 170 175
 Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ala Trp Pro
 180 185 190
 Ser Phe Ser Leu Tyr Asp Pro Phe Ala Pro Ala Leu Gly Ala Glu Val
 195 200 205
 Asn Asn Ala Ala Ser Arg Val Tyr Ala Val Glu Gly Ser Cys Phe Val
 210 215 220
 Leu Ala Pro Cys Ala Thr Val Ser Gln Ala Met Ile Asp Glu Leu Cys
 225 230 235 240
 Asp Arg Pro Asp Lys His Ala Leu Leu His Ala Gly Gly Gly Phe Ala
 245 250 255
 Ala Ile Tyr Gly Pro Asp Gly Ser Gln Ile Gly Glu Lys Leu Ala Pro
 260 265 270
 Asp Gln Glu Gly Leu Leu Ile Ala Glu Ile Asp Leu Gly Ala Ile Gly
 275 280 285
 Val Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
 290 295 300
 Val Thr Arg Leu Leu Leu Asn Lys Lys Arg Tyr Gln Arg Val Glu Gln
 305 310 315 320
 Phe Ala Leu Pro Ala Asp Met Val Glu Pro Ala Asp Ile Gly Ala Ala
 325 330 335
 Ala Ser

<210> 31
 <211> 933
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 31
 atgaccagaa tagccattat tcagcgaccg cccgtgctgc tcgatcgaag cgccaccatt 60
 gcccgggccg tgcaatcggg cgccgaagcg gcagcgcaag gcgcgaccct gattgtcttg 120
 cccgaatcgt acatccctgg ctatccctca tggatctggc ggctcgcgcc tggcaaagac 180
 ggcgcgatcg tgggccagtt gcatgcgcgc ttgctggcca atgcgggtcga cctgagcagc 240
 actgacctcg atgcgcttct tgaagcggcc cgtcagcacg gcgtgaccat tgtttgcggc 300
 atgaacgagt gcaaacggcg tcgcggcgcc ggacacctgt acaacacggg ggtcgtgatc 360
 ggaccggacg gcgtcatgct caaccggcat cgcaaattga tgccgaccac tcccgaagcg 420
 atggtgcatg gctttggcga tgcattccga ctgaaagcag ttgatacgcc tgccggccgg 480
 ctgggcacgc tgatctgctg ggagagctac atgccgctgg cacgctatgc cctgtacgag 540
 caaggcatcg agatctacat cgacccaact tatgacagtg gtgacggctg gatcagcacc 600
 atgcgccaca ttgcactcga agggcgctgc tgggtgattg gcagcggcac ggtcctgaaa 660
 ggcagtgata ttccggacga tttccggaa cgggcacgcc tgttcctga tccggatgag 720
 tggatcaacg atggtgattc ggtagttatc gatccgcagg gaaagatcgt tgccggtccg 780
 atgcgtaggg aagcaggcat tctatacgcc gatatcgacg tcgcgcgcgt agcaccatca 840
 cgccgcacgc tggatgtcgc ggggcattac gcgcgtccgg acgtcttcga gcttcgggta 900
 caccaggcac cgggggcacg agtaagtaat tga 933

<210> 32
 <211> 310
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 32

```

Met Thr Arg Ile Ala Ile Ile Gln Arg Pro Pro Val Leu Leu Asp Arg
1      5      10      15
Ser Ala Thr Ile Ala Arg Ala Val Gln Ser Val Ala Glu Ala Ala
20      25      30
Gln Gly Ala Thr Leu Ile Val Leu Pro Glu Ser Tyr Ile Pro Gly Tyr
35      40      45
Pro Ser Trp Ile Trp Arg Leu Ala Pro Gly Lys Asp Gly Ala Ile Val
50      55      60
Gly Gln Leu His Ala Arg Leu Leu Ala Asn Ala Val Asp Leu Ser Ser
65      70      75      80
Thr Asp Leu Asp Ala Leu Leu Glu Ala Ala Arg Gln His Gly Val Thr
85      90      95
Ile Val Cys Gly Met Asn Glu Cys Glu Arg Arg Arg Gly Gly Gly Thr
100     105     110
Leu Tyr Asn Thr Val Val Val Ile Gly Pro Asp Gly Val Met Leu Asn
115     120     125
Arg His Arg Lys Leu Met Pro Thr Asn Pro Glu Arg Met Val His Gly
130     135     140
Phe Gly Asp Ala Ser Gly Leu Lys Ala Val Asp Thr Pro Ala Gly Arg
145     150     155     160
Leu Gly Thr Leu Ile Cys Trp Glu Ser Tyr Met Pro Leu Ala Arg Tyr
165     170     175
Ala Leu Tyr Glu Gln Gly Ile Glu Ile Tyr Ile Ala Pro Thr Tyr Asp
180     185     190
Ser Gly Asp Gly Trp Ile Ser Thr Met Arg His Ile Ala Leu Glu Gly
195     200     205
Arg Cys Trp Val Ile Gly Ser Gly Thr Val Leu Lys Gly Ser Asp Ile
210     215     220
Pro Asp Asp Phe Pro Glu Arg Ala Arg Leu Phe Pro Asp Pro Asp Glu
225     230     235     240
Trp Ile Asn Asp Gly Asp Ser Val Val Ile Asp Pro Gln Gly Lys Ile
245     250     255
Val Ala Gly Pro Met Arg Arg Glu Ala Gly Ile Leu Tyr Ala Asp Ile
260     265     270
Asp Val Ala Arg Val Ala Pro Ser Arg Arg Thr Leu Asp Val Ala Gly
275     280     285
His Tyr Ala Arg Pro Asp Val Phe Glu Leu Arg Val His Gln Ala Pro
290     295     300
Gly Ala Arg Val Ser Asn
305     310

```

<210> 33

<211> 1026

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 33

```

atgttaagtc ccgtagcgca gtatcgcgcc gccgcggtgc aggcggcgcc atcttttctc 60
gatctcgacc gcaccgtcga gaagacgata gcgatcatcg agcaggcgcc cgagcaggat 120
gtgcgcctga tcgcgtttcc ggaaacctgg attcccggct atccgctctg gatctggctc 180
ggctcgccgg cctggggcat gcgcttcgtg cagcgctatt tcgagaactc gctggtgcgc 240
ggcagcaaac agtgaacgc gatcgccgat gcggcgcgcc gccaccgcat gaccgtcgtc 300
gtcggcttca gcgagcgcg gcggaggcagc ctctacatgg gccaggcgat cttcggtccc 360
gaaggcgagc tcatcgcgcc gcgcccgaag ctcaagccga cacacgccga gcgaacggtg 420
ttcggcgagg gcgacggcag ccacttggcc gtttacgaga cgggcgttgg tcgcatcgcc 480
gccctctgct gctgggagca catccagccg ctctcgaaat acgcgatgta tgcggccaac 540
gaacaggtgc atgtggcctc gtggccgtgc ttcagccttt atcgcgccat ggcctatgcg 600

```

```

ctcggggccgg aggtgaacac cgccgcgagc caggctctacg cggtcgaggg cggctgctac 660
gtgctggcct cctgtctcgt cgtgacaccc gagatcctga aggtgctgat cgacacgccc 720
gacaaggagc cgttgctgct cgccggcggg gggttctcga tgatcttcgg ccccgacggc 780
cgcgcgctcg cccagccgct gccggagacc gaagaggggc tcgtcacggc cgagatcgat 840
ctcggcgcgga tcgcgctcgc caaggccgcg gccgatcccc ccggccatta cgcgcgggccc 900
gacgtgacgc ggttggttgc gaacccgcgc cccgcggcgc gcgtcgaagc gctgggtccg 960
cgcttcgagg tcgtgcagag cgagcaggcc gagccgccca cgcaaccggc cgaagcggcg 1020
gattga 1026

```

<210> 34

<211> 341

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 34

```

Met Leu Ser Pro Val Thr Gln Tyr Arg Ala Ala Val Gln Ala Ala
1      5      10      15
Pro Ser Phe Leu Asp Leu Asp Arg Thr Val Glu Lys Thr Ile Ala Ile
20     25     30
Ile Glu Gln Ala Ala Glu Gln Asp Val Arg Leu Ile Ala Phe Pro Glu
35     40     45
Thr Trp Ile Pro Gly Tyr Pro Leu Trp Ile Trp Leu Gly Ser Pro Ala
50     55     60
Trp Gly Met Arg Phe Val Gln Arg Tyr Phe Glu Asn Ser Leu Val Arg
65     70     75     80
Gly Ser Lys Gln Trp Asn Ala Ile Ala Asp Ala Ala Arg Arg His Arg
85     90     95
Met Thr Val Val Val Gly Phe Ser Glu Arg Ala Gly Gly Ser Leu Tyr
100    105    110
Met Gly Gln Ala Ile Phe Gly Pro Glu Gly Glu Leu Ile Ala Ala Arg
115    120    125
Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly Glu Gly
130    135    140
Asp Gly Ser His Leu Ala Val Tyr Glu Thr Gly Val Gly Arg Ile Gly
145    150    155    160
Ala Leu Cys Cys Trp Glu His Ile Gln Pro Leu Ser Lys Tyr Ala Met
165    170    175
Tyr Ala Ala Asn Glu Gln Val His Val Ala Ser Trp Pro Cys Phe Ser
180    185    190
Leu Tyr Arg Gly Met Ala Tyr Ala Leu Gly Pro Glu Val Asn Thr Ala
195    200    205
Ala Ser Gln Val Tyr Ala Val Glu Gly Gly Cys Tyr Val Leu Ala Ser
210    215    220
Cys Leu Val Val Thr Pro Glu Ile Leu Lys Val Leu Ile Asp Thr Pro
225    230    235    240
Asp Lys Glu Pro Leu Leu Leu Ala Gly Gly Gly Phe Ser Met Ile Phe
245    250    255
Gly Pro Asp Gly Arg Ala Leu Ala Gln Pro Leu Pro Glu Thr Glu Glu
260    265    270
Gly Leu Val Thr Ala Glu Ile Asp Leu Gly Ala Ile Ala Leu Ala Lys
275    280    285
Ala Ala Ala Asp Pro Ala Gly His Tyr Ala Arg Pro Asp Val Thr Arg
290    295    300
Leu Leu Leu Asn Pro Arg Pro Ala Ala Arg Val Glu Ala Leu Gly Pro
305    310    315    320
Arg Phe Glu Val Val Gln Ser Glu Gln Ala Glu Pro Pro Thr Gln Pro
325    330    335
Ala Glu Ala Ala Asp

```


340

<210> 35

<211> 942

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 35

```

atgacagctc taaaaattgc tgctgttcaa atgtgcgccg aattgggccc tacagatcga      60
aacctgagtg cagctggatc attcgtgcgc gacgcatttc gcgaagggtc ccagtgggta      120
atcctcccag agttttttac ctccggcaatg gcattcgcac cttcgatggc gcaagcttgg      180
ttgccactgg aaggaaaggc gctagcgatg atgcgcagcc ttgcgcgtca attcgatggg      240
gttggttgag gctcatatgt tgccagagag gggaacgact gcgtaaatgc ctttcttctc      300
gtctttccgg atggaagcta ctaccggcat gacaaagata ttccaacaat gtgggagaac      360
tgttactaca tcggcggcgt cgacgatggg gtgctggaaa caccaattgg tgcggtggga      420
gttgactagt gttgggagtt catccgaaca caaacgcccc gaagactgaa ggatcgcgtt      480
caattagtgg ttggcgggtac ttgctggtgg gattttccga tgcctgtacc tgaacgatat      540
ctgaggctga ccaggcata ctccaggaac ttgagcgcgc atgctccggc gcggttggcc      600
agtatgttgg gtgtgcctgt tgtacacgct tcccatgctg gggattttac tgctgtcacc      660
ccaggcaatg aaacgaagaa ttaccgatcc aactatctgg gagagaccca gatcgtcgat      720
gccaatggaa atgtgttgaa gcgaatgaca gtgctgatg gtgaggggta cgtcattgct      780
gacgttcaat tgggggccat atcaaccggt cgaacttcga tccccgacac cttctggacc      840
tgcaagctaa cgccaggggc acaacaggct tgggatgaac aaaatgcttt tgggtgtggc      900
tactatgaga acgtcacacg caaacaccta atcggtcgat ga                      942

```

<210> 36

<211> 313

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 36

```

Met Thr Ala Leu Lys Ile Ala Ala Val Gln Met Cys Ala Glu Leu Gly
 1          5          10          15
Ala Thr Asp Arg Asn Leu Ser Ala Ala Gly Ser Phe Val Arg Asp Ala
          20          25          30
Phe Arg Glu Gly Ala Gln Trp Val Ile Leu Pro Glu Phe Phe Thr Ser
          35          40          45
Ala Met Ala Phe Ala Pro Ser Met Ala Gln Ala Trp Leu Pro Leu Glu
          50          55          60
Gly Lys Ala Leu Ala Met Met Arg Ser Leu Ala Arg Gln Phe Asp Gly
65          70          75          80
Val Val Gly Gly Ser Tyr Val Ala Arg Glu Gly Asn Asp Cys Val Asn
          85          90          95
Ala Phe Leu Leu Val Phe Pro Asp Gly Ser Tyr Tyr Arg His Asp Lys
          100          105          110
Asp Ile Pro Thr Met Trp Glu Asn Cys Tyr Tyr Ile Gly Gly Val Asp
          115          120          125
Asp Gly Val Leu Glu Thr Pro Ile Gly Ala Val Gly Val Ala Leu Cys
          130          135          140
Trp Glu Phe Ile Arg Thr Gln Thr Ala Arg Arg Leu Lys Asp Arg Val
          145          150          155          160
Gln Leu Val Val Gly Gly Thr Cys Trp Trp Asp Phe Pro Met Pro Val
          165          170          175
Pro Glu Arg Tyr Leu Arg Leu Thr Arg His Ile Ser Arg Asn Phe Glu
          180          185          190

```

Arg Asp Ala Pro Ala Arg Leu Ala Ser Met Leu Gly Val Pro Val Val
 195 200 205
 His Ala Ser His Ala Gly Asp Phe Thr Ala Val Thr Pro Gly Asn Glu
 210 215 220
 Thr Lys Asn Tyr Arg Ser Asn Tyr Leu Gly Glu Thr Gln Ile Val Asp
 225 230 235 240
 Ala Asn Gly Asn Val Leu Lys Arg Met Thr Val Ala Asp Gly Glu Gly
 245 250 255
 Tyr Val Ile Ala Asp Val Gln Leu Gly Ala Ile Ser Thr Gly Arg Thr
 260 265 270
 Ser Ile Pro Asp Thr Phe Trp Thr Cys Lys Leu Thr Pro Gly Ala Gln
 275 280 285
 Gln Ala Trp Asp Glu Gln Asn Ala Phe Gly Cys Gly Tyr Tyr Glu Asn
 290 295 300
 Val Thr Arg Lys His Leu Ile Gly Arg
 305 310

<210> 37
 <211> 993
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 37
 atggattcag atatgacgga tacttttaag gcagccatta ttcagcacgc gcctgttttt 60
 ttaaattctcg aagagagtct ggacaaagcc ggcagcctta tagaaaaggc tgccgatcaa 120
 ggcgcgaaag tgatcgccctt tcttgaaca tggctgcccgt gttatcccgt atggctcgac 180
 tactctccaa aagcgggtct gtgggactat cagcctgcaa aatctctcta tcgtctgcta 240
 gtcgataatt cagtcacctt acccgcaaaa cacctcgatc aactcctctc catagcgcaa 300
 aagaccggcg catatgttgt aatgggggca cacgaacgag tgggtggaac actctataac 360
 acgacgatct atgttgggat tgatgggaag gagtacaaac ttcatagaaa gctggtgccg 420
 acctataccg aaagattgat ctggggggcgg ggagacggca gcacattgag tgtgttgatg 480
 acggattatg gcgttcttgg aggattgatc tgctgggagc actggatgcc tctggcaaga 540
 gccgaatgc atgccagata tgaaaccctt catgtggcgc aatggccggc tgtaaaagat 600
 atccatcaga tagcaagcag acattatgct tttgaaggcc ggtgtttcgt gctcggcgga 660
 ggctctgttc tgactcgaag agatataata gaaggattca actcactggc tcgcgccgat 720
 agtgatgcat tggaaacttct gaaagctatt tcgggagaag atagtgtatc tattttgaat 780
 gggggaagcg cgataattgc gccgaatgga gagtatcttg cgggcccggc ctttaatgaa 840
 ccctccatta tttatgctga aattgatcct gcaactgataa gtgagggcca tcttacactg 900
 gatacaagcg gacactactc gcgccctgac atttttcgtc tggagataaa cgatcaacct 960
 caacatgatg taactttcag atcggggcat tag 993

<210> 38
 <211> 330
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 38
 Met Asp Ser Asp Met Thr Asp Thr Phe Lys Ala Ala Ile Ile Gln His
 1 5 10 15
 Ala Pro Val Phe Leu Asn Leu Glu Glu Ser Leu Asp Lys Ala Gly Ser
 20 25 30
 Leu Ile Glu Lys Ala Ala Asp Gln Gly Ala Lys Val Ile Ala Phe Pro
 35 40 45
 Glu Thr Trp Leu Pro Gly Tyr Pro Val Trp Leu Asp Tyr Ser Pro Lys
 50 55 60

Ala Gly Leu Trp Asp Tyr Gln Pro Ala Lys Ser Leu Tyr Arg Leu Leu
 65 70 75 80
 Val Asp Asn Ser Val Thr Leu Pro Gly Lys His Leu Asp Gln Leu Leu
 85 90 95
 Ser Ile Ala Gln Lys Thr Gly Ala Tyr Val Val Met Gly Ala His Glu
 100 105 110
 Arg Val Gly Gly Thr Leu Tyr Asn Thr Thr Ile Tyr Val Gly Ile Asp
 115 120 125
 Gly Lys Glu Tyr Lys Leu His Arg Lys Leu Val Pro Thr Tyr Thr Glu
 130 135 140
 Arg Leu Ile Trp Gly Arg Gly Asp Gly Ser Thr Leu Ser Val Leu Met
 145 150 155 160
 Thr Asp Tyr Gly Val Leu Gly Gly Leu Ile Cys Trp Glu His Trp Met
 165 170 175
 Pro Leu Ala Arg Ala Ala Met His Ala Arg Tyr Glu Thr Leu His Val
 180 185 190
 Ala Gln Trp Pro Ala Val Lys Asp Ile His Gln Ile Ala Ser Arg His
 195 200 205
 Tyr Ala Phe Glu Gly Arg Cys Phe Val Leu Ala Ala Gly Ser Val Leu
 210 215 220
 Thr Arg Arg Asp Ile Ile Glu Gly Phe Asn Ser Leu Ala Arg Ala Asp
 225 230 235 240
 Ser Asp Ala Leu Glu Leu Leu Lys Ala Ile Ser Gly Glu Asp Ser Asp
 245 250 255
 Leu Ile Leu Asn Gly Gly Ser Ala Ile Ile Ala Pro Asn Gly Glu Tyr
 260 265 270
 Leu Ala Gly Pro Val Phe Asn Glu Pro Ser Ile Ile Tyr Ala Glu Ile
 275 280 285
 Asp Pro Ala Leu Ile Ser Glu Gly His Leu Thr Leu Asp Thr Ser Gly
 290 295 300
 His Tyr Ser Arg Pro Asp Ile Phe Arg Leu Glu Ile Asn Asp Gln Pro
 305 310 315 320
 Gln His Asp Val Thr Phe Arg Ser Gly His
 325 330

<210> 39

<211> 1008

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 39

atgaaaaata	tcaaaaactc	agaaaaaagc	agcacagtaa	gagtcgctgc	ggtacaaatc	60
agtcgggtgt	tgtacaaccg	cgaagctacc	gttcaaaaag	tagtcaacaa	aatccttgaa	120
ctaggaaaac	aaggggtaca	attcgccact	tttccggaaa	cgatagtgcc	ttattatcct	180
tattttctctt	ttattcaggc	gccttatgcc	atgggc aaaag	aacacctgcg	cttgcttgaa	240
caatcagtta	ctgttccgtc	agccgcgacc	gatgccataa	gtgaggcggc	aaagggaagcc	300
aatatggtag	tgtctattgg	tgtcaatgaa	cgagacgggtg	gtaccattta	caatacgcaa	360
ctcctttttg	atgctgacgg	aacattaatt	cagcgcagac	gtaaacttac	accaacgtat	420
catgaaaagaa	tgatttgggg	acaagggtgac	gcttcagggtc	ttcgtgccac	agacagcgct	480
gttgggcgta	tcgggcagtt	ggcttgttgg	gaacattaca	atccattggt	ccgttatgct	540
ttgattgctg	atggagaaca	aatccattct	gccatgtatc	ccggatcatt	tttaggtgcg	600
ttgcacgggtg	aacaaaccga	aatcaatgta	cgccaacacg	ctttagaatc	ggccagcttc	660
gtcgtagtgg	ctaccggttg	gttggtatgcc	gatcaacaag	cacaaattgc	gaaagacacc	720
ggtggaccaaa	tcggaccaat	ttcgggaggt	tgttttacag	ccgttatagg	ccctgacgga	780
caactaatcg	gggaagccct	tacatcaggt	gaaggggaag	tgattgccga	tattgatttg	840
gcacaaattg	atgcccgcaa	aagattaatg	gatgccagtg	gtcactacaa	ccgtcctgaa	900
ttgttgagct	tgcatatcga	tcacactccg	actgctccta	tgcatgaaag	agtagtttac	960
actgagccgg	gattagcaaa	aagacaaaat	gaaaattcat	caaattaa		1008

<210> 40
 <211> 335
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 40
 Met Lys Asn Ile Lys Asn Ser Glu Lys Ser Ser Thr Val Arg Val Ala
 1 5 10 15
 Ala Val Gln Ile Ser Pro Val Leu Tyr Asn Arg Glu Ala Thr Val Gln
 20 25 30
 Lys Val Val Asn Lys Ile Leu Glu Leu Gly Lys Gln Gly Val Gln Phe
 35 40 45
 Ala Thr Phe Pro Glu Thr Ile Val Pro Tyr Tyr Pro Tyr Phe Ser Phe
 50 55 60
 Ile Gln Ala Pro Tyr Ala Met Gly Lys Glu His Leu Arg Leu Leu Glu
 65 70 75 80
 Gln Ser Val Thr Val Pro Ser Ala Ala Thr Asp Ala Ile Ser Glu Ala
 85 90 95
 Ala Lys Glu Ala Asn Met Val Val Ser Ile Gly Val Asn Glu Arg Asp
 100 105 110
 Gly Gly Thr Ile Tyr Asn Thr Gln Leu Leu Phe Asp Ala Asp Gly Thr
 115 120 125
 Leu Ile Gln Arg Arg Arg Lys Leu Thr Pro Thr Tyr His Glu Arg Met
 130 135 140
 Ile Trp Gly Gln Gly Asp Ala Ser Gly Leu Arg Ala Thr Asp Ser Ala
 145 150 155 160
 Val Gly Arg Ile Gly Gln Leu Ala Cys Trp Glu His Tyr Asn Pro Leu
 165 170 175
 Phe Arg Tyr Ala Leu Ile Ala Asp Gly Glu Gln Ile His Ser Ala Met
 180 185 190
 Tyr Pro Gly Ser Phe Leu Gly Ala Leu His Gly Glu Gln Thr Glu Ile
 195 200 205
 Asn Val Arg Gln His Ala Leu Glu Ser Ala Ser Phe Val Val Val Ala
 210 215 220
 Thr Gly Trp Leu Asp Ala Asp Gln Gln Ala Gln Ile Ala Lys Asp Thr
 225 230 235 240
 Gly Gly Pro Ile Gly Pro Ile Ser Gly Gly Cys Phe Thr Ala Val Ile
 245 250 255
 Gly Pro Asp Gly Gln Leu Ile Gly Glu Ala Leu Thr Ser Gly Glu Gly
 260 265 270
 Glu Val Ile Ala Asp Ile Asp Leu Ala Gln Ile Asp Ala Arg Lys Arg
 275 280 285
 Leu Met Asp Ala Ser Gly His Tyr Asn Arg Pro Glu Leu Leu Ser Leu
 290 295 300
 His Ile Asp His Thr Pro Thr Ala Pro Met His Glu Arg Val Val Tyr
 305 310 315 320
 Thr Glu Pro Gly Leu Ala Lys Arg Gln Asn Glu Asn Ser Ser Asn
 325 330 335

<210> 41
 <211> 966
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 41
atgcccaatg agaataacat cgctacattc aaagttgccg cagtccaggc cacaccggtg      60
tttcttgatc gtgaagcaac catcgacaaa gcttgcgggt tgattgccac tgccggcaat      120
gaaggagcgc gcctgattgt gtttccagaa gcgttcaccc caacctatcc tgaatgggtt      180
tggggtattc cttccgggtga gcaaggttta ctcaatgaac tctatgcaga gctgctcacc      240
aatgcggtca ctattcccag tgacgcgact gacaggctgt gcgaggccgc gcagcttgcg      300
aatgcctacg tagtgatggg aatgagcgaa cggaatgtcg aggcgagtgg cgcaagccta      360
tataatacgc tgtttgacat caatgcgcag ggggagattt tagggaaaca tcgaaagctg      420
gtgccaacgg gcggcgaaac cctgggatgg gcgcagggtg atggcagcac gctgcaggtc      480
tacgatacgc cattgggaaa actcgggtgt ctcatttgct gggaaaatta tatgccgctg      540
gcacgctatg ctatgtatgc ctgggggaca caaatctatg tcgcggcaac gtgggatcga      600
ggccaaccct ggctttctac attacggcat atcgccaaag aaggcagggt atacgtgatt      660
ggttgctgta tcgcgatgcg aaaagacgat attccggata gttactccat gaagcagaaa      720
taccatgctg aaatggatga atggattaat gttggcgaca gtgtgattgt caatcccga      780
ggacacttta tcgcagggcc tgtgcgcaag caagaagaaa ttctctacgc ggagatcgat      840
ccacgtatgg tgcaaggccc gaagtggatg ctcgatgtgg cggggcatta tgcgagacca      900
gatgtgttcc agttgacggt gcatacgaat gtgagagaga tgatgcgggt ggaagatgat      960
tcataa

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<210> 42
<211> 321
<212> PRT
<213> Unknown

```

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<220>
<223> Obtained from an environmental sample

```

```

<400> 42
Met Pro Asn Glu Asn Ile Ala Thr Phe Lys Val Ala Ala Val Gln
1      5      10      15
Ala Thr Pro Val Phe Leu Asp Arg Glu Ala Thr Ile Asp Lys Ala Cys
20     25     30
Gly Leu Ile Ala Thr Ala Gly Asn Glu Gly Ala Arg Leu Ile Val Phe
35     40     45
Pro Glu Ala Phe Ile Pro Thr Tyr Pro Glu Trp Val Trp Gly Ile Pro
50     55     60
Ser Gly Glu Gln Gly Leu Leu Asn Glu Leu Tyr Ala Glu Leu Leu Thr
65     70     75     80
Asn Ala Val Thr Ile Pro Ser Asp Ala Thr Asp Arg Leu Cys Glu Ala
85     90     95
Ala Gln Leu Ala Asn Ala Tyr Val Val Met Gly Met Ser Glu Arg Asn
100    105    110
Val Glu Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Ile Asn
115    120    125
Ala Gln Gly Glu Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly
130    135    140
Gly Glu Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Gln Val
145    150    155    160
Tyr Asp Thr Pro Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn
165    170    175
Tyr Met Pro Leu Ala Arg Tyr Ala Met Tyr Ala Trp Gly Thr Gln Ile
180    185    190
Tyr Val Ala Ala Thr Trp Asp Arg Gly Gln Pro Trp Leu Ser Thr Leu
195    200    205
Arg His Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys Ile
210    215    220
Ala Met Arg Lys Asp Asp Ile Pro Asp Ser Tyr Ser Met Lys Gln Lys
225    230    235    240
Tyr His Ala Glu Met Asp Glu Trp Ile Asn Val Gly Asp Ser Val Ile
245    250    255
Val Asn Pro Glu Gly His Phe Ile Ala Gly Pro Val Arg Lys Gln Glu

```

```

                260                265                270
Glu Ile Leu Tyr Ala Glu Ile Asp Pro Arg Met Val Gln Gly Pro Lys
                275                280                285
Trp Met Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Gln
                290                295                300
Leu Thr Val His Thr Asn Val Arg Glu Met Met Arg Val Glu Asp Asp
305                310                315                320
Ser

```

<210> 43
 <211> 993
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 43
atgagagtcg ttaaagccgc ggcgggtccaa ctgaaacctg tcctctatag ccgagagggga      60
actgtcgaac acgtcgtccg taaaatccac gagcttggac agcaaggggt acagttcgcg      120
acgtttccag agactgtggt gccttactac ccgtactttt cgatcgtgca gtccggctat      180
caaatctctg gcggtggtga gttcctgaag ctgcttgatc agtcagtaac cgtgccatct      240
ctcgctacgg aagcgatcgg cgaggcttgc aggcaggcgg gcgtcgttgt ctccatcggc      300
gtcaacgagc gtgatggagg aactctatac aacacgcaac ttctcttga tgccgacgga      360
acattgattc aaagacgacg caagatcaca cccacccatt acgagcgcac ggtctggggc      420
cagggcgatg gctcagggtt acgggccatt gacagcaagg tcgcgcgcac tggtaactg      480
gcgtgttttg agcactacaa ccctctcgca cgttacgcga tgatggccga tggcgagcag      540
atccattctg cgatgttccc cggtccatg ttcggcgata atttttcaga gaaggtggaa      600
atcaacataa ggcagcatgc aatggagtct ggggtgcttg tcgtttgcgc tactgcttg      660
ttgatgctg accagcaggc tcaaatcatg aaagacacgg gatgtgagat cggaccgatc      720
tcaggagggt gcttcacagc gatcgcgga ccagatggaa gccttatagg tgaacccatc      780
cgctcagggt aaggcggttg tattgccgac ctcgatttca aacttatcga caagcggaag      840
cacgtagtag acacacgcgg ccattatagc cggccagaat tgctcagcct cctgattgat      900
cggacgccga cggccacat acacgaaagg accgagcaac cgagggcggc catcgagaaa      960
gagtcgcagg atgttttcac cgctgttgct taa      993

```

<210> 44
 <211> 330
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 44
Met Arg Val Val Lys Ala Ala Val Gln Leu Lys Pro Val Leu Tyr
1          5          10          15
Ser Arg Glu Gly Thr Val Glu Asn Val Val Arg Lys Ile His Glu Leu
20        25        30
Gly Gln Gln Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
35        40        45
Tyr Tyr Pro Tyr Phe Ser Ile Val Gln Ser Gly Tyr Gln Ile Leu Gly
50        55        60
Gly Gly Glu Phe Leu Lys Leu Leu Asp Gln Ser Val Thr Val Pro Ser
65        70        75        80
Leu Ala Thr Glu Ala Ile Gly Glu Ala Cys Arg Gln Ala Gly Val Val
85        90        95
Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn Thr
100       105       110
Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln Arg Arg Arg Lys

```

$\langle 220 \rangle$

<223> Obtained from an environmental sample

<400> 46

```

Val Lys Pro Pro Thr Ser Phe Arg Val Ala Ala Val Gln Ala Cys Pro
 1          5          10          15
Val Tyr Leu Asp Arg Asp Leu Thr Ile Gly Lys Ala Glu Gly Leu Ile
 20          25          30
Ala Glu Ala Ala Gly Asn Gly Ala Asn Leu Ile Val Phe Pro Glu Ala
 35          40          45
Phe Val Pro Gly Tyr Pro Val Trp Val Trp Phe Ile Pro Pro Gly Arg
 50          55          60
Thr Ala Asp Leu Arg Glu Ala Tyr Ser Val Leu His Ala Asn Ser Ile
 65          70          75          80
Ala Val Pro Ser Gln Ser Thr Glu Arg Leu Cys Ala Ala Ala Arg Arg
 85          90          95
Ala Gly Val Ala Val Ala Ile Gly Val Asn Glu Arg Asn Ser Glu Ala
100          105          110
Ser Gly Gly Ser Leu Phe Asn Thr Leu Leu Tyr Ile Gly Pro Asp Gly
115          120          125
Thr Leu Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly Gly Glu Arg
130          135          140
Leu Val Trp Ala Ser Gly Asp Gly Ser Asp Leu Ala Val Phe Thr Leu
145          150          155          160
Pro Phe Ala Arg Val Gly Gly Leu Ile Cys Trp Glu Asn Tyr Met Pro
165          170          175
Leu Ala Arg Tyr Ala Leu Ala Ala Trp Gly Ala Gln Ile His Val Ala
180          185          190
Pro Thr Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Leu Arg His Val
195          200          205
Ala Lys Glu Gly Arg Ala Val Thr Ile Gly Cys Cys Gln Ala Val Arg
210          215          220
Lys Glu Asp Ile Pro Asp Gly Leu Ala Phe Lys Ser Arg Tyr Leu Ala
225          230          235          240
Asp Val Gly Ala Trp Val Asn Pro Gly Gly Ser Val Ile Val Asp Pro
245          250          255
Asp Gly Lys Ile Leu Ala Gly Pro Ala Asn Glu Thr Glu Gly Ile Leu
260          265          270
Tyr Ala Asp Ile Arg Ala Asp Gln Leu Val Gly Pro Arg Trp Gln Leu
275          280          285
Asp Ile Ala Gly His Tyr Ala Arg Pro Asp Val Phe Glu Leu Ile Val
290          295          300
His Arg Arg Ser Thr Pro Met Ile Arg Glu Val Ser Ala Pro Arg Arg
305          310          315          320
Arg Ala Arg Thr Gly Lys Arg Pro Arg Arg Arg
325          330

```

<210> 47

<211> 1014

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 47

```

gtgaaagaag caatcaaagt agcctgtgtg caagcagctc cagtctttct cgacctggac      60
gccacagtgg acaagaccgt cgccctgatt gaggaggcag cccgtaacgg cgcacgccta      120
atcgcccttc cagagacctg gattccaggc taccatgggt tcctttggct ggactcacca      180
gcctggggga tgcaattcgt ggcgcgatac cactgggtcct cgacagccct      240
caggccaagc gcatcagtga ggcgcgccag cgcgcggta tatacgtcgc gctagggtac      300
agcgaacgcg tgagcggaac cctctacatg gggcagtggc tcattgacga taaggcgcaa      360

```



```

acagctgggc tgcgccgaaa gctgaaacca acccatgtag agcgaaccct cttcggtgaa 420
ggcgacggat catccctttc cactttcgac acaccgttgg ggggtgctggg cggactctgc 480
tggtgggaac acttacaacc tctttcgaaa tatgcgctct acgcacagaa cgaggaaata 540
cacttcgccg cctggcctag cttcagcatc taccgtcaag cgacagaagt ccttggacca 600
gaagtaaata tgcagcttc tcggatctac gccgtggaag ggcagtgttt tgttctcgct 660
tcctgcgcgc tcgtctcgcc agagatgato gaaatgctct gcactgacga aagcaagcac 720
agccttcttc aggccggcgg cgggtactcc cgcattatcg gtcccgatgg cagcgacct 780
gcgcgccoct tgggcgaaaa cgaggaaggt attctctatg ccactctgga ccctgccgct 840
cgaatctatg caaagaccgc agctgatcca gccgggcaact actccagacc agacgtcact 900
cggctgctga tcaatcgag tgccaatcag ccagtcgtag aggttggaag ggaaatacct 960
gcatcgcccc aaggctttga agttgaggcg gccccgggt acgaaggcga ttga 1014

```

<210> 48

<211> 337

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 48

```

Val Lys Glu Ala Ile Lys Val Ala Cys Val Gln Ala Ala Pro Val Phe
1      5      10      15
Leu Asp Leu Asp Ala Thr Val Asp Lys Thr Val Ala Leu Ile Glu Glu
20     25     30
Ala Ala Arg Asn Gly Ala Arg Leu Ile Ala Phe Pro Glu Thr Trp Ile
35     40     45
Pro Gly Tyr Pro Trp Phe Leu Trp Leu Asp Ser Pro Ala Trp Gly Met
50     55     60
Gln Phe Val Arg Arg Tyr His Glu Asn Ser Leu Val Leu Asp Ser Pro
65     70     75     80
Gln Ala Lys Arg Ile Ser Glu Ala Ala Gln Arg Ala Gly Ile Tyr Val
85     90     95
Ala Leu Gly Tyr Ser Glu Arg Val Ser Gly Thr Leu Tyr Met Gly Gln
100    105    110
Trp Leu Ile Asp Asp Lys Gly Glu Thr Ala Gly Leu Arg Arg Lys Leu
115    120    125
Lys Pro Thr His Val Glu Arg Thr Leu Phe Gly Glu Gly Asp Gly Ser
130    135    140
Ser Leu Ser Thr Phe Asp Thr Pro Leu Gly Val Leu Gly Gly Leu Cys
145    150    155    160
Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr Ala Leu Tyr Ala Gln
165    170    175
Asn Glu Glu Ile His Phe Ala Ala Trp Pro Ser Phe Ser Ile Tyr Arg
180    185    190
Gln Ala Thr Glu Val Leu Gly Pro Glu Val Asn Val Ala Ala Ser Arg
195    200    205
Ile Tyr Ala Val Glu Gly Gln Cys Phe Val Leu Ala Ser Cys Ala Leu
210    215    220
Val Ser Pro Glu Met Ile Glu Met Leu Cys Thr Asp Glu Ser Lys His
225    230    235    240
Ser Leu Leu Gln Ala Gly Gly Gly Tyr Ser Arg Ile Ile Gly Pro Asp
245    250    255
Gly Ser Asp Leu Ala Arg Pro Leu Gly Glu Asn Glu Glu Gly Ile Leu
260    265    270
Tyr Ala Thr Leu Asp Pro Ala Ala Arg Ile Tyr Ala Lys Thr Ala Ala
275    280    285
Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val Thr Arg Leu Leu Ile
290    295    300
Asn Arg Ser Ala Asn Gln Pro Val Val Glu Val Gly Arg Glu Ile Pro
305    310    315    320

```

Ala Ser Ala Gln Gly Phe Glu Val Glu Ala Ala Pro Gly Tyr Glu Gly
 325 330 335

Asp

<210> 49

<211> 1038

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 49

```

atgaacaaag tcgtggctgc tgccgttcag tgcagcccgg tgctttactc ttgcgccgga      60
actgtaaaata aaatttgcga gtggattgca gatttgggca aacaaggggt tgagctggcg      120
gtgttcgcgg aaaccctggg gccttactac ccgtattttt cttttatcca ggctccttgt      180
gcgatgggcg cgcaacattt gttgttgatg caagaatcag tagaggttcc ttccatctac      240
acgcaacaaa ttgccgctgc agcaaaagca gcgaagatgg tgggtgtcagt tgggtattaac      300
gaacgcgacg gcggttctat ttataacgcg caattattat ttgatgcggg cgggtcagctt      360
gttcagcacc gccgaaaaat tacgccgaca ttcatgagc gcatgggtgtg ggggcagggc      420
gatggctccg gtttgtgctg agtggatacg gcagttggtc gtgttggttc gctcgttgc      480
tggaacattt acaaccact cgcggttac gcattgatgg cagatcgcg acaaattcac      540
gtgagtatgt ttcccggttc ttgggtcggc gaaatttttg ccgagcaaat tgaagcaact      600
attcgtcacc acgcattgga gtcgggttgc tttgtggtta atgcgacggg ctgggttaacg      660
ccggaacacg aagctcaaat cgtaaaagat actggtggtc ctatcgctgc cattagcggg      720
ggttgtttca ccgccattgt ttaccgggaa ggaaaattgc tcggcacgcc attgcgcagt      780
gattccgggg aggtgcctg tatcgccgaa ctggatttta atctcatcaa taagcgtaag      840
cgcatgatgg attctgtcgg ccattacagt cgtcctgaat tgctcagttt gctgattgat      900
aaaacaccga aaagtcatat acatccgctt aaaaaacctt tggctcccag tgaaaaaaat      960
acgccagagg atatgccac tggtttaaca ctggtcactc ccgtttcaaa tgcaaacctt     1020
ttcagcgcaa gcaactag                                     1038
  
```

<210> 50

<211> 345

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 50

```

Met Asn Lys Val Val Ala Ala Ala Val Gln Cys Ser Pro Val Leu Tyr
 1          5          10          15
Ser Cys Ala Gly Thr Val Asn Lys Ile Cys Glu Trp Ile Ala Asp Leu
          20          25          30
Gly Lys Gln Gly Val Glu Leu Ala Val Phe Ala Glu Thr Leu Val Pro
          35          40          45
Tyr Tyr Pro Tyr Phe Ser Phe Ile Gln Ala Pro Cys Ala Met Gly Ala
          50          55          60
Gln His Leu Leu Leu Met Gln Glu Ser Val Glu Val Pro Ser Ile Tyr
          65          70          75          80
Thr Gln Gln Ile Ala Ala Ala Lys Ala Ala Lys Met Val Val Ser
          85          90          95
Val Gly Ile Asn Glu Arg Asp Gly Gly Ser Ile Tyr Asn Ala Gln Leu
          100          105          110
Leu Phe Asp Ala Gly Gly Gln Leu Val Gln His Arg Arg Lys Ile Thr
          115          120          125
Pro Thr Phe His Glu Arg Met Val Trp Gly Gln Gly Asp Gly Ser Gly
          130          135          140
Leu Cys Ala Val Asp Thr Ala Val Gly Arg Val Gly Ser Leu Ala Cys
  
```

```

145          150          155          160
Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met Ala Asp Arg
          165          170          175
Glu Gln Ile His Val Ser Met Phe Pro Gly Ser Leu Val Gly Glu Ile
          180          185          190
Phe Ala Glu Gln Ile Glu Ala Thr Ile Arg His His Ala Leu Glu Ser
          195          200          205
Gly Cys Phe Val Val Asn Ala Thr Gly Trp Leu Thr Pro Glu Gln Gln
          210          215          220
Ala Gln Ile Val Lys Asp Thr Gly Gly Pro Ile Ala Ala Ile Ser Gly
225          230          235          240
Gly Cys Phe Thr Ala Ile Val Ser Pro Glu Gly Lys Leu Leu Gly Thr
          245          250          255
Pro Leu Arg Ser Asp Ser Gly Glu Gly Ala Cys Ile Ala Glu Leu Asp
          260          265          270
Phe Asn Leu Ile Asn Lys Arg Lys Arg Met Met Asp Ser Val Gly His
          275          280          285
Tyr Ser Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Lys Thr Pro Thr
          290          295          300
Ser His Thr His Pro Leu Lys Lys Pro Leu Ala Pro Ser Glu Lys Asn
305          310          315          320
Thr Pro Glu Asp Ile Ala Thr Gly Leu Thr Leu Val Thr Pro Val Ser
          325          330          335
Asn Ala Asn Leu Phe Ser Ala Ser Asn
          340          345

```

<210> 51
 <211> 897
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 51
gtgaacgtcc gcgtcgcggt ggtgcaggcc acgccggccg tgctcgacgg gccggcgctcg      60
gtgcggaagg cctgccgcct gatcggcgag gccgcggccg gcggcgccc cctgatcgcc      120
ctgcccaggg gcttcgtgcc catcatgccg cgctcctgct gggggcacca cttcgcgctg      180
atcgccctcg cgaagtcggc ggccctgcac cggcgcatct gggagaacgc cgtcgacgtc      240
ggcgggcccg tgcccgcga gctcggcgac gccgcgcgcc gcgcggacgc ctgggtggcc      300
atcgggggtga acgagcgca cggccgccgg ccgggcacgc tctggaacac gctgctctgg      360
ttcgcgccc acgggagcct ggcccggcgc caccgcaagc tcgtgcccac catgcacgag      420
cgcacgttct gggggcaggg cgcgggcgac gacctcgagg cgctggccgc ggacttcggc      480
cgccctggcg gctgatctg ctgggagaac ttcatgccc cgcgcgcgcc gcgcctgcac      540
cgggacgggg tcgacttcta cctggcccc acggcgagc accgggacat ctgggtcgcc      600
gcgatgcgca cgttcgcctt cgaggccggc gccttcgtcc tctcgccggt gcagtacctg      660
cggaccggcg acttcccga ggacttccc ctgcccggag agctcgccga ctgcccggag      720
gtccagttca ccggggggag cgtgatctgc gaccctggg gcaacctcct ggcgggggccg      780
gtccacgggg gcgaggagat cctctacgcc gactgcgac tcgacctcgt cctcgaggcc      840
cgacgggtgc tcgacacggc cggccactac gaccgcccgg acctcgccct ggccctga      897

```

<210> 52
 <211> 298
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 52
Val Asn Val Arg Val Ala Val Val Gln Ala Thr Pro Ala Val Leu Asp

```

[illegible]

cagatgcgcg gccccaaatg gatgctcgac gtggccggcc attacgctcg cccggatgtg 900
 tttagaactca tcgttcacg ggaggcgcg cccatgattg cgctaatttc atga 954

<210> 54
 <211> 317
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 54
 Met Val Asn Ser Lys Ser Gln Ile Lys Ile Ala Ala Val Gln Ala Ala
 1 5 10 15
 Pro Val Phe Leu Glu Arg Glu Ala Thr Ile Asp Lys Ala Cys Arg Leu
 20 25 30
 Ile Ala Glu Ala Gly Glu Gln Gly Ala Asn Leu Val Val Phe Pro Glu
 35 40 45
 Ser Phe Val Pro Ala Tyr Pro Asp Trp Val Trp Ala Val Pro Ala Gly
 50 55 60
 Glu Thr Thr Leu Leu Asn Thr Leu Tyr Ala Glu Leu Leu Ala Asn Ala
 65 70 75 80
 Val Glu Ile Pro Gly Pro Ala Thr Glu Arg Leu Ser Gln Ala Ala Asn
 85 90 95
 Leu Ala Gly Val Tyr Val Ala Ile Gly Leu Thr Glu Arg Asn Ile Glu
 100 105 110
 Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Phe Leu Asp Ser Ala
 115 120 125
 Gly Gly Met Leu Gly Lys His Arg Lys Leu Ile Pro Thr Gly Gly Glu
 130 135 140
 Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Ala Val Tyr Glu
 145 150 155 160
 Thr Arg Phe Gly Lys Met Gly Gly Leu Ile Cys Trp Glu Asn Tyr Met
 165 170 175
 Pro Leu Ala Arg Tyr Ala Leu Tyr Ala Trp Gly Thr Gln Ile Tyr Ile
 180 185 190
 Ala Ala Thr Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Leu Arg His
 195 200 205
 Ile Ala Ala Glu Gly Arg Val Val Val Gly Cys Gly Met Ala Leu
 210 215 220
 Arg Lys Ala Asp Leu Pro Asp Arg Phe Glu Leu Lys Gln Arg Phe Tyr
 225 230 235 240
 Gln Asn Ala Asp Glu Trp Ile Asn Val Gly Asp Ser Ala Ile Val Asn
 245 250 255
 Pro Asp Gly Glu Phe Ile Ala Gly Pro Leu Arg Glu Gln Glu Gly Ile
 260 265 270
 Leu Tyr Ala Glu Ile Asp Leu Ala Gln Met Arg Gly Pro Lys Trp Met
 275 280 285
 Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Glu Leu Ile
 290 295 300
 Val His Arg Glu Ala Arg Pro Met Ile Ala Leu Ile Ser
 305 310 315

<210> 55
 <211> 1017
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 55
atgggtatcg aacatccgaa gtacaaggtc gccgtggtgc aggcagctcc cgcttggtc 60
gatctcgacg cgtcgatcga caagtcgacg gcgctgatcg aggaggcggc ccaaaaaggc 120
gccaaagctga tcgcattccc cgaggccttc attcccggct atccctggca catctggatg 180
gactcgccgg cctggggcat cggccgcggc tttgtgcagc gctattttga caattcgctc 240
gcctatgaca gcccgcaggc cgagaagctg cgcgcggcgg tgcgcaaggc aaagctcacc 300
gccgtgctcg ggctgtccga gcgcgacggc ggcaagtctt atctggcgca atggttgatc 360
gggcccgatg gcgagaccat cgcaaaacgc cgcaagctgc ggccgacaca tgccgagcgc 420
acggtgtacg gcgagggcga cggcagcgat ctgcagctcc acaaccgtcc cgatatcggc 480
cgcctcggcg cgctctgctg ctgggagcat ttgcagccac tgtcgaaata cgcgatgtac 540
gcgcagaacg agcaggtgca tgctcgcggc tggccgagct tttcgctcta cgatcccttt 600
gcggtggcgc tcggcgccga ggtgaacaac gcggcctcgc gcgtctatgc agtcgaaggc 660
tcctgcttcg tgctggcgcc atgcgccacc gtctcgagg ccgatgatcga cgagctctgc 720
gaccgaccgg acaagcatac gctgctgcat gtcggcgccg gttttgccgc gatctatggt 780
cctgacggca gccagatcgg cgacaagctc gcgcccgacc aggaagggct gttgatcgcg 840
gagatcgacc ttggggccat tggcgctgcc aagaacgcgg ccgatcccgc cgggcattat 900
tcgcggcccg acgtgacggc gctcctgctc aacaagaaac cgtacaagcg cgtcgagcag 960
ttctcgccac cggccgaggc ggtcgagccc acagatatcg cagcggcggc aagctga 1017

```

<210> 56

<211> 338

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 56

```

Met Gly Ile Glu His Pro Lys Tyr Lys Val Ala Val Val Gln Ala Ala
1      5      10      15
Pro Ala Trp Leu Asp Leu Asp Ala Ser Ile Asp Lys Ser Ile Ala Leu
20     25     30
Ile Glu Glu Ala Ala Gln Lys Gly Ala Lys Leu Ile Ala Phe Pro Glu
35     40     45
Ala Phe Ile Pro Gly Tyr Pro Trp His Ile Trp Met Asp Ser Pro Ala
50     55     60
Trp Ala Ile Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
65     70     75     80
Ala Tyr Asp Ser Pro Gln Ala Glu Lys Leu Arg Ala Ala Val Arg Lys
85     90     95
Ala Lys Leu Thr Ala Val Leu Gly Leu Ser Glu Arg Asp Gly Gly Ser
100    105    110
Leu Tyr Leu Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
115    120    125
Lys Arg Arg Lys Leu Arg Pro Thr His Ala Glu Arg Thr Val Tyr Gly
130    135    140
Glu Gly Asp Gly Ser Asp Leu Ala Val His Asn Arg Pro Asp Ile Gly
145    150    155    160
Arg Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys
165    170    175
Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ala Trp Pro
180    185    190
Ser Phe Ser Leu Tyr Asp Pro Phe Ala Val Ala Leu Gly Ala Glu Val
195    200    205
Asn Asn Ala Ala Ser Arg Val Tyr Ala Val Glu Gly Ser Cys Phe Val
210    215    220
Leu Ala Pro Cys Ala Thr Val Ser Gln Ala Met Ile Asp Glu Leu Cys
225    230    235    240
Asp Arg Pro Asp Lys His Thr Leu Leu His Val Gly Gly Gly Phe Ala
245    250    255
Ala Ile Tyr Gly Pro Asp Gly Ser Gln Ile Gly Asp Lys Leu Ala Pro

```

```

                260                265                270
Asp Gln Glu Gly Leu Leu Ile Ala Glu Ile Asp Leu Gly Ala Ile Gly
                275                280                285
Val Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
                290                295                300
Val Thr Arg Leu Leu Leu Asn Lys Lys Pro Tyr Lys Arg Val Glu Gln
305                310                315                320
Phe Ser Pro Pro Ala Glu Ala Val Glu Pro Thr Asp Ile Ala Ala Ala
                325                330                335
Ala Ser

```

<210> 57
 <211> 1014
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 57
gtgaaagaag caatcaaagt agcctgtgtg caagcagctc cagtctttct cgacctggac      60
gccacagtgg acaagaccgt cgccctgatt gaggaggcag cccgtaacgg cgcacgccta      120
atcgcccttc cagagacctg gattccaggc taccatgggt tcctttgggt ggactcacca      180
gcctggggga tgcaattcgt gcgccgatac cacgagaact cactggtcct cgacagccct      240
caggccaagc gcatcagtga ggccgcccag cgcgccggtg tatacgtcgc gctagggtag      300
agcgaacgcg tgagcggaac cctctacatg gggcagtggc tcattgacga taagggcgaa      360
acagctgggc tgcgccgaaa gctgaaacca acccatgtag agcgaaccct cttcgtgaa      420
ggcgacggat catccctttc cactttcgac acaccgttgg ggggtgctggg cggactctgc      480
tgttgggaac acttacaacc tctttcgaaa tatgcgtctt acgcacagaa cgaggaaata      540
cacttcgccc cctggcctag cttcagcacc taccgtcaag cgacagaagt ccttggacca      600
gaagtataatg tcgcagcttc tcggatctac gccgtggaag ggcagtgttt tgttctcgct      660
tcctgcgcgc tcgtctcgcc agagatgata gaaatgctct gcaactgacga aagcaagcac      720
agccttcttc aggccggcgg cgggtactcc cgcattatcg gtcccgatgg cagcgaccta      780
gcgcgccctt tgggcgaaaa cgagggaagg attctctatg ccactctgga ccctgccgct      840
cgaatctatg caaagaccgc agctgatcca gccgggcact actccagacc agacgtcact      900
cggctgctga tcaatcgag tgccaatcag ccagtcgtag aggttggacg ggaaatacct      960
gcatcgccc aaggcttga agttgaggcg gccccgggt acggaggcga ttga      1014

```

<210> 58
 <211> 337
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 58
Val Lys Glu Ala Ile Lys Val Ala Cys Val Gln Ala Ala Pro Val Phe
1          5          10          15
Leu Asp Leu Asp Ala Thr Val Asp Lys Thr Val Ala Leu Ile Glu Glu
20          25          30
Ala Ala Arg Asn Gly Ala Arg Leu Ile Ala Phe Pro Glu Thr Trp Ile
35          40          45
Pro Gly Tyr Pro Trp Phe Leu Trp Leu Asp Ser Pro Ala Trp Gly Met
50          55          60
Gln Phe Val Arg Arg Tyr His Glu Asn Ser Leu Val Leu Asp Ser Pro
65          70          75          80
Gln Ala Lys Arg Ile Ser Glu Ala Ala Gln Arg Ala Gly Ile Tyr Val
85          90          95
Ala Leu Gly Tyr Ser Glu Arg Val Ser Gly Thr Leu Tyr Met Gly Gln

```

100 105 110
 Trp Leu Ile Asp Asp Lys Gly Glu Thr Ala Gly Leu Arg Arg Lys Leu
 115 120 125
 Lys Pro Thr His Val Glu Arg Thr Leu Phe Gly Glu Gly Asp Gly Ser
 130 135 140
 Ser Leu Ser Thr Phe Asp Thr Pro Leu Gly Val Leu Gly Gly Leu Cys
 145 150 155 160
 Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr Ala Leu Tyr Ala Gln
 165 170 175
 Asn Glu Glu Ile His Phe Ala Ala Trp Pro Ser Phe Ser Ile Tyr Arg
 180 185 190
 Gln Ala Thr Glu Val Leu Gly Pro Glu Val Asn Val Ala Ala Ser Arg
 195 200 205
 Ile Tyr Ala Val Glu Gly Gln Cys Phe Val Leu Ala Ser Cys Ala Leu
 210 215 220
 Val Ser Pro Glu Met Ile Glu Met Leu Cys Thr Asp Glu Ser Lys His
 225 230 235 240
 Ser Leu Leu Gln Ala Gly Gly Gly Tyr Ser Arg Ile Ile Gly Pro Asp
 245 250 255
 Gly Ser Asp Leu Ala Arg Pro Leu Gly Glu Asn Glu Glu Gly Ile Leu
 260 265 270
 Tyr Ala Thr Leu Asp Pro Ala Ala Arg Ile Tyr Ala Lys Thr Ala Ala
 275 280 285
 Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val Thr Arg Leu Leu Ile
 290 295 300
 Asn Arg Ser Ala Asn Gln Pro Val Val Glu Val Gly Arg Glu Ile Pro
 305 310 315 320
 Ala Ser Ala Gln Gly Phe Glu Val Glu Ala Ala Pro Gly Tyr Gly Gly
 325 330 335
 Asp

<210> 59
 <211> 987
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 59
 atgcgagata ggaatttcaa actggcggcc attcaggcgg agccggtttt ctttaatcgc 60
 cgggcctcga cggaaaaggc ctgcagattg atcaaagaag cgggcgcgat gggcgccgat 120
 atcgcgggat tcagcgagac ctggcttccc gggtatccct ttttatctg gggcgcaagc 180
 gccgatccat ccctgctctg gaaggtctct gcggaatacc tggccaatgc cgttcaaata 240
 cccggtccc agacggatca attatgcgag gcggcgaaaa aggccggcat cgatgtggcg 300
 atcggagtgg ttgaactcga cgagtttacg aagggaacgg cttactgcac gctgctcttc 360
 atcggcaaa aagggaagat cctgggaaag caccgcaaac tcaagccgac gcaccgggag 420
 cgacacgtat ggggagaggg cgatgcgacg ggactcagtg tccatgagcg tccttacggg 480
 cggatcagcg gcctgaactg ctgggagcat aatatgggtc tggccgggta tgcctctgatg 540
 tctcagggca cgcacattca tatcgcgcc tggccgggtt cggaagggaa agcacctccc 600
 gcgcgctctc cgatgtggga gcgccagctt ctgctctccc gcgctttcgc ttcgcaatcc 660
 gccgcatacg tgattctggt cggaggactc ctgaaccgc agaatttcc ggcgccctac 720
 gatgaacttg ccgtcaagta cgggggagac agtttcatca tcgatccgcg cggggagatc 780
 atcgccgggc cggccaagg ggaaccatt ctcacgccc aaggctcgat ggaacaggtc 840
 ctgcgggcaa agtccgcctt cgatgtcgcg ggacattatt cccgcccga cgtcttcaa 900
 ctctgcgtca accgcaaac gtaccggcgt gtaagggaaa cttcgagca ggaccaacc 960
 gttctgaaa gagaatcgga atcgtaa 987

<210> 60
 <211> 328

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 60

```

Met Arg Asp Arg Asn Phe Lys Leu Ala Ala Ile Gln Ala Glu Pro Val
 1           5           10           15
Phe Phe Asn Arg Arg Ala Ser Thr Glu Lys Ala Cys Arg Leu Ile Lys
 20           25           30
Glu Ala Gly Ala Met Gly Ala Asp Ile Ala Gly Phe Ser Glu Thr Trp
 35           40           45
Leu Pro Gly Tyr Pro Phe Phe Ile Trp Gly Ala Ser Ala Asp Pro Ser
 50           55           60
Leu Leu Trp Lys Ala Ser Ala Glu Tyr Leu Ala Asn Ala Val Gln Ile
 65           70           75           80
Pro Gly Pro Glu Thr Asp Gln Leu Cys Glu Ala Ala Lys Lys Ala Gly
 85           90           95
Ile Asp Val Ala Ile Gly Val Val Glu Leu Asp Glu Phe Thr Lys Gly
100           105           110
Thr Ala Tyr Cys Thr Leu Leu Phe Ile Gly Lys Glu Gly Lys Ile Leu
115           120           125
Gly Lys His Arg Lys Leu Lys Pro Thr His Arg Glu Arg Thr Val Trp
130           135           140
Gly Glu Gly Asp Ala Thr Gly Leu Ser Val His Glu Arg Pro Tyr Gly
145           150           155           160
Arg Ile Ser Gly Leu Asn Cys Trp Glu His Asn Met Val Leu Pro Gly
165           170           175
Tyr Val Leu Met Ser Gln Gly Thr His Ile His Ile Ala Ala Trp Pro
180           185           190
Gly Ser Glu Gly Lys Ala Pro Pro Ala Pro Ser Pro Met Trp Glu Arg
195           200           205
Gln Leu Leu Leu Ser Arg Ala Phe Ala Ser Gln Ser Ala Ala Tyr Val
210           215           220
Ile Leu Val Gly Gly Leu Leu Asn Pro Gln Asn Ile Pro Ala Pro Tyr
225           230           235           240
Asp Glu Leu Ala Val Lys Tyr Arg Gly Asp Ser Phe Ile Ile Asp Pro
245           250           255
Arg Gly Glu Ile Ile Ala Gly Pro Ala Lys Gly Glu Thr Ile Leu Ile
260           265           270
Ala Glu Gly Ser Met Glu Gln Val Leu Ala Ala Lys Ser Ala Phe Asp
275           280           285
Val Ala Gly His Tyr Ser Arg Pro Asp Val Phe Gln Leu Cys Val Asn
290           295           300
Arg Lys Pro Tyr Arg Arg Val Arg Glu Thr Ser Glu Gln Asp Gln Pro
305           310           315           320
Ala Ser Glu Arg Glu Ser Glu Ser
325

```

<210> 61

<211> 966

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 61

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atgactcgat cttacccgaa tgacacactc acggttgggc ttgcgcaa at tgctccagtc      60
tggttggatc gtacagggac aatttcaaag atattagctc aagtcctatgc ggcaaatgaa    120

```

```

gcgggctgtc atcttgctgc gtttggcgaa ggtctcctcc ccgatatcc gttttggatt 180
gagcgaacaa atgggtgcagt cttcaactcg cccacgcaga aagaaattca cgcgcattat 240
ctggatcagg ctgtccagat cgaagcagg catcttgagg cgctttgcga agcagccaag 300
gaatatgaga tcgcaattgt cctgggatgc attgaacgtc cgcaagatcg tggagggcac 360
agtctgtatg caagccttgt atatattgat tcagacggca tcaccaatc tgtgcatcga 420
aagttaatgc caacatatga agaacggctc acctggctcg caggtgacgg acatggatta 480
cggtgacaca aattagggtgc ctttacggtt ggcgccctca actgttggga aaactggatg 540
cctttggcac gcgcggccat gtatggtcaa ggcgaggatt tgcattatgc catttgcccc 600
ggcggtctccc acaatagca agacattaca cgctttattg cactagaatc gcgttcctat 660
gttttatctg tgtcagggtt aatgcgctca ggcgattttc caaaagagac cccacatctt 720
gcatccatcc tggctaaagg tgaggatatt cttgccaacg gtggttcacg tatcgccggt 780
cctgacggca aatggatcgt tgagccgctt gtaggagaag agaagttaat tgttgcaacg 840
attgatcatt gtcgtgtgcg cgaagagcgt caaaattttg atccttcagg acattacagc 900
aggccagatg tattgcaact gaaaataaac aggcaacgcc agagtacaat ctcgtttgga 960
gagtaa

```

<210> 62

<211> 321

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 62

```

Met Thr Arg Ser Tyr Pro Asn Asp Thr Leu Thr Val Gly Leu Ala Gln
1      5      10      15
Ile Ala Pro Val Trp Leu Asp Arg Thr Gly Thr Ile Ser Lys Ile Leu
20      25      30
Ala Gln Val His Ala Ala Asn Glu Ala Gly Cys His Leu Val Ala Phe
35      40      45
Gly Glu Gly Leu Leu Pro Gly Tyr Pro Phe Trp Ile Glu Arg Thr Asn
50      55      60
Gly Ala Val Phe Asn Ser Pro Thr Gln Lys Glu Ile His Ala His Tyr
65      70      75      80
Leu Asp Gln Ala Val Gln Ile Glu Ala Gly His Leu Glu Ala Leu Cys
85      90      95
Glu Ala Ala Lys Glu Tyr Glu Ile Ala Ile Val Leu Gly Cys Ile Glu
100     105     110
Arg Pro Gln Asp Arg Gly Gly His Ser Leu Tyr Ala Ser Leu Val Tyr
115     120     125
Ile Asp Ser Asp Gly Ile Ile Gln Ser Val His Arg Lys Leu Met Pro
130     135     140
Thr Tyr Glu Glu Arg Leu Thr Trp Ser Pro Gly Asp Gly His Gly Leu
145     150     155     160
Arg Val His Lys Leu Gly Ala Phe Thr Val Gly Gly Leu Asn Cys Trp
165     170     175
Glu Asn Trp Met Pro Leu Ala Arg Ala Ala Met Tyr Gly Gln Gly Glu
180     185     190
Asp Leu His Ile Ala Ile Trp Pro Gly Gly Ser His Asn Thr Gln Asp
195     200     205
Ile Thr Arg Phe Ile Ala Leu Ser Arg Ser Tyr Val Leu Ser Val
210     215     220
Ser Gly Leu Met Arg Ser Gly Asp Phe Pro Lys Glu Thr Pro His Leu
225     230     235     240
Ala Ser Ile Leu Ala Lys Gly Glu Asp Ile Leu Ala Asn Gly Gly Ser
245     250     255
Cys Ile Ala Gly Pro Asp Gly Lys Trp Ile Val Glu Pro Leu Val Gly
260     265     270
Glu Glu Lys Leu Ile Val Ala Thr Ile Asp His Cys Arg Val Arg Glu
275     280     285

```

Glu Arg Gln Asn Phe Asp Pro Ser Gly His Tyr Ser Arg Pro Asp Val
 290 295 300
 Leu Gln Leu Lys Ile Asn Arg Gln Arg Gln Ser Thr Ile Ser Phe Gly
 305 310 315 320
 Glu

<210> 63
 <211> 978
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 63
 atgcaagata gaggaccgat tgtacgagct gcggtatcc aggctgaacc catagtcctt 60
 gattgtgacg cgaccgtgga aaaagcctgc cgattgatcg gtgaagcagc agaaaatggt 120
 gcaaaccatga tcgtgtttcc cgaagccttc attcccgttt atcccaatgc ggcgatctgg 180
 ggtcgaggtc tggccacttt tggcggacag cgccagaaat acgtatggac ggcactatgg 240
 aacaattcgg tggaaatccc tggccggcc accgacaggc tggcaaaggc agcacacgag 300
 gctcgagcca ccgttgtcat gggattgaat gagcgcgcg tcgataacaa cacgctttac 360
 aacacccctgc tatttattgg gccagacggg cgcttgctgg gcaagcaccg taagctcatg 420
 cccaccaatc acgaacggat gatctgggg atgggagatg ggagcaccct gcgggttttt 480
 gatacacctt gtggaaaagt aggcggtctc atctgctggg aaaactacat gcctctggcg 540
 cgttatgcac tctatggaca gggcgaacaa atccatgtcg cgccgactgc gcacgatggt 600
 gagatcactc tggccaatgc acgcaatacc gcctatgagg gacgcttatt cgtcatctcc 660
 gtgtgcatga tccttcgcaa gtccagcttt ccccatgatt ttgagctggg cgaggaattg 720
 gcggaggcag atgacttcat aaaatcaggc ggcagcgcca tcgttggggc agatggcgag 780
 gtgctggcgg gtccattgtg gaatgaagag aatatactgt atgccgatct tgacttgaat 840
 cgaattgtgg atgagagacg agtatattgat gtgacggggc attattcacg tccagatggt 900
 ctacgactgc actttaatgc ttccctcag aaaactattg aaagatatga gcaacctctc 960
 gatccgtctg aggggttaa 978

<210> 64
 <211> 325
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 64
 Met Gln Asp Arg Val Pro Ile Val Arg Ala Ala Ala Ile Gln Ala Glu
 1 5 10 15
 Pro Ile Val Leu Asp Cys Asp Ala Thr Val Glu Lys Ala Cys Arg Leu
 20 25 30
 Ile Gly Glu Ala Ala Glu Asn Gly Ala Asn Leu Ile Val Phe Pro Glu
 35 40 45
 Ala Phe Ile Pro Val Tyr Pro Asn Ala Ala Ile Trp Gly Arg Gly Leu
 50 55 60
 Ala Thr Phe Gly Gly Gln Arg Gln Lys Tyr Val Trp Thr Arg Leu Trp
 65 70 75 80
 Asn Asn Ser Val Glu Ile Pro Gly Pro Ala Thr Asp Arg Leu Ala Lys
 85 90 95
 Ala Ala His Glu Ala Arg Ala Thr Val Val Met Gly Leu Asn Glu Arg
 100 105 110
 Ala Val Asp Asn Asn Thr Leu Tyr Asn Thr Leu Leu Phe Ile Gly Pro
 115 120 125
 Asp Gly Arg Leu Leu Gly Lys His Arg Lys Leu Met Pro Thr Asn His
 130 135 140

Glu Arg Met Ile Trp Gly Met Gly Asp Gly Ser Thr Leu Arg Val Phe
 145 150 155 160
 Asp Thr Pro Cys Gly Lys Val Gly Gly Leu Ile Cys Trp Glu Asn Tyr
 165 170 175
 Met Pro Leu Ala Arg Tyr Ala Leu Tyr Gly Gln Gly Glu Gln Ile His
 180 185 190
 Val Ala Pro Thr Ala His Asp Gly Glu Ile Thr Leu Val Asn Ala Arg
 195 200 205
 Asn Thr Ala Tyr Glu Gly Arg Leu Phe Val Ile Ser Val Cys Met Ile
 210 215 220
 Leu Arg Lys Ser Ser Phe Pro His Asp Phe Glu Leu Gly Glu Glu Leu
 225 230 235 240
 Ala Glu Ala Asp Asp Phe Ile Lys Ser Gly Gly Ser Ala Ile Val Gly
 245 250 255
 Pro Asp Gly Glu Val Leu Ala Gly Pro Leu Trp Asn Glu Glu Asn Ile
 260 265 270
 Leu Tyr Ala Asp Leu Asp Leu Asn Arg Ile Val Asp Glu Arg Arg Val
 275 280 285
 Phe Asp Val Thr Gly His Tyr Ser Arg Pro Asp Val Leu Arg Leu His
 290 295 300
 Phe Asn Ala Ser Pro Gln Lys Thr Ile Glu Arg Tyr Glu Gln Pro Leu
 305 310 315 320
 Asp Pro Ser Glu Gly
 325

<210> 65
 <211> 1002
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 65
 atgccgaccc ccacttcaaa attcaaaatc ggcgccgtgc aggcacgcgc ggtttttctg 60
 gaccgggaag ccactgcgca aaaagcctgc aaattgattg ccgaagcggg agggcagggc 120
 gcgcggctga tcgttttccc ggagtctttc attccacact atcctgattg ggtctgggcg 180
 gtccccgccg gaagaggaaa agtggttaagc gaactttacg ccgagctgct ggccaatgcc 240
 gtggaagtcc ccgggcccgt caccgatcag ctgggtgaag cagcccaaaa aacgggcgcc 300
 tatgtcgtca tgggcgtcac ggaaaaggac accgacgcaa gcggcgcgag cctttacaac 360
 acgtctctct atttcaaccc cgcggggggac ctctgggaa aacaccggaa gcttgttcct 420
 accggcgggg agcggctggt ctgggcgcag ggcgacggca gcaccctgga agtgtagcgc 480
 actccccctg gaaaaatcgg aggcctcatc tgctgggaaa actacatgcc cctcgcccgg 540
 tacacgatgt atgcctgggg gaccagatt tatatcgcg ccacatggga ccagggggag 600
 acgtggcttg ccaccctgcg gcatatcgct aaggaaggac ggggtgtacgt catcgctgc 660
 tgcacgcgc tgcggcgga cgacatcccc gaccggctgg aatacaagaa gaagttctac 720
 tcggggtcgc gggaatgat caatatggg gacagcgcca tcgtgaaccc ggaaggcgaa 780
 ttcatgtccg gccccgtgcg gatgaaggag gagatcctgt atgccgaggt ggacccctc 840
 ctgatggcgg gatcgaaatg gatgctcgac gtcgcggggc attacgcgcg ccccgacgtc 900
 tttgaactca tcgtccaccg ccagccccac ccgatgatcc gggtaatcga gaaagaggga 960
 ggggccggaa gaaccgggga cgagaagaag gaaaatgagt ga 1002

<210> 66
 <211> 333
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 66

Met Pro Thr Pro Thr Ser Lys Phe Lys Ile Gly Ala Val Gln Ala Ser
 1 5 10 15
 Pro Val Phe Leu Asp Arg Glu Ala Thr Ala Gln Lys Ala Cys Lys Leu
 20 25 30
 Ile Ala Glu Ala Gly Gly Gln Gly Ala Arg Leu Ile Val Phe Pro Glu
 35 40 45
 Ser Phe Ile Pro Thr Tyr Pro Asp Trp Val Trp Ala Val Pro Pro Gly
 50 55 60
 Arg Gly Lys Val Leu Ser Glu Leu Tyr Ala Glu Leu Leu Ala Asn Ala
 65 70 75 80
 Val Glu Val Pro Gly Pro Val Thr Asp Gln Leu Gly Glu Ala Ala Gln
 85 90 95
 Lys Thr Gly Ala Tyr Val Val Met Gly Val Thr Glu Lys Asp Thr Asp
 100 105 110
 Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Phe Asn Pro Ala
 115 120 125
 Gly Asp Leu Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly Gly Glu
 130 135 140
 Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Glu Val Tyr Asp
 145 150 155 160
 Thr Pro Leu Gly Lys Ile Gly Gly Leu Ile Cys Trp Glu Asn Tyr Met
 165 170 175
 Pro Leu Ala Arg Tyr Thr Met Tyr Ala Trp Gly Thr Gln Ile Tyr Ile
 180 185 190
 Ala Ala Thr Trp Asp Gln Gly Glu Thr Trp Leu Ala Thr Leu Arg His
 195 200 205
 Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys Ile Ala Leu
 210 215 220
 Arg Arg Asp Asp Ile Pro Asp Arg Leu Glu Tyr Lys Lys Lys Phe Tyr
 225 230 235 240
 Ser Gly Ser Arg Glu Trp Ile Asn Met Gly Asp Ser Ala Ile Val Asn
 245 250 255
 Pro Glu Gly Glu Phe Ile Ala Gly Pro Val Arg Met Lys Glu Glu Ile
 260 265 270
 Leu Tyr Ala Glu Val Asp Pro Leu Leu Met Ala Gly Ser Lys Trp Met
 275 280 285
 Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Glu Leu Ile
 290 295 300
 Val His Arg Gln Pro His Pro Met Ile Arg Val Ile Glu Lys Glu Gly
 305 310 315 320
 Gly Ala Gly Arg Thr Gly Asp Glu Lys Lys Glu Asn Glu
 325 330

<210> 67

<211> 936

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 67

atgccccgtg	tggcggtggt	ccagcgcccg	ccggtgtttc	tcgaccgcgc	cgcgaccctc	60
gagaacgccg	tggcttcgct	cgccgagggc	gcgtcgaaacg	gggctcgccct	cgcggtcttt	120
ccggaagccc	tggttcccgg	ctatccggcg	tgatgtggc	ggctgcggcc	cgggcccagc	180
atggcgctca	ccgagcggat	tcacgcgcgc	ttgcgggcga	actcggtgag	cctcgccgcc	240
gacgagctcg	cgccgctgcg	cgagggcgcc	cggcgccacg	agctcaccgt	agtgtgcggc	300
ctgcacgagc	gcgacgaggc	gctcggcggc	ggcacgctct	ataacaccgt	cgtcacgatc	360
ggcgccgacg	gcgcggtgct	caaccgccac	cggaagctga	tgcccaccaa	ccccgagcgc	420
atggtctggg	gctgcggcga	tgccagcggg	ctcaggacgg	tccccaccca	gtgcggggcg	480
gtcggcgccc	tgatctgctg	ggaaagctac	atgccgcttg	cacgctacgc	gctgtacgcc	540

```

cagggaatcg acctctacgt cacgccgacc tacgacagcg gcgagcgggc ggttgcgacc 600
atgcagcaca ttgcccgca aggcggctgc tgggtggtga gctgcggctc ggcgtttcag 660
gcgcgcgacg tcccgacgc gtttccgggg aagagcgagc ttttccgca caacgacgag 720
tggatcaacc cggcgactc ggtcgtggtc gcgccgggcg gcaaggtcgt cgccggggccg 780
ctgcacaaag aacgcgcgat cctgtacgcc gagatcgacc tcgagcgggt cggcgtggcg 840
cgccgcagcc tggacgtggt cggccattat gcgcggcccg acctcttcga cctgcacgtg 900
aacgcccgcc cgcaaagcgt ggttgaattg cgctga 936

```

<210> 68
 <211> 311
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 68

Met	Pro	Arg	Val	Ala	Val	Val	Gln	Arg	Pro	Pro	Val	Phe	Leu	Asp	Arg
1				5					10					15	
Ala	Ala	Thr	Leu	Glu	Asn	Ala	Val	Ala	Ser	Leu	Ala	Glu	Ala	Ala	Ser
			20					25					30		
Asn	Gly	Ala	Arg	Leu	Ala	Val	Phe	Pro	Glu	Ala	Leu	Val	Pro	Gly	Tyr
	35					40						45			
Pro	Ala	Trp	Met	Trp	Arg	Leu	Arg	Pro	Gly	Pro	Asp	Met	Ala	Leu	Thr
	50				55						60				
Glu	Arg	Ile	His	Ala	Arg	Leu	Arg	Ala	Asn	Ser	Val	Ser	Leu	Ala	Ala
65				70					75						80
Asp	Glu	Leu	Ala	Pro	Leu	Arg	Glu	Ala	Ala	Arg	Arg	His	Glu	Leu	Thr
				85				90					95		
Val	Val	Cys	Gly	Leu	His	Glu	Arg	Asp	Glu	Ala	Leu	Gly	Gly	Gly	Thr
		100						105					110		
Leu	Tyr	Asn	Thr	Val	Val	Thr	Ile	Gly	Ala	Asp	Gly	Ala	Val	Leu	Asn
		115				120						125			
Arg	His	Arg	Lys	Leu	Met	Pro	Thr	Asn	Pro	Glu	Arg	Met	Val	Trp	Gly
	130				135						140				
Cys	Gly	Asp	Ala	Ser	Gly	Leu	Arg	Thr	Val	Pro	Thr	Gln	Cys	Gly	Arg
145				150					155						160
Val	Gly	Ala	Leu	Ile	Cys	Trp	Glu	Ser	Tyr	Met	Pro	Leu	Ala	Arg	Tyr
			165					170						175	
Ala	Leu	Tyr	Ala	Gln	Gly	Ile	Asp	Leu	Tyr	Val	Thr	Pro	Thr	Tyr	Asp
		180					185						190		
Ser	Gly	Glu	Arg	Ala	Val	Ala	Thr	Met	Gln	His	Ile	Ala	Arg	Glu	Gly
		195				200						205			
Gly	Cys	Trp	Val	Val	Ser	Cys	Gly	Ser	Ala	Phe	Gln	Ala	Arg	Asp	Val
	210				215						220				
Pro	Asp	Ala	Phe	Pro	Gly	Lys	Ser	Glu	Leu	Phe	Arg	Asp	Asn	Asp	Glu
225				230					235						240
Trp	Ile	Asn	Pro	Gly	Asp	Ser	Val	Val	Val	Ala	Pro	Gly	Gly	Lys	Val
			245					250						255	
Val	Ala	Gly	Pro	Leu	His	Lys	Glu	Arg	Ala	Ile	Leu	Tyr	Ala	Glu	Ile
		260					265						270		
Asp	Leu	Glu	Arg	Val	Gly	Val	Ala	Arg	Arg	Ser	Leu	Asp	Val	Val	Gly
		275				280						285			
His	Tyr	Ala	Arg	Pro	Asp	Leu	Phe	Asp	Leu	His	Val	Asn	Ala	Arg	Pro
	290				295						300				
Gln	Ser	Val	Val	Glu	Leu	Arg									
305					310										

<210> 69
 <211> 939
 <212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 69

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gtgaccgagt ttccggacggg gcgggtcgca gcgggtgcagg cgacgccggg gaccctcgac      60
gccgatgcct cggtcgagaa ggcgatcggg ctgatcggcg aggcgggtggc cggtgaggcg      120
cagctcgtcg tgctgcccga ggccttcgtg tcgctctacc cgtcgaacgc gtgggcgcga      180
gcggccgcgc gattcggcgg cttcgacgag ctctgggagc ggatgtgggc cagctcgtc      240
gacgtcccgc gcccgctggg cgaccggctg gtcgatcggt gccgcaggca tgacgtggta      300
tgcggtgatcg gcgtgaacga gcgcgaaagc gaaaggccgg ggtcgcttta caacacgatg      360
ctgaccctcg gcccgtcggg cctcctgcac cggcaccgca agctcatgcc gacgcaccac      420
gagcgctgtg tccatgggat cggcgacggg caagacctcg gcgttggtga gaccgacgcg      480
ggacggatcg ggggactgat ctgctgggag aaccgaatgc cgctcgcgcg ctacgcggtc      540
taccagggtg gaccgcagat ctgggtcgcg ccgacggccg atgactccga cggctggctc      600
gcgagcatgc gccacatcgc gatcgagtcg ggcgcgttcg tcgtgtcggg gccgcagttc      660
atcccgcgct ccgcgttccc cgacgatttc ccgctcgagc taccgcccgg caaggagggt      720
ttcggccgcg gcgggtcgcc gatcgtcgag ccgacctggg gcgaggtaat cgcggggccg      780
ctctacgata gggaggggat cgtgttcgcc gactgtgacc tgcgacgcgg cttgcatgcc      840
aagcgctggg tcgactccgt cggccattac agccgcgcgg aggtgctcga tggcggcgct      900
gagcgcgctc cggcgccggg ggacggcgaa tcgccgtga      939

```

<210> 70

<211> 312

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 70

```

Val Thr Glu Phe Arg Thr Val Arg Val Ala Ala Val Gln Ala Thr Pro
 1          5          10          15
Val Thr Leu Asp Ala Asp Ala Ser Val Glu Lys Ala Ile Gly Leu Ile
          20          25          30
Gly Glu Ala Val Ala Gly Gly Ala Gln Leu Val Val Leu Pro Glu Ala
          35          40          45
Phe Val Ser Leu Tyr Pro Ser Asn Ala Trp Ala Arg Ala Ala Ala Gly
          50          55          60
Phe Gly Gly Phe Asp Glu Leu Trp Glu Arg Met Trp Ala Ser Ser Leu
          65          70          75          80
Asp Val Pro Gly Pro Leu Val Asp Arg Leu Val Asp Ala Cys Arg Arg
          85          90          95
His Asp Val Val Cys Val Ile Gly Val Asn Glu Arg Glu Ser Glu Arg
          100          105          110
Pro Gly Ser Leu Tyr Asn Thr Met Leu Thr Leu Gly Pro Ser Gly Leu
          115          120          125
Leu His Arg His Arg Lys Leu Met Pro Thr His His Glu Arg Leu Phe
          130          135          140
His Gly Ile Gly Asp Gly Gln Asp Leu Gly Val Val Glu Thr Asp Ala
          145          150          155          160
Gly Arg Ile Gly Gly Leu Ile Cys Trp Glu Asn Arg Met Pro Leu Ala
          165          170          175
Arg Tyr Ala Val Tyr Gln Gly Gly Pro Gln Ile Trp Val Ala Pro Thr
          180          185          190
Ala Asp Asp Ser Asp Gly Trp Leu Ala Ser Met Arg His Ile Ala Ile
          195          200          205
Glu Ser Gly Ala Phe Val Val Ser Val Pro Gln Phe Ile Pro Ala Ser
          210          215          220
Ala Phe Pro Asp Asp Phe Pro Val Glu Leu Pro Pro Gly Lys Glu Val

```

```

225          230          235          240
Phe Gly Arg Gly Gly Ala Ala Ile Val Glu Pro Thr Trp Gly Glu Val
          245          250          255
Ile Ala Gly Pro Leu Tyr Asp Arg Glu Gly Ile Val Phe Ala Asp Cys
          260          265          270
Asp Leu Arg Arg Gly Leu His Ala Lys Arg Trp Phe Asp Ser Val Gly
          275          280          285
His Tyr Ser Arg Ala Glu Val Leu Asp Gly Gly Val Glu Arg Val Pro
          290          295          300
Ala Pro Val Asp Gly Glu Ser Pro
305          310

```

<210> 71
 <211> 966
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 71
atgccaaacg agaacaccaa cgccacattc aaagttgccg ctgtgcaggc ttcgcctgtg      60
tttcttgatc gtgccgcaac aatcgacaag gcttgcgatt tgatcgccgc tgctggcggg      120
gaaggggcac gcttgattgt ctttccagaa gcattcatcc cgtcttatcc tgattgggta      180
tgggcaattc cttcgggtga agagggcgta ctcaatgagt tgtacgcaga tctgctatcc      240
aactcgggtca cgattcccag tgactcgacg gacaaactgt gcagagcagc caggcttgct      300
aatgcctacg tggatgatgg tatgagcgaa cgcaatgctg aggcagcgcg cgcgagcatg      360
tataaacacgc tattgtatat tgatgcacag ggggagattc tgggcaagca tcggaagttg      420
gtgccaacgg gcgcgagcgc gctagtctgg gcgcagggcg atggcagtac actgcaggtc      480
tatgatactc ccttagggaa actcgggtggc ttaatttgct gggagaatta tatgccactg      540
gcccgctata ccatgtatgc ctggggcaca caaatctatg tcgcggcaac gtgggatcgg      600
ggtcagccct ggctctctac ttacgccac attgccaag aaggcagggt gtatgtgatt      660
ggttgttgta tcgcgatgcg taaagacgat atccagacc attatacaat gaaacagaag      720
ttttactcag atgcagatga gtggattaat attggcgata gtgcgattgt taatcccgaa      780
gggcaattta tcgctggacc ggtgcgcaag caggaagaga ttctctatgc ggagattgat      840
ccgcgcatgg tccaagggcc gaagtggatg ctgcacgtgg cgggacatta tgccaggccg      900
gatgtgttcg aactgattgt ccacacggat attcgaagga tgatcaaadc ggaaaagaat      960
tcataa

```

<210> 72
 <211> 321
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 72
Met Pro Asn Glu Asn Thr Asn Ala Thr Phe Lys Val Ala Ala Val Gln
1          5          10          15
Ala Ser Pro Val Phe Leu Asp Arg Ala Ala Thr Ile Asp Lys Ala Cys
          20          25          30
Asp Leu Ile Ala Ala Ala Gly Gly Glu Gly Ala Arg Leu Ile Val Phe
          35          40          45
Pro Glu Ala Phe Ile Pro Ser Tyr Pro Asp Trp Val Trp Ala Ile Pro
          50          55          60
Ser Gly Glu Glu Gly Val Leu Asn Glu Leu Tyr Ala Asp Leu Leu Ser
65          70          75          80
Asn Ser Val Thr Ile Pro Ser Asp Ser Thr Asp Lys Leu Cys Arg Ala
          85          90          95
Ala Arg Leu Ala Asn Ala Tyr Val Val Met Gly Met Ser Glu Arg Asn

```



```

      100      105      110
Ala Glu Ala Ser Gly Ala Ser Met Tyr Asn Thr Leu Leu Tyr Ile Asp
      115      120      125
Ala Gln Gly Glu Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly
      130      135      140
Gly Glu Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Gln Val
      145      150      155      160
Tyr Asp Thr Pro Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn
      165      170      175
Tyr Met Pro Leu Ala Arg Tyr Thr Met Tyr Ala Trp Gly Thr Gln Ile
      180      185      190
Tyr Val Ala Ala Thr Trp Asp Arg Gly Gln Pro Trp Leu Ser Thr Leu
      195      200      205
Arg His Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys Ile
      210      215      220
Ala Met Arg Lys Asp Asp Ile Pro Asp His Tyr Thr Met Lys Gln Lys
      225      230      235      240
Phe Tyr Ser Asp Ala Asp Glu Trp Ile Asn Ile Gly Asp Ser Ala Ile
      245      250      255
Val Asn Pro Glu Gly Gln Phe Ile Ala Gly Pro Val Arg Lys Gln Glu
      260      265      270
Glu Ile Leu Tyr Ala Glu Ile Asp Pro Arg Met Val Gln Gly Pro Lys
      275      280      285
Trp Met Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Glu
      290      295      300
Leu Ile Val His Thr Asp Ile Arg Arg Met Ile Lys Ser Glu Lys Asn
      305      310      315      320
Ser

```

<210> 73

<211> 1035

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

```

<400> 73
atgacagcaa tagactcaac gtttaaagtc gccgccgttc aggctgcgcc ggtcttcctc 60
aatcgcgacg caaccgtgga gaaggcgtgc cggctgatca agtccgcggc agagggaggc 120
gcgcgtctga tcgttttccc ggaagcgttc ataccggcct acccgactg ggtgtggacg 180
gtccctgccg gtgagcaagg cctgctcaac gacctctacg gccaaactcg cgaccagtcc 240
gtgacgattc ccagcgacat caccaccgag ttatgtaacg cggcacgggc agcaaacgcc 300
tatgtcgtga ttggtgtcaa cgagcgcaac gcggaggcaa gcaatggaag cctctacaac 360
tcgctcctct acatcgacgc aaacggcaaa attctcggta agcacgcaa gctcgttccc 420
acaggcggag aacggctcgt gtgggcgcag ggcgatggca gcacgctcga agcctacgac 480
acggagctgg gcaaactcgg cgtctctatt tgctgggaga actatatgcc gctggcacgc 540
tacgcgatgt acgcatgggg agtgacgctc tatgtcggcg cgacctggga ccgtggcggc 600
ccctggactg ccacgctgcg tcatgtcgcc aaggaaggtc agatgtacgt catcgggtgc 660
tgccaggccc tgcacaagga tgacctgccg gagctagacg ggctgaagga gaagtactac 720
gccaacgcac gagagtggat caatgttggc gacagcgcta ttgtcggccc ggacggacaa 780
ttccttgctg agcccgtccg aatgcgggaa gacatcctct acgccgaggt ggacactcgc 840
aacttccgcg gcccgaaagt gatgttcgac gcggctggac actacgcgcg tcccgcacatt 900
ttccaactca cagtgaaccg cgagcagcgg ccgatggctc gcgtcgtcgg tgacagcagt 960
gaccagaagg agcggccgct cccggacgac ggacggctct ggtacgccta cagcaccaat 1020
cagcaccacg actga 1035

```

<210> 74

<211> 344

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 74

```

Met Thr Ala Ile Asp Ser Thr Phe Lys Val Ala Ala Val Gln Ala Ala
 1          5          10          15
Pro Val Phe Leu Asn Arg Asp Ala Thr Val Glu Lys Ala Cys Arg Leu
      20          25          30
Ile Lys Ser Ala Ala Glu Gly Gly Ala Arg Leu Ile Val Phe Pro Glu
      35          40          45
Ala Phe Ile Pro Ala Tyr Pro Asp Trp Val Trp Thr Val Pro Ala Gly
      50          55          60
Glu Gln Gly Leu Leu Asn Asp Leu Tyr Gly Gln Leu Val Asp Gln Ser
65          70          75          80
Val Thr Ile Pro Ser Asp Ile Thr Thr Glu Leu Cys Asn Ala Ala Arg
      85          90          95
Ala Ala Asn Ala Tyr Val Val Ile Gly Val Asn Glu Arg Asn Ala Glu
      100          105          110
Ala Ser Asn Gly Ser Leu Tyr Asn Ser Leu Leu Tyr Ile Asp Ala Asn
      115          120          125
Gly Lys Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly Gly Glu
      130          135          140
Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Glu Ala Tyr Asp
145          150          155          160
Thr Glu Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn Tyr Met
      165          170          175
Pro Leu Ala Arg Tyr Ala Met Tyr Ala Trp Gly Val Gln Leu Tyr Val
      180          185          190
Ala Ala Thr Trp Asp Arg Gly Gly Pro Trp Thr Ala Thr Leu Arg His
      195          200          205
Val Ala Lys Glu Gly Gln Met Tyr Val Ile Gly Cys Cys Gln Ala Leu
      210          215          220
His Lys Asp Asp Leu Pro Glu Leu Asp Gly Leu Lys Glu Lys Tyr Tyr
225          230          235          240
Ala Asn Ala Arg Glu Trp Ile Asn Val Gly Asp Ser Ala Ile Val Gly
      245          250          255
Pro Asp Gly Gln Phe Leu Val Glu Pro Val Arg Met Arg Glu Asp Ile
      260          265          270
Leu Tyr Ala Glu Val Asp Thr Arg Asn Phe Arg Gly Pro Lys Trp Met
      275          280          285
Phe Asp Ala Ala Gly His Tyr Ala Arg Pro Asp Ile Phe Gln Leu Thr
      290          295          300
Val Asn Arg Glu Gln Arg Pro Met Val Arg Val Val Gly Asp Ser Ser
305          310          315          320
Asp Gln Lys Glu Arg Pro Leu Pro Asp Asp Gly Arg Leu Trp Tyr Ala
      325          330          335
Tyr Ser Thr Asn Gln His His Asp
      340

```

<210> 75

<211> 1125

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 75

atgagcacca ttgttaaagc cgctgcgggt caaatcagcc cagtcctcta cagccgcgag

60

```

gggacagtcg caaaagtgtg gcggaagatc cacgaacttg gccaaaaggg ggtgcggttc 120
gccacgttcc cggagaccgt gggtccctac tatccatatt tttccgccgt ccagaccccc 180
attcaactat tgtccggaac cgagtacctg aagttgctcg accaaggcgt gaccgtgccg 240
tccacgacta ccgacgcaat cggggaggct gcccggaacg ccggcatggt tgtatctatc 300
ggcgtgaatg agcgtgacgg cgggaccctg tacaacgcgc agttgctctt cgatgcggat 360
gggaccttga ttcagcgtcg ccgcaagatc actcctacgc attacgagcg catgatctgg 420
ggccaggagg atggttcggg ttgctggggc gtcaagagcc aggttggtcg tattggccaa 480
cttgcattgt ttgagcacia caaccactg gcgcgttacg cgatgatggc cgatggcgag 540
caaatccatt cggccatgta tccaggttcc gcgttcggcg aggggttcgc ggaaaagatg 600
gaaatcaata tccgccagca tgcgttggag tccgggtgct tcgttggtgaa tgcaacggcc 660
tggcttgacg ccagccagca ggcacaaatc atgaatgaca cgggttgcca aatcgttccg 720
atctcgggcg gttgctttac cagcatcgta acaccgcagc gcacgtttct gggcgaacct 780
ctccggtcgg gtgagggcga ggtcatcgcc gatctcgatt tcaagctgat cgacaaacgc 840
aagatgttga tggactcgcg cggccactac agtcgcccg aattgctcag tctgctgatc 900
gaccgcaccc ccaccgcgca cattcatgag cgaggtgcgc cgcagacgtc aggcgtgtg 960
caagaggcga cgaaagtggg ttcacacgcg ccgctcctgc gtgacggaca atgggatcag 1020
ctcaatgcgg gagcgggccg acatacaggg aatggagaag cacagataga aatcatggcc 1080
gcggccact cgggcacccg tggaattgaa gcgaaggag cctaa 1125

```

<210> 76

<211> 374

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 76

```

Met Ser Thr Ile Val Lys Ala Ala Val Gln Ile Ser Pro Val Leu
1      5      10      15
Tyr Ser Arg Glu Gly Thr Val Ala Lys Val Val Arg Lys Ile His Glu
20     25     30
Leu Gly Gln Lys Gly Val Arg Phe Ala Thr Phe Pro Glu Thr Val Val
35     40     45
Pro Tyr Tyr Pro Tyr Phe Ser Ala Val Gln Thr Pro Ile Gln Leu Leu
50     55     60
Ser Gly Thr Glu Tyr Leu Lys Leu Leu Asp Gln Gly Val Thr Val Pro
65     70     75     80
Ser Thr Thr Thr Asp Ala Ile Gly Glu Ala Ala Arg Asn Ala Gly Met
85     90     95
Val Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn
100    105    110
Ala Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln Arg Arg Arg
115    120    125
Lys Ile Thr Pro Thr His Tyr Glu Arg Met Ile Trp Gly Gln Gly Asp
130    135    140
Gly Ser Gly Leu Arg Ala Val Lys Ser Gln Val Gly Arg Ile Gly Gln
145    150    155    160
Leu Ala Cys Phe Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Met Met
165    170    175
Ala Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Ala Phe
180    185    190
Gly Glu Gly Phe Ala Glu Lys Met Glu Ile Asn Ile Arg Gln His Ala
195    200    205
Leu Glu Ser Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala
210    215    220
Ser Gln Gln Ala Gln Ile Met Asn Asp Thr Gly Cys Gln Ile Gly Pro
225    230    235    240
Ile Ser Gly Gly Cys Phe Thr Thr Ile Val Thr Pro Asp Gly Thr Phe
245    250    255
Leu Gly Glu Pro Leu Arg Ser Gly Glu Gly Glu Val Ile Ala Asp Leu

```

```

                260                265                270
Asp Phe Lys Leu Ile Asp Lys Arg Lys Met Leu Met Asp Ser Arg Gly
      275                280                285
His Tyr Ser Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro
      290                295                300
Thr Ala His Ile His Glu Arg Gly Ala Pro Gln Thr Ser Gly Ala Val
305                310                315                320
Gln Glu Ala Thr Lys Val Gly Ser His Ala Pro Leu Leu Arg Asp Gly
      325                330                335
Gln Trp Asp Gln Leu Asn Ala Gly Ala Gly Arg His Thr Gly Asn Gly
      340                345                350
Glu Ala Gln Ile Glu Ile Met Ala Ala Ala His Ser Gly Thr Arg Gly
      355                360                365
Ile Glu Ala Lys Gly Ala
      370

```

<210> 77

<211> 1056

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 77

```

atgccaaaccc ccagcgatca tttcaaaatc gccgctgttc aggcctcgcc cgtgtttctg      60
gaccgggagg ccactgtgga aaaggcctgc cggttgatcg ccgaagccgc aaagcagggc      120
gtccgcctca tcgtctttcc ggaatcggtc atcccgacct acccgactg ggtatgggcc      180
gttcccccg gaagggaaag aatcctgaac cagctgtatt ctgaattcct ggccaatgcc      240
gtcgatgttc ccggcgcggc gaccgaacaa ctgcccagg ctgcacgaat ggccggcgcc      300
tatgtgatta tgggcgtcac cgaaagagac acctcggcc gcggggccag cctctacaac      360
acctgctct acttcagccc cgaaggcatc ctaatgggca aacaccgga gctggttccc      420
acggggggcg aacggctggt ctgggcctac ggagacggca gcacgctgga ggtctacgac      480
actccgctgg gaaagatcgg cgggctgac tgctgggaga actacatgcc cctggcccgg      540
tacacgatgt acgcctgggg caccagatt tacatcgccg ccacctggga ccgcggggaa      600
ccgtggctct ccacctgcg gcataatcgca aaggaaggaa gggctctacgt catcgggtgc      660
tgcacgccc tgcgccagg ggatatcccg gaccggttcg agtacaaggg aaaattttat      720
tccgggtccc gggagtggat caatgagggc gacagcgcca tcgtgaaccc ggacggggaa      780
ttcatcgccg ggcgggtgcg gacgaaggag gagatcctgt atgccgagat agacccccgg      840
cagatgcggg gcccgaagt gatgctcgat gtggccggtc attacgccc ggcggatatc      900
ttcgaactca tcgtccaccg gaatccccac ccgatgatca aaatcgccga agacaggggc      960
acggggatcg cctcaagttt gattcgcccc cgccctaacc ttccccatc aagggggagg      1020
aaatcgcaaa gaagcaaacg caagcccaaa aatga                                1056

```

<210> 78

<211> 351

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 78

```

Met Pro Thr Pro Ser Asp His Phe Lys Ile Ala Ala Val Gln Ala Ser
  1                5                10                15
Pro Val Phe Leu Asp Arg Glu Ala Thr Val Glu Lys Ala Cys Arg Leu
      20                25                30
Ile Ala Glu Ala Ala Lys Gln Gly Val Arg Leu Ile Val Phe Pro Glu
      35                40                45
Ser Phe Ile Pro Thr Tyr Pro Asp Trp Val Trp Ala Val Pro Pro Gly
      50                55                60

```

```

Arg Glu Arg Ile Leu Asn Gln Leu Tyr Ser Glu Phe Leu Ala Asn Ala
65          70          75          80
Val Asp Val Pro Gly Ala Ala Thr Glu Gln Leu Ala Gln Ala Ala Arg
          85          90          95
Met Ala Gly Ala Tyr Val Ile Met Gly Val Thr Glu Arg Asp Thr Ser
          100          105          110
Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Phe Ser Pro Glu
          115          120          125
Gly Ile Leu Met Gly Lys His Arg Lys Leu Val Pro Thr Gly Gly Glu
          130          135          140
Arg Leu Val Trp Ala Tyr Gly Asp Gly Ser Thr Leu Glu Val Tyr Asp
145          150          155          160
Thr Pro Leu Gly Lys Ile Gly Gly Leu Ile Cys Trp Glu Asn Tyr Met
          165          170          175
Pro Leu Ala Arg Tyr Thr Met Tyr Ala Trp Gly Thr Gln Ile Tyr Ile
          180          185          190
Ala Ala Thr Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Leu Arg His
          195          200          205
Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys Ile Ala Leu
          210          215          220
Arg Gln Gly Asp Ile Pro Asp Arg Phe Glu Tyr Lys Gly Lys Phe Tyr
225          230          235          240
Ser Gly Ser Arg Glu Trp Ile Asn Glu Gly Asp Ser Ala Ile Val Asn
          245          250          255
Pro Asp Gly Glu Phe Ile Ala Gly Pro Val Arg Thr Lys Glu Glu Ile
          260          265          270
Leu Tyr Ala Glu Ile Asp Pro Arg Gln Met Arg Gly Pro Lys Trp Met
          275          280          285
Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Ile Phe Glu Leu Ile
          290          295          300
Val His Arg Asn Pro His Pro Met Ile Lys Ile Ala Glu Asp Arg Gly
305          310          315          320
Thr Gly Ile Ala Ser Ser Leu Ile Arg Pro Arg Pro Asn Leu Pro Pro
          325          330          335
Ser Arg Gly Arg Lys Ser Ala Arg Ser Lys Arg Lys Pro Lys Lys
          340          345          350

```

<210> 79

<211> 990

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 79

```

atgacgaaga aaagcggccg cgattcgttt cgggtcgtcg cggtcaggc ctcgtccgtc 60
tacctggatc gggaacggag catcgagaaa gcgtgccggc tgatcgacga cgcgggacga 120
aacgacgccg acctcgtcgt gttccccgaa gccttcgtgc ccggataccc actgtgggtg 180
tggtcgtctc cgccggggcg caccgcagac ttgcgtcccg cttatgcgac gctccacgcc 240
aacgcgatca gcattccgga cgactccacc gatcggtcgt gcgccgccgc aaaagacgcc 300
ggcgtcgcgc tcgcgatcgg cgtcaacgaa cgcaacaccg aagcgagcgg catgagcctg 360
ttcaacacgc tgctctatat cggagcggac ggccggattc tcggaaaaca ccggaagctg 420
gtaccgaccg gcggcgaaac gctcgtctgg gcattctggc acggcagcga cctcgaggtc 480
tactcgtcgc cgttcgtcgc cgtaagcgga ctgatctgct gggagcacta catgccgtc 540
gcccggtatg cgctcgcgcg gtggggcgaa caggtgcacg tcgctccaac ctgggatcgt 600
ggcgagccgt ggctgtccac gctaaggcac atcgcgagg aagggccgct tctcgtcgtc 660
ggctgctgtc aagccgtgcg caaggacgac atccctgaca cgctcgcgtt caagtccaaa 720
tacctcgacg acgtggacgg ctggatcaac ccaggtggca gcgtcatcat caatcctgac 780
ggcaaggtcg tcgcgggacc gcgatggaa accgaaactg tactgtacgc ggaccttcgc 840
accgagcagc tcgtcggacc gcgctggcag ctcgacgtcg gcggacatta cgctcgtccg 900

```

gacgtcttcg agctcgtcgt ccacgcgcat ccgaagccgt tgattcggac agcgaccggt 960
 gtcaggcgcc gcaagcgtgc acgtcgcctaa 990

<210> 80
 <211> 329
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 80
 Met Thr Lys Lys Ser Gly Arg Asp Ser Phe Arg Val Ala Ala Val Gln
 1 5 10 15
 Ala Ser Ser Val Tyr Leu Asp Arg Glu Arg Ser Ile Glu Lys Ala Cys
 20 25 30
 Arg Leu Ile Asp Asp Ala Gly Arg Asn Asp Ala Asp Leu Val Val Phe
 35 40 45
 Pro Glu Ala Phe Val Pro Gly Tyr Pro Leu Trp Val Trp Leu Val Pro
 50 55 60
 Pro Gly Arg Thr Ala Asp Leu Arg Ser Ala Tyr Ala Thr Leu His Ala
 65 70 75 80
 Asn Ala Ile Ser Ile Pro Asp Asp Ser Thr Asp Arg Leu Cys Ala Ala
 85 90 95
 Ala Lys Asp Ala Gly Val Ala Val Ala Ile Gly Val Asn Glu Arg Asn
 100 105 110
 Thr Glu Ala Ser Gly Met Ser Leu Phe Asn Thr Leu Leu Tyr Ile Gly
 115 120 125
 Ala Asp Gly Arg Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly
 130 135 140
 Gly Glu Arg Leu Val Trp Ala Ser Gly Asp Gly Ser Asp Leu Glu Val
 145 150 155 160
 Tyr Ser Leu Pro Phe Gly Arg Val Ser Gly Leu Ile Cys Trp Glu His
 165 170 175
 Tyr Met Pro Leu Ala Arg Tyr Ala Leu Ala Ala Trp Gly Glu Gln Val
 180 185 190
 His Val Ala Pro Thr Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Leu
 195 200 205
 Arg His Ile Ala Lys Glu Gly Arg Val Leu Val Val Gly Cys Cys Gln
 210 215 220
 Ala Val Arg Lys Asp Asp Ile Pro Asp Thr Leu Ala Phe Lys Ser Lys
 225 230 235 240
 Tyr Leu Ala Asp Val Asp Gly Trp Ile Asn Pro Gly Gly Ser Val Ile
 245 250 255
 Ile Asn Pro Asp Gly Lys Val Val Ala Gly Pro Ala Met Glu Thr Glu
 260 265 270
 Thr Val Leu Tyr Ala Asp Leu Arg Thr Glu Gln Leu Val Gly Pro Arg
 275 280 285
 Trp Gln Leu Asp Val Gly Gly His Tyr Ala Arg Pro Asp Val Phe Glu
 290 295 300
 Leu Val Val His Arg His Pro Lys Pro Leu Ile Arg Thr Ala Thr Gly
 305 310 315 320
 Val Arg Arg Arg Lys Arg Ala Arg Arg
 325

<210> 81
 <211> 993
 <212> DNA
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 81
 atgaaagtcg tcaaagccgc cgctgtccag ttcagcccgg tgctctatag ccgcaagcg 60
 accgtcgcca aggtcgccg gaaaatccac gagctcggc agaaaggcgt gcagttcgcc 120
 acctttcctg aaacggtcgt gccttattac ccttacttcg cggccgtcca gacgggcac 180
 gagctcttgt cgggcaccga acatctgcgc ctgctogaac aggccgtgac tgtgccctcc 240
 gctgcgaccg atgcaatcgg cgaagccgcg cgacaggccg gcatgggtcg gtccatcggc 300
 gtcaatgagc gtgacggcgg cagcgtttac aacacgcaac tgctcttcga tgccgacgg 360
 acgctgatcc agcggccgcg caagatcacg ccgacccatt tcgaacgcat gatctggggg 420
 cagggagatg gctcgggctt gcgtgcagtc gacagcgagc tcggccgcat cggccagctc 480
 gcatgcttcg agcacaacaa cccgcttgca cgttacgcaa tgatcgccga cggcgagcag 540
 atccattcag cgatgtaccc tggctcggcc tttggcgagg gcttcgcccc gcgtatggag 600
 atcaacatcc gccagcatgc gctcagagtc gccgctttcg tcgtcaacgc aacggcgtgg 660
 cttgacgccc accagcaggc gcaaatcatg aaggacaccg gttgtggaat cggcccgatc 720
 tcgggcccgt gcttcaccac gatcgtttct cctgacggta tgctgatggc cgatccgctt 780
 cgctcggggc aaggcgaagt gattgtcgat ctcgacttca cgcagatcga ccgccgcaag 840
 atgctgatgg actcggcccg cactacaac cgccctgaac tgctgagtct gatgatcgac 900
 cgtacgccgg ctgcgcatgt tcacgaacgc gcttcgcgcc cgaatgaccgt cgacgaccag 960
 agttccggcg atctgcgcac ccaggttgca tga 993

<210> 82
 <211> 330
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 82
 Met Lys Val Val Lys Ala Ala Ala Val Gln Phe Ser Pro Val Leu Tyr
 1 5 10 15
 Ser Arg Glu Ala Thr Val Ala Lys Val Val Arg Lys Ile His Glu Leu
 20 25 30
 Gly Gln Lys Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
 35 40 45
 Tyr Tyr Pro Tyr Phe Ala Ala Val Gln Thr Gly Ile Glu Leu Leu Ser
 50 55 60
 Gly Thr Glu His Leu Arg Leu Leu Glu Gln Ala Val Thr Val Pro Ser
 65 70 75 80
 Ala Ala Thr Asp Ala Ile Gly Glu Ala Ala Arg Gln Ala Gly Met Val
 85 90 95
 Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn Thr
 100 105 110
 Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln Arg Arg Lys
 115 120 125
 Ile Thr Pro Thr His Phe Glu Arg Met Ile Trp Gly Gln Gly Asp Gly
 130 135 140
 Ser Gly Leu Arg Ala Val Asp Ser Ala Val Gly Arg Ile Gly Gln Leu
 145 150 155 160
 Ala Cys Phe Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Met Ile Ala
 165 170 175
 Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Ala Phe Gly
 180 185 190
 Glu Gly Phe Ala Gln Arg Met Glu Ile Asn Ile Arg Gln His Ala Leu
 195 200 205
 Glu Ser Ala Ala Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp
 210 215 220
 Gln Gln Ala Gln Ile Met Lys Asp Thr Gly Cys Gly Ile Gly Pro Ile
 225 230 235 240
 Ser Gly Gly Cys Phe Thr Thr Ile Val Ser Pro Asp Gly Met Leu Met

```

                245                250                255
Ala Asp Pro Leu Arg Ser Gly Glu Gly Glu Val Ile Val Asp Leu Asp
                260                265                270
Phe Thr Gln Ile Asp Arg Arg Lys Met Leu Met Asp Ser Ala Gly His
                275                280                285
Tyr Asn Arg Pro Glu Leu Leu Ser Leu Met Ile Asp Arg Thr Pro Ala
                290                295                300
Ala His Val His Glu Arg Ala Ser Arg Pro Met Thr Val Asp Asp Gln
305                310                315                320
Ser Ser Gly Asp Leu Arg Thr Gln Val Ala
                325                330

```

<210> 83
 <211> 1071
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 83
atgatgagtt cagcccggtgt aataaaactc gccgcagcac agctttcacc tgtgctgccg      60
ggggagtcca caaatagccg cgacggcacc attgccaaag tcgtcgcggc gattgctggag      120
gctgcgcgcg ccggcgcgca gctgatcgtg ttcccgaaa cgggtggtgcc gtattaccgc      180
tatttctcgt tcattacgcc gccggtgacg atgggggcgg agcatttgcg cttgtacgat      240
cagtctgtcg tgggtgccgag cgcgcgcaact gatactgttg ccgccgctgc aaaaaaacac      300
agcatggtgg tcgtgctcgg tattaacgaa cgcgatcacg gcacgctcta caacgcgcaa      360
ttaattttcg atgcgagcgg cgaattatta ttaaacgcc gaaaaattac cccgacctat      420
cacgagcgca tgggtgtgggg tcagggcgac gccagcggtt tgaaaaccgt cgacaccgcg      480
atcggccgtg tcggtgcgct cgctgctgg gaacattaca acccattggc gcgttacagc      540
ctgatggccc agcacgaaga aattcattgc agtcaatttc cggggtcatt ggtcgggcca      600
attttcgccc agcaaagga agtgacaatg cgccaccacg cgctcgaatc cggttgcttc      660
gtcggttaatg caacggcggtg gttatcggaa gcgcaaattc aatcgatcag cagcgatccc      720
gcgatgcaaa aagcactgcg cggcggttgc tacaccgcaa ttatttcgcc cgaaggcaaa      780
catctgtgcg agccgctacg cgaagggtgaa ggtttgattt ttgccgaagc cgatatggcg      840
ctcattacca aacgcaaacg catgatggat tcggttggtc attacgcgcg acccgaattg      900
ctgtcgctgt taatcgacca tcgcgccacc acaccattgc atagcgctac cgcgagtgat      960
gccgcgcgcg taaaaaatac tcggagttcc gtcctgaat cagccgatag tgaaccatc      1020
cgcgagtcag ttaataacg aactccaatc gcacggcttg cgcctagttg a              1071

```

<210> 84
 <211> 356
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 84
Met Met Ser Ser Ala Arg Val Ile Lys Leu Ala Ala Ala Gln Leu Ser
 1                5                10                15
Pro Val Leu Pro Gly Glu Ser Thr Asn Ser Arg Asp Gly Thr Ile Ala
                20                25                30
Lys Val Val Ala Ala Ile Ala Glu Ala Ala Arg Ala Gly Ala Gln Leu
                35                40                45
Ile Val Phe Pro Glu Thr Val Val Pro Tyr Tyr Pro Tyr Phe Ser Phe
 50                55                60
Ile Thr Pro Ala Val Thr Met Gly Ala Glu His Leu Arg Leu Tyr Asp
 65                70                75                80
Gln Ser Val Val Val Pro Ser Ala Ala Thr Asp Thr Val Ala Ala Ala
                85                90                95

```


Ala Lys Lys His Ser Met Val Val Val Leu Gly Ile Asn Glu Arg Asp
 100 105 110
 His Gly Thr Leu Tyr Asn Ala Gln Leu Ile Phe Asp Ala Ser Gly Glu
 115 120 125
 Leu Leu Leu Lys Arg Arg Lys Ile Thr Pro Thr Tyr His Glu Arg Met
 130 135 140
 Val Trp Gly Gln Gly Asp Gly Ser Gly Leu Lys Thr Val Asp Thr Ala
 145 150 155 160
 Ile Gly Arg Val Gly Ala Leu Ala Cys Trp Glu His Tyr Asn Pro Leu
 165 170 175
 Ala Arg Tyr Ser Leu Met Ala Gln His Glu Glu Ile His Cys Ser Gln
 180 185 190
 Phe Pro Gly Ser Leu Val Gly Pro Ile Phe Ala Glu Gln Met Glu Val
 195 200 205
 Thr Met Arg His His Ala Leu Glu Ser Gly Cys Phe Val Val Asn Ala
 210 215 220
 Thr Ala Trp Leu Ser Glu Ala Gln Ile Gln Ser Ile Ser Ser Asp Pro
 225 230 235 240
 Ala Met Gln Lys Ala Leu Arg Gly Gly Cys Tyr Thr Ala Ile Ile Ser
 245 250 255
 Pro Glu Gly Lys His Leu Cys Glu Pro Leu Arg Glu Gly Glu Gly Leu
 260 265 270
 Ile Phe Ala Glu Ala Asp Met Ala Leu Ile Thr Lys Arg Lys Arg Met
 275 280 285
 Met Asp Ser Val Gly His Tyr Ala Arg Pro Glu Leu Leu Ser Leu Leu
 290 295 300
 Ile Asp His Arg Ala Thr Thr Pro Leu His Ser Val Thr Ala Ser Asp
 305 310 315 320
 Ala Ala Ala Val Lys Asn Thr Arg Ser Ser Ala His Glu Ser Ala Asp
 325 330 335
 Ser Glu Thr Ile Arg Glu Ser Val Asn Asn Gly Thr Pro Ile Ala Arg
 340 345 350
 Leu Ala Pro Ser
 355

<210> 85

<211> 1014

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 85

atgggtctg	ttcatcagaa	atacaaggtt	gcggtggttc	aggcggcgcc	ggtctttctc	60
gacctcgatg	cgacggtgga	caagacgac	gccctgatcg	agcaggccgc	agcacagggc	120
gcgaagctga	tcgctgttcc	cgagaccttc	attcccggat	atccgtggca	gatctggctt	180
ggggcgcccg	cctgggcgat	cgcccggtgc	ttcgtgcagc	gctatttcga	taactcgttg	240
tcatttgaca	gcccgcaggc	cgaaaaaatt	cgcaaggccg	tcaagcgcg	caagctgacc	300
gcggtgatcg	gcgtctccga	acgcgacggc	ggcagcctct	atatcgccca	atggctgac	360
ggtcccgcag	gcgagaccat	tgcgaagcgc	cgcaagctgc	ggccgaccca	tgccgaacgc	420
accgtgttcg	gcgagggcga	cggcagcgac	ctcgccgtcc	atgatcgcg	cgacgtggga	480
cggctcggtg	caatgtgctg	ctgggagcat	ctgcagccgc	tgctcgaaata	cgcatgttac	540
gccagaacg	agcaggttca	cgtcggcgcc	tggccgagct	tctcattgta	cgacccattc	600
gcccatgcgc	ttggctggga	agtaaacac	gcggcgagca	aggtttatgc	tgctgagggc	660
tcatgtttct	tcctcgcccc	gtgcgcgggt	gtctcgagg	ccatgatcga	cgagctctgc	720
gattcccccg	aaaagcacgc	cttctgcac	gctggcggcg	gccacgcggt	aatctatggg	780
ccggacggga	gttcgcttgc	cgacaaactt	ccacccgatc	aggagggcac	tctgtatgcc	840
gatatcgatc	tcggcatgat	cggcgtggca	aagaacgcgc	ccgaccccg	aggacactat	900
tccaggcccg	acgtcacgcg	gctgctgctc	aacacttccc	gcgccaatcg	cgctcgagcat	960
ttttcattgc	cgatcgatgc	cgaggtcatg	agcgaaatca	gacttcaggc	ctga	1014

<210> 86
 <211> 337
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 86
 Met Gly Leu Val His Gln Lys Tyr Lys Val Ala Val Val Gln Ala Ala
 1 5 10 15
 Pro Val Phe Leu Asp Leu Asp Ala Thr Val Asp Lys Thr Ile Ala Leu
 20 25 30
 Ile Glu Gln Ala Ala Ala Gln Gly Ala Lys Leu Ile Ala Phe Pro Glu
 35 40 45
 Thr Phe Ile Pro Gly Tyr Pro Trp Gln Ile Trp Leu Gly Ala Pro Ala
 50 55 60
 Trp Ala Ile Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
 65 70 75 80
 Ser Phe Asp Ser Pro Gln Ala Glu Lys Ile Arg Lys Ala Val Lys Arg
 85 90 95
 Ala Lys Leu Thr Ala Val Ile Gly Val Ser Glu Arg Asp Gly Ser
 100 105 110
 Leu Tyr Ile Gly Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
 115 120 125
 Lys Arg Arg Lys Leu Arg Pro Thr His Ala Glu Arg Thr Val Phe Gly
 130 135 140
 Glu Gly Asp Gly Ser Asp Leu Ala Val His Asp Arg Ala Asp Val Gly
 145 150 155 160
 Arg Leu Gly Ala Met Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys
 165 170 175
 Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Gly Ala Trp Pro
 180 185 190
 Ser Phe Ser Leu Tyr Asp Pro Phe Ala His Ala Leu Gly Trp Glu Val
 195 200 205
 Asn Asn Ala Ala Ser Lys Val Tyr Ala Val Glu Gly Ser Cys Phe Phe
 210 215 220
 Leu Gly Pro Cys Ala Val Val Ser Gln Ala Met Ile Asp Glu Leu Cys
 225 230 235 240
 Asp Ser Pro Glu Lys His Ala Phe Leu His Ala Gly Gly Gly His Ala
 245 250 255
 Val Ile Tyr Gly Pro Asp Gly Ser Ser Leu Ala Asp Lys Leu Pro Pro
 260 265 270
 Asp Gln Glu Gly Ile Leu Tyr Ala Asp Ile Asp Leu Gly Met Ile Gly
 275 280 285
 Val Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
 290 295 300
 Val Thr Arg Leu Leu Leu Asn Thr Ser Arg Ala Asn Arg Val Glu His
 305 310 315 320
 Phe Ser Leu Pro Ile Asp Ala Glu Val Met Ser Glu Ile Arg Leu Gln
 325 330 335
 Ala

<210> 87
 <211> 1062
 <212> DNA
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 87

atggcggaat	cgaagctgaa	ggtcgccgca	attcaagttg	cgcccgtgtt	catggatcgc	60
gatgccacga	tcgcccgcgc	ctgcgagcgg	atcgccgaag	ccgcccgcgc	cggcgcggag	120
ttggtggtct	ttcccaggc	attcgtgccc	gggtatccc	actggatctg	ggtggcgcgg	180
ccaagccaac	gcaaaactgct	caatgatctt	tacgcgcacc	tcgtctcgca	gtcggtcgac	240
gtgccgtcgg	cctccgtgga	tcgttttcgc	gacgcgcctc	gcgacgcggg	ggtcacggtg	300
gtgatcggcg	tcaacgagcg	caacaccgaa	gcgagcggcg	cgagcctcta	caacaccgcg	360
ctcgtgatcg	gtccactggg	gcagctgata	ggccgccacc	gcaagcttgt	gccgaccggg	420
ccggagcgca	tggtgtgggc	gcagggcgac	ggcagcacgc	tcgacgtcta	cgacacaccc	480
gtcggcaagc	tttcgacggt	gatctgctgg	gagaactaca	tgccgctcgc	gcgctacgcc	540
atggcggcgt	ggggcgcgcg	catccacgtc	gccggcacgt	gggaccgcgg	cgagccgtgg	600
atctcgacca	tgcgctcatgt	ggcgacggag	ggccgcgtat	tcgtgattag	ctgttgcatg	660
gcgctgcgca	aacgagacat	tccggccgag	ctcgagttcg	cgatgctcta	tcccgacggg	720
cgcaaatgga	tcaacgccgg	tgattcgctg	gtcgtgaatc	ccgctggcca	gatcatcgct	780
gggcccgttc	acgagcagga	aggaatcctc	tacgccgagc	tcgagcgcaa	tcagatgacc	840
ggtcccggtt	ggatgttcga	cgccgcccgc	cattacgcgc	gaccggacgt	cttccaactc	900
acggtaaacc	gctccccgcg	cccgatgctg	cgggagggcg	gggcaaagac	gagtgaaggca	960
aacacgagag	atgccgtacc	catggacagc	acgccctcga	gatcgcgggc	ccgcgcgggtg	1020
gcgcgaaagg	ccgcacgcac	cggtcgctcc	aagcggcggt	ga		1062

<210> 88

<211> 353

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 88

Met	Ala	Glu	Ser	Lys	Leu	Lys	Val	Ala	Ala	Ile	Gln	Val	Ala	Pro	Val
1				5					10					15	
Phe	Met	Asp	Arg	Asp	Ala	Thr	Ile	Ala	Arg	Ala	Cys	Glu	Arg	Ile	Ala
			20					25				30			
Glu	Ala	Ala	Arg	Ala	Gly	Ala	Glu	Leu	Val	Val	Phe	Pro	Glu	Ala	Phe
	35					40					45				
Val	Pro	Gly	Tyr	Pro	Asp	Trp	Ile	Trp	Val	Ala	Arg	Pro	Ser	Gln	Arg
	50				55						60				
Lys	Leu	Leu	Asn	Asp	Leu	Tyr	Ala	His	Leu	Val	Ser	Gln	Ser	Val	Asp
65				70					75					80	
Val	Pro	Ser	Ala	Ser	Val	Asp	Arg	Leu	Arg	Asp	Ala	Ala	Arg	Asp	Gly
			85						90					95	
Gly	Val	Thr	Val	Val	Ile	Gly	Val	Asn	Glu	Arg	Asn	Thr	Glu	Ala	Ser
		100					105						110		
Gly	Ala	Ser	Leu	Tyr	Asn	Thr	Ala	Leu	Val	Ile	Gly	Pro	Leu	Gly	Gln
	115				120						125				
Leu	Ile	Gly	Arg	His	Arg	Lys	Leu	Val	Pro	Thr	Gly	Pro	Glu	Arg	Met
	130				135						140				
Val	Trp	Ala	Gln	Gly	Asp	Gly	Ser	Thr	Leu	Asp	Val	Tyr	Asp	Thr	Pro
145				150					155					160	
Val	Gly	Lys	Leu	Ser	Thr	Leu	Ile	Cys	Trp	Glu	Asn	Tyr	Met	Pro	Leu
			165						170					175	
Ala	Arg	Tyr	Ala	Met	Ala	Ala	Trp	Gly	Ala	Arg	Ile	His	Val	Ala	Gly
		180						185					190		
Thr	Trp	Asp	Arg	Gly	Glu	Pro	Trp	Ile	Ser	Thr	Met	Arg	His	Val	Ala
	195					200					205				
Thr	Glu	Gly	Arg	Val	Phe	Val	Ile	Ser	Cys	Cys	Met	Ala	Leu	Arg	Lys
	210				215						220				
Arg	Asp	Ile	Pro	Ala	Glu	Leu	Glu	Phe	Ala	Met	Leu	Tyr	Pro	Asp	Gly
225				230					235					240	

Arg Glu Trp Ile Asn Ala Gly Asp Ser Leu Val Val Asn Pro Ala Gly
 245 250 255
 Gln Ile Ile Ala Gly Pro Leu His Glu Gln Glu Gly Ile Leu Tyr Ala
 260 265 270
 Glu Leu Glu Arg Asn Gln Met Thr Gly Pro Arg Trp Met Phe Asp Ala
 275 280 285
 Ala Gly His Tyr Ala Arg Pro Asp Val Phe Gln Leu Thr Val Asn Arg
 290 295 300
 Ser Pro Arg Pro Met Leu Arg Glu Ala Gly Ala Lys Thr Ser Glu Ala
 305 310 315 320
 Asn Thr Arg Asp Ala Val Pro Met Asp Ser Thr Pro Ser Arg Ser Arg
 325 330 335
 Pro Arg Ala Val Ala Arg Lys Ala Ala Arg Thr Gly Arg Ser Lys Arg
 340 345 350
 Arg

<210> 89
 <211> 918
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 89
 atgaataacca aagaagtaaa ggtcgcagcc gctcaatttg cccacattt tctgaatttg 60
 agcaaaacgg tggaaaaaac ctgcaacttg atttccgaag caggcaaaaa tggagcaaa 120
 ctcatgtat ttccggaagc ctctctctct gggtatcccg attgggtctg gttattccc 180
 aatggaaatt caacaatgct ggatgattta tatcaggaat tgggtgagaa cgctgtaaca 240
 atccctgatt caacaacaca gaaactctgt caggcagcaa aagatgccgg ggtatatgtc 300
 gcagtcggtta tccatgaaag aaatgcagaa gcaagtggct tcacactttt caataccctt 360
 ctatacatta atgatcaagg cagcatcatt ggaaaacacc gaaaactgat cccaacaggg 420
 ggcgaaacgcc tggctctggg gcagggtaat ggggatacgc ttgctgcatt cgatacacac 480
 tttggcaaat tgggaggatt gctttgctgg gaaaactaca tgcccctggc tcggcaagct 540
 atgtacgcag ttgggactga agtttatgtt gcccacactt gggactccag tgagaattgg 600
 ttgctgagta tgcgccatat agccagagag ggcggcatgt ttgtgatcaa tgtttgccag 660
 gctgtccgaa aagacgatat tcctgaccgc tatgcattca agcaactcta ttctggtaat 720
 tcagaatgga tcaatagcgg caacagttgc atcatcaatc cgcgcggtga aatcattgcc 780
 ggaccatcct caaacaggca agaaatactc tacgcagatt tagatctgag tttgattaca 840
 aaatctaaac gcatgttcga tgttaccggg cattatgccc ggcgggatgt gtttagatat 900
 gaaatcaaaa aaagctag 918

<210> 90
 <211> 305
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 90
 Met Asn Thr Lys Glu Val Lys Val Ala Ala Ala Gln Phe Ala Pro His
 1 5 10 15
 Phe Leu Asn Leu Ser Lys Thr Val Glu Lys Thr Cys Asn Leu Ile Ser
 20 25 30
 Glu Ala Gly Lys Asn Gly Ala Lys Leu Ile Val Phe Pro Glu Ala Phe
 35 40 45
 Leu Ser Gly Tyr Pro Asp Trp Val Trp Leu Ile Pro Asn Gly Asn Ser
 50 55 60
 Thr Met Leu Asp Asp Leu Tyr Gln Glu Leu Val Glu Asn Ala Val Thr

```

65          70          75          80
Ile Pro Asp Ser Thr Gln Lys Leu Cys Gln Ala Ala Lys Asp Ala
      85          90          95
Gly Val Tyr Val Ala Val Gly Ile His Glu Arg Asn Ala Glu Ala Ser
      100          105          110
Gly Phe Thr Leu Phe Asn Thr Leu Leu Tyr Ile Asn Asp Gln Gly Ser
      115          120          125
Ile Ile Gly Lys His Arg Lys Leu Ile Pro Thr Gly Gly Glu Arg Leu
      130          135          140
Val Trp Gly Gln Gly Asn Gly Asp Thr Leu Ala Ala Phe Asp Thr His
      145          150          155          160
Phe Gly Lys Leu Gly Gly Leu Leu Cys Trp Glu Asn Tyr Met Pro Leu
      165          170          175          180
Ala Arg Gln Ala Met Tyr Ala Val Gly Thr Glu Val Tyr Val Ala Pro
      185          190
Thr Trp Asp Ser Ser Glu Asn Trp Leu Leu Ser Met Arg His Ile Ala
      195          200          205
Arg Glu Gly Gly Met Phe Val Ile Asn Val Cys Gln Ala Val Arg Lys
      210          215          220
Asp Asp Ile Pro Asp Arg Tyr Ala Phe Lys Gln Leu Tyr Ser Gly Asn
      225          230          235          240
Ser Glu Trp Ile Asn Ser Gly Asn Ser Cys Ile Ile Asn Pro Arg Gly
      245          250          255
Glu Ile Ile Ala Gly Pro Ser Ser Asn Arg Gln Glu Ile Leu Tyr Ala
      260          265          270
Asp Leu Asp Leu Ser Leu Ile Thr Lys Ser Lys Arg Met Phe Asp Val
      275          280          285
Thr Gly His Tyr Ala Arg Pro Asp Val Phe Arg Tyr Glu Ile Lys Lys
      290          295          300
Ser
305

```

<210> 91

<211> 939

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 91

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atgacacaaa tcgctgtcat tcaagaacct ccggtctatc tgaatctgag taaatcgatg      60
gacagagcgg tcgacttgat tgccaatgct gcaagcaagg ggtgtgagtt gattgtgttt      120
cccgaagcct ggcttgcagg ttaccccacc ttctgtcggc gtcttgcgcc gggcagcgga      180
atgggaaaaa ctgatgagct ttacgcgcgt ttgtctcgcca actcgggtcga ccgtagcaaaa      240
gaggggctta gaccattgca ggaggccgca aaggagcatg gcgttgtcat tgtgctgggt      300
tatcaagagg tggatggcgc gggaagcagc agcacgatct tcaacagctg tgcgattatt      360
gatgcggacg ggcgactggc caacaatcat cgcaagttga tgcccaccaa tccggagagg      420
atggtttggg gttttggcga cggttcaggc ctgaacgctg ttgacaccgc ggtgggcagg      480
atcggcacgc tgatttgctg ggaaaactac atgccgtagc cgcgctacgc gctgtatgtc      540
caaaacatcg aaatctatgt tgccccgact tgggacagtg gtgccatgtg gcaggcgacc      600
ctgcagcata tcgcgcgcga aggtggctgc tgggtcatcg gatgtgcaac gtcgctggaa      660
gcctctgaca tcccgacga cgttccccat cgggatgagc tattcccga caaagacgaa      720
tgggtaaac ctggcgatgc ggtggtttat aagccatttg gcgacattgt ggccggcccc      780
atgcatcagg aaaaggggct tctcatcgca gagttggacg tcgccgctgt tcagtcgtca      840
cgtcggaagt tcgatgcgag cgggcactac gctcgccccg atgtcttcaa actgcattgt      900
aatcgcaccg cgatgcggcc agttgatttc acgaattag      939

```

<210> 92

<211> 312

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 92

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Met Thr Lys Ile Ala Val Ile Gln Glu Pro Pro Val Tyr Leu Asn Leu
 1           5           10           15
Ser Lys Ser Met Asp Arg Ala Val Asp Leu Ile Ala Asn Ala Ala Ser
      20           25           30
Lys Gly Cys Glu Leu Ile Val Phe Pro Glu Ala Trp Leu Ala Gly Tyr
      35           40           45
Pro Thr Phe Val Trp Arg Leu Ala Pro Gly Ser Gly Met Gly Lys Thr
      50           55           60
Asp Glu Leu Tyr Ala Arg Leu Leu Ala Asn Ser Val Asp Arg Ser Lys
      65           70           75           80
Glu Gly Leu Arg Pro Leu Gln Glu Ala Ala Lys Glu His Gly Val Val
      85           90           95
Ile Val Leu Gly Tyr Gln Glu Val Asp Gly Ala Gly Ser Ser Ser Thr
      100          105          110
Ile Phe Asn Ser Cys Ala Ile Ile Asp Ala Asp Gly Arg Leu Ala Asn
      115          120          125
Asn His Arg Lys Leu Met Pro Thr Asn Pro Glu Arg Met Val Trp Gly
      130          135          140
Phe Gly Asp Gly Ser Gly Leu Asn Val Val Asp Thr Ala Val Gly Arg
      145          150          155          160
Ile Gly Thr Leu Ile Cys Trp Glu Asn Tyr Met Pro Leu Ala Arg Tyr
      165          170          175
Ala Leu Tyr Val Gln Asn Ile Glu Ile Tyr Val Ala Pro Thr Trp Asp
      180          185          190
Ser Gly Ala Met Trp Gln Ala Thr Leu Gln His Ile Ala Arg Glu Gly
      195          200          205
Gly Cys Trp Val Ile Gly Cys Ala Thr Ser Leu Glu Ala Ser Asp Ile
      210          215          220
Pro Asp Asp Val Pro His Arg Asp Glu Leu Phe Pro Asn Lys Asp Glu
      225          230          235          240
Trp Val Asn Pro Gly Asp Ala Val Val Tyr Lys Pro Phe Gly Gly Ile
      245          250          255
Val Ala Gly Pro Met His Gln Glu Lys Gly Leu Leu Ile Ala Glu Leu
      260          265          270
Asp Val Ala Ala Val Gln Ser Ser Arg Arg Lys Phe Asp Ala Ser Gly
      275          280          285
His Tyr Ala Arg Pro Asp Val Phe Lys Leu His Val Asn Arg Thr Ala
      290          295          300
Met Arg Pro Val Asp Phe Thr Asn
      305          310

```

<210> 93

<211> 978

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 93

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atgcccacatca tcaaagccgc tgccgtgcaa atcagcccgg tgctttacag tcgcgaaggc      60
accgtggaca aggtctgtca acagatcatc gacctcggtc ggcaaggcgt gcagttcgcc      120
gtctttccgg aaacggtggt gccttactac ccgtactttt cgtttgtgca gccggccttt      180
gccatgggag cacagcacct caagttgctg gatcaatcgg tgacagtgcc gtcggccgcc      240
accttggccca tcggtgaagc ttgcaagcaa gcagggatag tggtgtccat cggcgtaaac      300

```

```

gaacgcgatg gcggtacgat ctacaacgcg caattactct tcgatgccga cggcagcctg 360
attcagcatc gccgcaaaat caccgccgacc tatcacgaac gcatgggtctg ggggcaaggc 420
gatgggttccg gcctgcgcgc catcgacagt gcagtggggc gcattggctc cctggcctgt 480
tgggagcatt acaacccgct ggctcgttat gccttgatgg ccgatggcga gcagatccac 540
gccgcgatgt ttcccggtc gctggtgggc gacatttttg ccgagcagat cgaagtcacc 600
atccgccatc acgccttgga gtccggctgt ttcgtgggtca acgccaccgc ctggctggagc 660
gccgatcagc agggccaaat catgcaagac accggttgca gcctcggcc gatctcgggt 720
ggctgcttca ccgccatcgt ttcccctgaa ggcaagtgc tcggtgagcc gctgcgttcc 780
ggcgaagggg tggatgatcg cgatctcgat ctggcactga tcgataagcg taaacggatg 840
atggattcgg tcgggcatta cagtcgcccg gaactgctca gcctgttgat cgaccgcacg 900
cccacagcgc atgtgcatga acgcagcgcg cacctggtgg ctgtcgctac cgaggagttc 960
gatcatgcaa accaatga 978

```

<210> 94

<211> 325

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 94

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Met Pro Ile Ile Lys Ala Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
1      5      10      15
Ser Arg Glu Gly Thr Val Asp Lys Val Cys Gln Gln Ile Ile Asp Leu
20     25     30
Gly Arg Gln Gly Val Gln Phe Ala Val Phe Pro Glu Thr Val Val Pro
35     40     45
Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Pro Ala Phe Ala Met Gly Ala
50     55     60
Gln His Leu Lys Leu Leu Asp Gln Ser Val Thr Val Pro Ser Ala Ala
65     70     75     80
Thr Leu Ala Ile Gly Glu Ala Cys Lys Gln Ala Gly Ile Val Val Ser
85     90     95
Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Ile Tyr Asn Ala Gln Leu
100    105    110
Leu Phe Asp Ala Asp Gly Ser Leu Ile Gln His Arg Arg Lys Ile Thr
115    120    125
Pro Thr Tyr His Glu Arg Met Val Trp Gly Gln Gly Asp Gly Ser Gly
130    135    140
Leu Arg Ala Ile Asp Ser Ala Val Gly Arg Ile Gly Ser Leu Ala Cys
145    150    155    160
Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met Ala Asp Gly
165    170    175
Glu Gln Ile His Ala Ala Met Phe Pro Gly Ser Leu Val Gly Asp Ile
180    185    190
Phe Ala Glu Gln Ile Glu Val Thr Ile Arg His His Ala Leu Glu Ser
195    200    205
Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp Gln Gln
210    215    220
Gly Gln Ile Met Gln Asp Thr Gly Cys Ser Leu Gly Pro Ile Ser Gly
225    230    235    240
Gly Cys Phe Thr Ala Ile Val Ser Pro Glu Gly Lys Leu Leu Gly Glu
245    250    255
Pro Leu Arg Ser Gly Glu Gly Val Val Ile Ala Asp Leu Asp Leu Ala
260    265    270
Leu Ile Asp Lys Arg Lys Arg Met Met Asp Ser Val Gly His Tyr Ser
275    280    285
Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro Thr Ala His
290    295    300
Val His Glu Arg Ser Ala His Leu Val Ala Val Ala Thr Glu Glu Phe

```

305
Asp His Ala Asn Gln
325

315

320

<210> 95
<211> 966
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 95
atgtccaacg agaataacat tgctacattc aaagttgccg cagtccaggc cacacctgtg 60
tttcttgatc gtgaagcaac catcgacaaa gcttgcgcggt tgattgccac tgctggcagt 120
gaaggagcgc gcttgattgt gtttccagaa gcattcatcc caacttatcc tgaatgggta 180
tggggtattc cctccggtga gcaagggtta ctcaacgaac tctatgcaga gttgctcacc 240
aatgcggtca ccattcccag cgatgcgact gacaggctgt gcgaggctgc gcagcttgcg 300
aatgcctacg tagtgatggg catgagcgaa cggaacgtcg aggcgagtg gcaagccctg 360
tataatacgc tgttgtacat aaatgcgcag ggggagattt tagggaaaca tcgaaagctg 420
gtgccaacgg gcggcgaaacg cctggtatgg gcgcagggtg atggcagtag gctgcagggtc 480
tacgatactc cattgggaaa actcgggtggc ttaatttgct gggaaaatta tatgccgctg 540
gcacggtatg ctatgtatgc ctggggaaca caaatctatg tcgcggcaac gtgggatcgc 600
ggtcaaccct ggctttctac attaaggcat atcgccaaag aaggcagggt atacgtgatt 660
ggttgctgta tcgcgatgcg taaagacgat attccagatc gttacaccat gaagcaaaaa 720
tattatgctg aaatggatga atggatgaat gttggtgaca gtgtgattgt caatcccagag 780
gggcacttta ttgccgggcc tgtgcgcaag caggaagaaa ttctctacgc ggagattgat 840
cctcgcatgg tgcaaggccc gaagtggatg ctcgatgtgg cagggcatta tgcgagaccg 900
gatgtgttcc agttgacggg gcatacggat gtgaggcgga tgatgcgggt ggaagatgat 960
tcataa 966

<210> 96
<211> 321
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 96
Met Ser Asn Glu Asn Asn Ile Ala Thr Phe Lys Val Ala Ala Val Gln
1 5 10 15
Ala Thr Pro Val Phe Leu Asp Arg Glu Ala Thr Ile Asp Lys Ala Cys
20 25 30
Ala Leu Ile Ala Thr Ala Gly Ser Glu Gly Ala Arg Leu Ile Val Phe
35 40 45
Pro Glu Ala Phe Ile Pro Thr Tyr Pro Glu Trp Val Trp Gly Ile Pro
50 55 60
Ser Gly Glu Gln Gly Leu Leu Asn Glu Leu Tyr Ala Glu Leu Leu Thr
65 70 75 80
Asn Ala Val Thr Ile Pro Ser Asp Ala Thr Asp Arg Leu Cys Glu Ala
85 90 95
Ala Gln Leu Ala Asn Ala Tyr Val Val Met Gly Met Ser Glu Arg Asn
100 105 110
Val Glu Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Ile Asn
115 120 125
Ala Gln Gly Glu Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly
130 135 140
Gly Glu Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Gln Val
145 150 155 160
Tyr Asp Thr Pro Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn

165 170 175
 Tyr Met Pro Leu Ala Arg Tyr Ala Met Tyr Ala Trp Gly Thr Gln Ile
 180 185 190
 Tyr Val Ala Ala Thr Trp Asp Arg Gly Gln Pro Trp Leu Ser Thr Leu
 195 200 205
 Arg His Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys Ile
 210 215 220
 Ala Met Arg Lys Asp Asp Ile Pro Asp Arg Tyr Thr Met Lys Gln Lys
 225 230 235 240
 Tyr Tyr Ala Glu Met Asp Glu Trp Met Asn Val Gly Asp Ser Val Ile
 245 250 255
 Val Asn Pro Glu Gly His Phe Ile Ala Gly Pro Val Arg Lys Gln Glu
 260 265 270
 Glu Ile Leu Tyr Ala Glu Ile Asp Pro Arg Met Val Gln Gly Pro Lys
 275 280 285
 Trp Met Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Gln
 290 295 300
 Leu Thr Val His Thr Asp Val Arg Arg Met Met Arg Val Glu Asp Asp
 305 310 315 320
 Ser

<210> 97
 <211> 1017
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 97
 atgggcatcg aacatccgaa atacaaggtc gccgtggtgc aagctgcgcc cgcctggctc 60
 gacctcgacg cgctcgatcga caagacgatc gggctgatcg aggaggcggc gaagaaaggc 120
 gccaagctga tcgctttccc cgaagccttc attcccggct acccttgga catctggctc 180
 gactcaccgg cctgggcat cgcccgcggt ttcgtgcagc gctatttcga caattcgctc 240
 gcctacgaca gcccacaggc ggaaaggctg cgacaggccg tgcggaaggc caagctcacc 300
 gccgtgatcg gcctgtccga gcgcgacggc ggcagcctct atctcgcgca gtggctgac 360
 gggcccgcag gtgagaccat cgcaaagcgc cgcaagctgc ggccgaccca tgccgagcgc 420
 accgtctatg gcgaaggcga cggcagcgat ctcccggtcc atgagcgggc cgacatcggc 480
 cggctcgcg cgctgtgctg ctgggagcat ctgcagccgc tgcgaaatt cgccatgtac 540
 gcccagaacg agcaggtaca tgcgcgggcc tggccgagct tctcgtctta cgatcccttc 600
 gcgcctgcgc tgggcgcgga ggtgaacaac gccgcctccc gcatctatgc ggtggaaggc 660
 tcctgcttcg tgctcgacac gtgcgcgacg gtctcgagc ccatgatcga cgagctctgc 720
 gatcgccgg acaagcacgc gctgctgcat gccgcggcg gcttcgccgc gatctacggg 780
 cccgacggca gccagatcgg cgacaagctg ccgcccagc aggaggccct gctgatcgcc 840
 gagatcgatc tgggcgcgat cggcgtcgcc aagaacgcgg ccgatccgc cgggcattat 900
 tcgcggcccg acgtcacgcg gctcctgctc aacaggaagc cgaacaagcg cgtggagcag 960
 ttgcgctgc ccgtcgacac ggtcgagccc gtcgacgtcg cggcggcagc aagctga 1017

<210> 98
 <211> 338
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 98
 Met Gly Ile Glu His Pro Lys Tyr Lys Val Ala Val Val Gln Ala Ala
 1 5 10 15
 Pro Ala Trp Leu Asp Leu Asp Ala Ser Ile Asp Lys Thr Ile Gly Leu

```

      20      25      30
Ile Glu Glu Ala Ala Lys Lys Gly Ala Lys Leu Ile Ala Phe Pro Glu
      35      40      45
Ala Phe Ile Pro Gly Tyr Pro Trp His Ile Trp Leu Asp Ser Pro Ala
      50      55      60
Trp Ala Ile Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
      65      70      75      80
Ala Tyr Asp Ser Pro Gln Ala Glu Arg Leu Arg Gln Ala Val Arg Lys
      85      90      95
Ala Lys Leu Thr Ala Val Ile Gly Leu Ser Glu Arg Asp Gly Gly Ser
      100      105      110
Leu Tyr Leu Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
      115      120      125
Lys Arg Arg Lys Leu Arg Pro Thr His Ala Glu Arg Thr Val Tyr Gly
      130      135      140
Glu Gly Asp Gly Ser Asp Leu Ala Val His Glu Arg Ala Asp Ile Gly
      145      150      155      160
Arg Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys
      165      170      175
Phe Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ala Trp Pro
      180      185      190
Ser Phe Ser Leu Tyr Asp Pro Phe Ala Pro Ala Leu Gly Ala Glu Val
      195      200      205
Asn Asn Ala Ala Ser Arg Ile Tyr Ala Val Glu Gly Ser Cys Phe Val
      210      215      220
Leu Ala Pro Cys Ala Thr Val Ser Gln Ala Met Ile Asp Glu Leu Cys
      225      230      235      240
Asp Arg Pro Asp Lys His Ala Leu Leu His Ala Gly Gly Gly Phe Ala
      245      250      255
Ala Ile Tyr Gly Pro Asp Gly Ser Gln Ile Gly Asp Lys Leu Pro Pro
      260      265      270
Glu Gln Glu Gly Leu Leu Ile Ala Glu Ile Asp Leu Gly Ala Ile Gly
      275      280      285
Val Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
      290      295      300
Val Thr Arg Leu Leu Leu Asn Arg Lys Pro Asn Lys Arg Val Glu Gln
      305      310      315      320
Phe Ala Leu Pro Val Asp Thr Val Glu Pro Val Asp Val Ala Ala Ala
      325      330      335
Ala Ser

```

<210> 99
 <211> 1014
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 99
atgcctgaca agagaatcgt ccgcgcgcc gcggtccaga tagcaccgga cctcgaacgg      60
cccgtggca cgctcgagaa ggtcctcgag acgatcgacg acgccgcacg ccagggcgtg      120
cagctcatcg tcttccccga gaccttcctg ccctactacc cgtacttttc gttcgtgcgg      180
gcccgggtgg catcggtgac agagcacatg cggctctatg acgaagcggg ggtcgtgccc      240
gggccgggtga cgcagtcggt ggccgagcgg gcacggcgcc acggcatggt cgtcgtgctc      300
ggcgtgaacg agcgcgatca cggcagctta tacaacgcac aactgatctt cgataccgac      360
ggcagactgc tgctcaagcg ccgcaagatc acgccgacgt ttcacgaacg gatgatctgg      420
ggcatggggc acgcagccgg cctgaaggta gcggaaacgc gtatcggccg ggtgggtgca      480
ctcgttgct gggaacacta caaccgcgtt gcacgttatg cactgatgac ccagcacgaa      540
gagattcatt gcagccagtt tcccggtcgt ctggtcggac ccattctcgg tgaacagatc      600

```

```

gaagtgacca tccggcatca cgcactggaa tccggctgct tcgtgatcaa ttccaccggc 660
tggctgaccg agccgcagat cgagtcgata acgaaagatc cgggcctgca gaaggcgctt 720
cgcgccgggt gcaacacggc gatcatctcg cccgaaggcc agcatctcgc cccgccgctg 780
cgtgaggggc agggcatggt catcgctgac ctggacatgt cgctgatcac caaacgcaaa 840
cgcatgatgg attctgtcgg ccactacgcg cggcccgaac tgctgagcct cgccatcaac 900
gaccggcccg cggtcacgtc ggcacccatg aacagcttct catcttcaac cgggggattg 960
caccttgaa cgcgaacgaga cctgtcggc cgtgagcccg caattgatga ctga 1014

```

<210> 100

<211> 337

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 100

```

Met Pro Asp Lys Arg Ile Val Arg Ala Ala Val Gln Ile Ala Pro
1      5      10      15
Asp Leu Glu Arg Pro Gly Gly Thr Leu Glu Lys Val Leu Glu Thr Ile
20     25     30
Asp Asp Ala Ala Arg Gln Gly Val Gln Leu Ile Val Phe Pro Glu Thr
35     40     45
Phe Leu Pro Tyr Tyr Pro Tyr Phe Ser Phe Val Arg Ala Pro Val Ala
50     55     60
Ser Gly Ala Glu His Met Arg Leu Tyr Asp Glu Ala Val Val Val Pro
65     70     75     80
Gly Pro Val Thr His Ala Val Ala Glu Arg Ala Arg Arg His Gly Met
85     90     95
Val Val Val Leu Gly Val Asn Glu Arg Asp His Gly Ser Leu Tyr Asn
100    105    110
Ala Gln Leu Ile Phe Asp Thr Asp Gly Glu Leu Leu Leu Lys Arg Arg
115    120    125
Lys Ile Thr Pro Thr Phe His Glu Arg Met Ile Trp Gly Met Gly Asp
130    135    140
Ala Ala Gly Leu Lys Val Ala Glu Thr Arg Ile Gly Arg Val Gly Ala
145    150    155    160
Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met
165    170    175
Thr Gln His Glu Glu Ile His Cys Ser Gln Phe Pro Gly Ser Leu Val
180    185    190
Gly Pro Ile Phe Gly Glu Gln Ile Glu Val Thr Ile Arg His His Ala
195    200    205
Leu Glu Ser Gly Cys Phe Val Ile Asn Ser Thr Gly Trp Leu Thr Glu
210    215    220
Pro Gln Ile Glu Ser Ile Thr Lys Asp Pro Gly Leu Gln Lys Ala Leu
225    230    235    240
Arg Gly Gly Cys Asn Thr Ala Ile Ile Ser Pro Glu Gly Gln His Leu
245    250    255
Ala Pro Pro Leu Arg Glu Gly Glu Gly Met Val Ile Ala Asp Leu Asp
260    265    270
Met Ser Leu Ile Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His
275    280    285
Tyr Ala Arg Pro Glu Leu Leu Ser Leu Ala Ile Asn Asp Arg Pro Ala
290    295    300
Val Thr Ser Ala Pro Met Asn Ser Phe Ser Ser Thr Gly Gly Leu
305    310    315    320
His Leu Glu Arg Glu Arg Asp Leu Val Gly Arg Glu Pro Ala Ile Asp
325    330    335
Asp

```

<210> 101
 <211> 1065
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 101
 atggcgacag tccatccgaa atttaaagta gccgccgtcc aggcggcccc ggcctttctc 60
 gacctcgacg cgtcgggtgga aaaagcgggtg cgcctgattg atgaagccgg cgccgctggg 120
 gcccggtcca tcgcgtttcc agagactttt atccccgggt atccgtgggt gatctggctc 180
 ggtgctccgg cctgggcgat catgcgcggc ttctctctcc gctatttcga caactcgctg 240
 cagtacggca ccccggaagc cgaccggctg cgggcagccg ccaaacgcaa caaatgttc 300
 gtcgcgctcg gactgtcaga gcgcgacggc ggagctctct acatcgccca atggattatc 360
 ggacccgacg gcgagacggg cgcaacgcgc cgcaagctca agcctactca cgccgagcgg 420
 acggtgttcg gcgaaggcga tggctcgcac cttgcgggtc acgaacttga tatcgggcgg 480
 gtcggtgcgc tgtgctgttg ggagcacctg cagccactgt cgaagtacgc gatgtatgcg 540
 cagaacgagc aagttcatat cgcggcgttg cggagctttt cgctttacga tccgttcgcg 600
 catgcgcttg gcgccgaggt caacaacgcg gcgagcaaga tctacgcggg cgaaggctca 660
 tgctttgtga ttgcgccatg cgcgaccgtt tcccaggcga tgatcgacga attgtgtgac 720
 tcgcccagaga agcatcagtt cctgcacgtc ggccggcggt tcgccgtgat ctatggtccc 780
 gacggcgcgc cactcgccaa gccactggcg cccgatcagg aggggtctcct ttacgcggat 840
 atcgacctcg gcatgatttc ggtcgcgaaa gcggcgccg atccggctgg acattacgcg 900
 cgcccgagc tgaccgctct gttgttcaac aatcgtcctg ggaaccgggt ggagacactc 960
 gcgctgccgg tcgaccagga ggagagggc ggagcagggc gcaaacctgc gcccaagtca 1020
 ccgagtgtcg ctgcgttcac actgacgcag gcggcagccg agtag 1065

<210> 102
 <211> 354
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 102
 Met Ala Thr Val His Pro Lys Phe Lys Val Ala Ala Val Gln Ala Ala
 1 5 10 15
 Pro Ala Phe Leu Asp Leu Asp Ala Ser Val Glu Lys Ala Val Arg Leu
 20 25 30
 Ile Asp Glu Ala Gly Ala Ala Gly Ala Arg Leu Ile Ala Phe Pro Glu
 35 40 45
 Thr Phe Ile Pro Gly Tyr Pro Trp Trp Ile Trp Leu Gly Ala Pro Ala
 50 55 60
 Trp Ala Ile Met Arg Gly Phe Val Ser Arg Tyr Phe Asp Asn Ser Leu
 65 70 75 80
 Gln Tyr Gly Thr Pro Glu Ala Asp Arg Leu Arg Ala Ala Ala Lys Arg
 85 90 95
 Asn Lys Met Phe Val Ala Leu Gly Leu Ser Glu Arg Asp Gly Gly Ser
 100 105 110
 Leu Tyr Ile Ala Gln Trp Ile Ile Gly Pro Asp Gly Glu Thr Val Ala
 115 120 125
 Thr Arg Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly
 130 135 140
 Glu Gly Asp Gly Ser His Leu Ala Val His Glu Leu Asp Ile Gly Arg
 145 150 155 160
 Val Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr
 165 170 175
 Ala Met Tyr Ala Gln Asn Glu Gln Val His Ile Ala Ala Trp Pro Ser

```

      180      185      190
Phe Ser Leu Tyr Asp Pro Phe Ala His Ala Leu Gly Ala Glu Val Asn
      195      200      205
Asn Ala Ala Ser Lys Ile Tyr Ala Val Glu Gly Ser Cys Phe Val Ile
      210      215      220
Ala Pro Cys Ala Thr Val Ser Gln Ala Met Ile Asp Glu Leu Cys Asp
225      230      235      240
Ser Pro Glu Lys His Gln Phe Leu His Val Gly Gly Gly Phe Ala Val
      245      250      255
Ile Tyr Gly Pro Asp Gly Ala Pro Leu Ala Lys Pro Leu Ala Pro Asp
      260      265      270
Gln Glu Gly Leu Leu Tyr Ala Asp Ile Asp Leu Gly Met Ile Ser Val
      275      280      285
Ala Lys Ala Ala Ala Asp Pro Ala Gly His Tyr Ala Arg Pro Asp Val
      290      295      300
Thr Arg Leu Leu Phe Asn Asn Arg Pro Gly Asn Arg Val Glu Thr Leu
305      310      315      320
Ala Leu Pro Val Asp Gln Glu Ala Glu Ala Gly Ala Gly Gly Lys Pro
      325      330      335
Ala Pro Lys Ser Pro Ser Val Ala Ala Phe Thr Leu Thr Gln Ala Ala
      340      345      350
Ala Glu

```

<210> 103
 <211> 945
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 103
atgggcgagt tcggcgaggt gacgctgggg gtggcgagg cggcgcggt gtacttcgac      60
cgggaggcgt cgacggagaa ggctcgcggc ctgatccggg aggcggggga gaagggcgctc      120
gacctgttgg cgttcgggga gacgtggctg acgggggtacc cgtactggaa ggatgcgccg      180
tggtctcggg agtacaacga cctgcgcgcg cggtagctgg cgaatggcgt gatgataccg      240
gggccggaga cggacgcgct atgccaggca gcggcggaag cgggggtgga cgtggcaatc      300
ggcgtggtgg agctggagcc ggggagcctt tcgagcgtgt attgcacgtt gctgttcac      360
tcgcgcgagg gcgagatcct ggggcggcac cggagctga agccgacgga ttcggaacgg      420
cggtagctgt cagaggtgga tgcgacgggg ctgcgggtgt acgagcggcc atatggccgg      480
ttgagcggat tgaactgctg ggaacacctt atgatgttg cggggtacgc gctggcgga      540
caggggacgc agtttcatgt ggcagcgtgg ccgaacatgg cgagctcggc gagcgagctg      600
ctgtcgcggg cgtatgcgta ccaggccgga tgctacgtgt tgtgcgcggg cgggctcggg      660
cctgcgccgg gagagctacc ggacggcatc gcggcgaggt cgctggacca cctgacgggc      720
gagagctgca tcatcgaccc gtggggaaaa gtgatcgagg ggccggtgtc gtgcgaggag      780
acgctgatta cggcgcggtg atcgaccgcg tcaatctacc ggcgcaagtc gctgacggac      840
gtgggtggcc actactcgcg accggacgtg ttccggttcg aggtggatag gtcggagcgc      900
ccgcgagtggt tgtttcgga tggggatgtg gacgaccggg ggtaa      945

```

<210> 104
 <211> 314
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 104
Met Gly Glu Phe Gly Glu Val Thr Leu Gly Val Ala Gln Ala Ala Pro
  1           5           10           15

```

Val Tyr Phe Asp Arg Glu Ala Ser Thr Glu Lys Ala Arg Gly Leu Ile
 20 25 30
 Arg Glu Ala Gly Glu Lys Gly Val Asp Leu Leu Ala Phe Gly Glu Thr
 35 40 45
 Trp Leu Thr Gly Tyr Pro Tyr Trp Lys Asp Ala Pro Trp Ser Arg Glu
 50 55 60
 Tyr Asn Asp Leu Arg Ala Arg Tyr Val Ala Asn Gly Val Met Ile Pro
 65 70 75 80
 Gly Pro Glu Thr Asp Ala Leu Cys Gln Ala Ala Glu Ala Gly Val
 85 90 95
 Asp Val Ala Ile Gly Val Val Glu Leu Glu Pro Gly Ser Leu Ser Ser
 100 105 110
 Val Tyr Cys Thr Leu Leu Phe Ile Ser Arg Glu Gly Glu Ile Leu Gly
 115 120 125
 Arg His Arg Lys Leu Lys Pro Thr Asp Ser Glu Arg Arg Tyr Trp Ser
 130 135 140
 Glu Gly Asp Ala Thr Gly Leu Arg Val Tyr Glu Arg Pro Tyr Gly Arg
 145 150 155 160
 Leu Ser Gly Leu Asn Cys Trp Glu His Leu Met Met Leu Pro Gly Tyr
 165 170 175
 Ala Leu Ala Ala Gln Gly Thr Gln Phe His Val Ala Ala Trp Pro Asn
 180 185 190
 Met Ala Ser Ser Ala Ser Glu Leu Leu Ser Arg Ala Tyr Ala Tyr Gln
 195 200 205
 Ala Gly Cys Tyr Val Leu Cys Ala Gly Gly Leu Gly Pro Ala Pro Gly
 210 215 220
 Glu Leu Pro Asp Gly Ile Ala Ala Glu Ser Leu Asp His Leu Thr Gly
 225 230 235 240
 Glu Ser Cys Ile Ile Asp Pro Trp Gly Lys Val Ile Ala Gly Pro Val
 245 250 255
 Ser Cys Glu Glu Thr Leu Ile Thr Ala Arg Val Ser Thr Ala Ser Ile
 260 265 270
 Tyr Arg Arg Lys Ser Leu Thr Asp Val Gly Gly His Tyr Ser Arg Pro
 275 280 285
 Asp Val Phe Arg Phe Glu Val Asp Arg Ser Glu Arg Pro Arg Val Val
 290 295 300
 Phe Arg Asp Gly Asp Val Asp Asp Arg Gly
 305 310

<210> 105

<211> 975

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 105

atgaccattg	tcaaagccgc	tgccgtccag	attgccccg	ttctctacag	ccgtgaaggc	60
actgtagaaa	aggtcgtaa	caagattcgc	gaactcggcg	agaagggcgt	gcagttcgcc	120
gttttccctg	aaaccgctgt	accgtactac	ccgtactttt	cctttgtgca	gagcccttcc	180
aaaatgggtt	ccgagcacta	caaattgctc	gaccaggccg	ttgtcgtgcc	gtcggcgacc	240
accgatgcca	tcggcaaaagc	ggccaaggaa	gccaacatgg	tggtgtccat	cggcgtcaac	300
gaacgcgatg	gcagcaccct	ctacaacacg	cagttgctgt	ttgatgccga	cggcactttg	360
attcaggccc	gtcgcgaagat	ttcacccgacc	taccacgaac	gcatgatctg	gggcatgggc	420
gacggttccg	gcctgcgcgc	caccgacagc	gcggtcgggc	gcatcggaca	attggcctgc	480
tgggaacatt	acaatccgct	ggcgcgttac	gccttgatcg	aagacggcga	acagatccac	540
gcctcgatgt	acccgggctc	gttcgcaggt	cctttattca	ctcgccagat	ggaagtcagc	600
atccgcatgc	atgccctgga	atcggcgtgc	ttcgtggtca	actcgaccgc	gtggttgtag	660
ccggaacagc	aagcccagat	catggccgac	accggttgcg	agatcgggcc	gatctccggc	720
ggctgctaca	ccgcgatcat	cgacccacag	ggtgaagtcg	tcggcgcact	gaccgaaggc	780

gagggcgaag tgattgccga catcgatctg ttccagatcg aaatccgtaa acgtcagatg 840
gacggccgtg gtcactacag ccgtccggaa atcctgagcc tgaacatcga ccgtacgccg 900
catcgccatg ttcacgaacg caacgaccag cagaaaccgg gtgtgatcga cactgctgaa 960
gaaaccgggc gttga 975

<210> 106
<211> 324
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 106
Met Thr Ile Val Lys Ala Ala Ala Val Gln Ile Ala Pro Val Leu Tyr
1 5 10 15
Ser Arg Glu Gly Thr Val Glu Lys Val Val Asn Lys Ile Arg Glu Leu
20 25 30
Gly Glu Lys Gly Val Gln Phe Ala Val Phe Pro Glu Thr Val Val Pro
35 40 45
Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Ser Pro Phe Lys Met Gly Ser
50 55 60
Glu His Tyr Lys Leu Leu Asp Gln Ala Val Val Pro Ser Ala Thr
65 70 75 80
Thr Asp Ala Ile Gly Lys Ala Ala Lys Glu Ala Asn Met Val Val Ser
85 90 95
Ile Gly Val Asn Glu Arg Asp Gly Ser Thr Leu Tyr Asn Thr Gln Leu
100 105 110
Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln Ala Arg Arg Lys Ile Ser
115 120 125
Pro Thr Tyr His Glu Arg Met Ile Trp Gly Met Gly Asp Gly Ser Gly
130 135 140
Leu Arg Ala Thr Asp Ser Ala Val Gly Arg Ile Gly Gln Leu Ala Cys
145 150 155 160
Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Ile Glu Asp Gly
165 170 175
Glu Gln Ile His Ala Ser Met Tyr Pro Gly Ser Phe Ala Gly Pro Leu
180 185 190
Phe Thr Arg Gln Met Glu Val Ser Ile Arg Met His Ala Leu Glu Ser
195 200 205
Ala Cys Phe Val Val Asn Ser Thr Ala Trp Leu Tyr Pro Glu Gln Gln
210 215 220
Ala Gln Ile Met Ala Asp Thr Gly Cys Glu Ile Gly Pro Ile Ser Gly
225 230 235 240
Gly Cys Tyr Thr Ala Ile Ile Asp Pro Gln Gly Glu Val Val Gly Ala
245 250 255
Leu Thr Glu Gly Glu Gly Glu Val Ile Ala Asp Ile Asp Leu Phe Gln
260 265 270
Ile Glu Ile Arg Lys Arg Gln Met Asp Gly Arg Gly His Tyr Ser Arg
275 280 285
Pro Glu Ile Leu Ser Leu Asn Ile Asp Arg Thr Pro His Arg His Val
290 295 300
His Glu Arg Asn Asp Gln Gln Lys Pro Gly Val Ile Asp Thr Ala Glu
305 310 315 320
Glu Thr Gly Arg

<210> 107
<211> 981
<212> DNA
<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 107

```

atggccatca ttcgcgcagc agccgtacag atcagcccgg ttctttacag ccgcgaaggc      60
accgtggaca aggtctgcca gcagatcatc acccttgcca aacagggtgt gcagttcgcc      120
gtgttcccgg aaacgggtgt gccgtactac ccctattttt cctttgtgca gccggcggtc      180
gccatgggtg cgcaacacct caaattgcta gatcaatctg taaccgtgcc atcgcccgcc      240
accctggcga ttggcgaagc gtgcaagcaa gcaggaatgg tcgtttccat cggagtcaat      300
gaacgcgatg gcggtacgat ttacaacgcg caattactct tcgatgctga cggcacgctg      360
attcagcatc ggcgcaaaat caccocgacc taccacgagc gcatggtctg ggggcagggc      420
gatggttcog gtctgcgcgc catcgacagc gcggtcgggc gcatcggtc cctggcatgc      480
tggaacatt acaaccggct ggcccgttac gccttgatgg cagacggcga acagatccac      540
gccgcgatgt ttcccggttc cctggtgggt gacatcttcg ccgagcagat cgaggtcacc      600
atccgccatc acgcattgga gtcaggatgc ttcgtggtca atgcaacagc ctggctggat      660
gcggatcagc agggccaaat aatgcaggac acagggttgc gccttggtcc catctcgggc      720
ggctgcttca ccgcgatcgt atcgccggaa ggaagctac ttggagagcc gcttcgctcc      780
ggggaaggcg tagtgattgc cgacctgat acggccttga tcgacaagcg caaacggatg      840
atggattcag taggtcatta cagtcgtccc gagctgctca gcctattgat cgatcgatcg      900
ccgactgcgc atgttcatga acgcgccggc tttgtttcga gcaacgccgg tttgcaggag      960
gtgccccatg cagaccaatg a                                     981

```

<210> 108

<211> 326

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 108

```

Met Ala Ile Ile Arg Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
 1          5          10          15
Ser Arg Glu Gly Thr Val Asp Lys Val Cys Gln Gln Ile Ile Thr Leu
 20          25          30
Gly Lys Gln Gly Val Gln Phe Ala Val Phe Pro Glu Thr Val Val Pro
 35          40          45
Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Pro Ala Phe Ala Met Gly Ala
 50          55          60
Gln His Leu Lys Leu Leu Asp Gln Ser Val Thr Val Pro Ser Ala Ala
 65          70          75          80
Thr Leu Ala Ile Gly Glu Ala Cys Lys Gln Ala Gly Met Val Val Ser
 85          90          95
Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Ile Tyr Asn Ala Gln Leu
100          105          110
Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln His Arg Arg Lys Ile Thr
115          120          125
Pro Thr Tyr His Glu Arg Met Val Trp Gly Gln Gly Asp Gly Ser Gly
130          135          140
Leu Arg Ala Ile Asp Ser Ala Val Gly Arg Ile Gly Ser Leu Ala Cys
145          150          155          160
Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met Ala Asp Gly
165          170          175
Glu Gln Ile His Ala Ala Met Phe Pro Gly Ser Leu Val Gly Asp Ile
180          185          190
Phe Ala Glu Gln Ile Glu Val Thr Ile Arg His His Ala Leu Glu Ser
195          200          205
Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp Gln Gln
210          215          220
Gly Gln Ile Met Gln Asp Thr Gly Cys Gly Leu Gly Pro Ile Ser Gly

```



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225          230          235          240
Gly Cys Phe Thr Ala Ile Val Ser Pro Glu Gly Lys Leu Leu Gly Glu
          245          250          255
Pro Leu Arg Ser Gly Glu Gly Val Val Ile Ala Asp Leu Asp Thr Ala
          260          265          270
Leu Ile Asp Lys Arg Lys Arg Met Met Asp Ser Val Gly His Tyr Ser
          275          280          285
Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Ser Pro Thr Ala His
          290          295          300
Val His Glu Arg Ala Gly Phe Val Ser Ser Asn Ala Gly Leu Gln Glu
305          310          315          320
Val Ala His Ala Asp Gln
          325

```

<210> 109

<211> 1092

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 109

```

atggccatca ttcgcgcagc agccgtacag atcagcccgg ttctttacag ccgcgaaggc      60
accgtggaca gggctctgcca gcagatcatc acccttggca aacaagggtgt gcagttcgcc      120
gtgttcccg aaacgggtggt gccgtactac ccctatTTTT cctttgtgca gccggcattt      180
gcgatgggtg cacaacacct caaattgctc gatcaatctg taaccgtgcc atcggccgcc      240
accctggcga ttggcgaagc gtgcaagcaa gcaggaatgg tcgtttccat cggcgtaaat      300
gaacgcgatg gcgttacgat ttacaacgcg caattactct tcgatgctga cggcactctg      360
attcagcatc ggcgcaaaat caccgcgacc taccacgagc gcattggtctg ggggcagggc      420
gatggttccg gtctgcgcgc catcgacagc gcggtcgggc gcattcgctc cctggcatgc      480
tggaacatt acaacccgct ggcgcgttac gccttgatgg cagacggcga acagatccac      540
gccgcgatgt ttcccggttc cctggtgggt gacatcttcg ccgagcagat cgaggtcacc      600
atccgccatc acgcattgga atcaggatgc ttctggttca atgcaacagc ttggctggat      660
gcggatcagc agggccaaat aatgcaggac acaggttgcg gccttgggcc catctcgggc      720
ggctgcttca ccgcgatcgt atcgccggaa ggggaagctac ttggagagcc gcttcgctca      780
ggggaaggcg tagtgattgc cgacctcgat atggccttga tcgacaagcg caaacggatg      840
atggattcag taggtcatta cagtcgtccc gagctgctca gcctattgat cgatcgatcg      900
ccgactgcgc attttcatga acgcgcgggg ctttggttcc agcgcgccc gtttcagga      960
ggtcgcgcgc gcagaccaat gaattgctcg ctgacctgca aatccaaggc ctgctgtggc     1020
cgccgcgcga aatggcttgt cgcgccaagg cggcgccggg ccttcagacc acaaggcgct     1080
gagcctaggt aa                                     1092

```

<210> 110

<211> 363

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 110

```

Met Ala Ile Ile Arg Ala Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
 1          5          10          15
Ser Arg Glu Gly Thr Val Asp Arg Val Cys Gln Gln Ile Ile Thr Leu
          20          25          30
Gly Lys Gln Gly Val Gln Phe Ala Val Phe Pro Glu Thr Val Val Pro
          35          40          45
Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Pro Ala Phe Ala Met Gly Ala
          50          55          60
Gln His Leu Lys Leu Leu Asp Gln Ser Val Thr Val Pro Ser Ala Ala

```

```

65          70          75          80
Thr Leu Ala Ile Gly Glu Ala Cys Lys Gln Ala Gly Met Val Val Ser
      85          90          95
Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Ile Tyr Asn Ala Gln Leu
      100        105        110
Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln His Arg Arg Lys Ile Thr
      115        120        125
Pro Thr Tyr His Glu Arg Met Val Trp Gly Gln Gly Asp Gly Ser Gly
      130        135        140
Leu Arg Ala Ile Asp Ser Ala Val Gly Arg Ile Gly Ser Leu Ala Cys
      145        150        155
Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met Ala Asp Gly
      165        170        175
Glu Gln Ile His Ala Ala Met Phe Pro Gly Ser Leu Val Gly Asp Ile
      180        185        190
Phe Ala Glu Gln Ile Glu Val Thr Ile Arg His His Ala Leu Glu Ser
      195        200        205
Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp Gln Gln
      210        215        220
Gly Gln Ile Met Gln Asp Thr Gly Cys Gly Leu Gly Pro Ile Ser Gly
      225        230        235
Gly Cys Phe Thr Ala Ile Val Ser Pro Glu Gly Lys Leu Leu Gly Glu
      245        250        255
Pro Leu Arg Ser Gly Glu Gly Val Val Ile Ala Asp Leu Asp Met Ala
      260        265        270
Leu Ile Asp Lys Arg Lys Arg Met Met Asp Ser Val Gly His Tyr Ser
      275        280        285
Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Ser Pro Thr Ala His
      290        295        300
Phe His Glu Arg Ala Gly Leu Cys Ser Glu Arg Arg Arg Phe Ala Gly
      305        310        315
Gly Arg Ala Cys Arg Pro Met Asn Cys Ser Leu Thr Cys Lys Ser Lys
      325        330        335
Ala Cys Val Gly Arg Pro Arg Lys Trp Leu Val Ala Pro Arg Arg Arg
      340        345        350
Arg Ser Phe Arg Pro Gln Gly Ala Glu Pro Arg
      355        360

```

<210> 111
 <211> 990
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 111
atgcccaaaa cagtacgtgc cgcagcagtc cagatcgcg cccgacctgac gtcacgcgcc      60
ggcaccgtcg agcgggtcct caatgcaatc gccgaagctg ctgacaaagg cgccgagctg      120
atcgatttcc ccgagacctt cgtgccctgg tatccctatt tcagtttctg tctgccacct      180
gtccagcaag gccctgagca tcttcgtctt tatgaggaag cagtcacggt accatcagca      240
gaaacacggg ccgtcgcgga cgccgcgcgc aaacgcaatg cgggttatcg ccttggcgctc      300
aatgagcgcg accacggctc gctctataac actcagctga tcttcgacgc ggatggcagc      360
ctgaaactca agcgtcgcaa gatcacgcgc acctatcacg aacggatgat ctggggccaa      420
ggcgtatggc cggcctgaa ggttgctgac actgccgtcg gtcgcgtggg tgccctggca      480
tgctgggagc attacaatcc tctggccgcg tatactttga tggcccagca tgaggaaatt      540
cacgcctctc atttccggg ctcactggtc ggcccgatat tcggcgagca aatcgaagtc      600
accatgcgcc accacgcggt ggaatcgggc tgtttcgtgg tcaatgccac cggctggctg      660
agcggaggagc agatcgcatc tattcatccg gaccccgcc tgcataaggg cctgcgcgat      720
ggctgcatga cctgcatcat cagcccgaa ggacgcatg tcgtaccgcc gctgacctcg      780
ggcgaaggca tcttgatcgg cgatctggac atgcggctca ttaccaagcg caagcggatg      840

```

```

atggattcgg tcggacacta tgctcggcct gaactgctgc accttgcca tgacacgacg      900
cccgcacgcg cagcgagca ggtcggcctt tcaggcgatt ttcccgatgc ggagcaagac      960
aaactatttg aggaggttca taatgcgtga      990

```

<210> 112
 <211> 329
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 112
 Met Pro Lys Thr Val Arg Ala Ala Val Gln Ile Ala Pro Asp Leu
 1 5 10 15
 Thr Ser Arg Ala Gly Thr Val Glu Arg Val Leu Asn Ala Ile Ala Glu
 20 25 30
 Ala Ala Asp Lys Gly Ala Glu Leu Ile Val Phe Pro Glu Thr Phe Val
 35 40 45
 Pro Trp Tyr Pro Tyr Phe Ser Phe Val Leu Pro Pro Val Gln Gln Gly
 50 55 60
 Pro Glu His Leu Arg Leu Tyr Glu Glu Ala Val Thr Val Pro Ser Ala
 65 70 75 80
 Glu Thr Arg Ala Val Ala Asp Ala Ala Arg Lys Arg Asn Ala Val Ile
 85 90 95
 Val Leu Gly Val Asn Glu Arg Asp His Gly Ser Leu Tyr Asn Thr Gln
 100 105 110
 Leu Ile Phe Asp Ala Asp Gly Ser Leu Lys Leu Lys Arg Arg Lys Ile
 115 120 125
 Thr Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly Asp Gly Ala
 130 135 140
 Gly Leu Lys Val Val Asp Thr Ala Val Gly Arg Val Gly Ala Leu Ala
 145 150 155 160
 Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Thr Leu Met Ala Gln
 165 170 175
 His Glu Glu Ile His Ala Ser His Phe Pro Gly Ser Leu Val Gly Pro
 180 185 190
 Ile Phe Gly Glu Gln Ile Glu Val Thr Met Arg His His Ala Leu Glu
 195 200 205
 Ser Gly Cys Phe Val Val Asn Ala Thr Gly Trp Leu Ser Glu Glu Gln
 210 215 220
 Ile Ala Ser Ile His Pro Asp Pro Ala Leu Gln Lys Gly Leu Arg Asp
 225 230 235 240
 Gly Cys Met Thr Cys Ile Ile Thr Pro Glu Gly Arg His Val Val Pro
 245 250 255
 Pro Leu Thr Ser Gly Glu Gly Ile Leu Ile Gly Asp Leu Asp Met Arg
 260 265 270
 Leu Ile Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His Tyr Ala
 275 280 285
 Arg Pro Glu Leu Leu His Leu Val His Asp Thr Thr Pro Ala Arg Ala
 290 295 300
 Arg Glu Gln Val Gly Leu Ser Gly Asp Phe Pro Asp Ala Glu Gln Asp
 305 310 315 320
 Lys Leu Phe Glu Glu Val His Asn Ala
 325

<210> 113
 <211> 993
 <212> DNA
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 113

```

atgacgaagg aacgcgccgc gcgcagcctg cgcgcagctg ccatacagct tgaagccgaa      60
gtcggcgaca tcgccgcca tctcgcacgc atcgaggcga tggtcgagga ggctgcgggc      120
aagggcgccg aactgatcgc cattccggag ttctgcacct cccgcatgcc cttcgatgca      180
cgcgtgcacg acgccgtgct gccgccggac aacttcgtgg tcgatgcctt tcgccgcatg      240
gcagcgacgc acaactgccg gctcggcggc tccatgtcga ttgccgacgg tggcgagatc      300
tacaaccgct accacttcgt cgaacccgac ggagcgctgc atctgcacga caaggatctg      360
ccgacgatgt gggagaacgc cttctacacc ggcggtccg acgacggcgt cttcgacacc      420
ggcatcggcg gcgtcggcgc cgcggtgtgc tgggaactgg tacgcaccgg caccgtgcga      480
cgcatgctcg gtcgcgtcga cgtcgccatg accggcacgc attggtggac gatgccgcac      540
aactggggca gcgccgtcgc gcgcacgctg gccgcgatga cgcagtacaa ccgtacatg      600
tccgagaatg caccacccga attcgcccgc cgcctgggtg tgccggtgct gcaggcctcg      660
cactgcgga gtttcgcac cggtttcttg ctgctgccag gcagcggcg tgcaactgcc      720
tatgacaccg agtacgtcgg cgccacacag atcgtcgatg ccgatggcca catcctcgcc      780
caccgtcgca cgcaggaagg ccccggtgtc gtcgtcgccg acatcacgct cgggtgccgc      840
acgcccagac tgccactgga agaccgcttc tggattcccg agctgccgct cttcctcaag      900
gcctactggc accaccagaa cctgtgcggc aagtcctact accgtcgcgt cggccgcgat      960
gccggcctgg cggcggcgga gcgttcggca tga      993

```

<210> 114

<211> 330

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 114

```

Met Thr Lys Glu Arg Ala Ala Arg Ser Leu Arg Ala Ala Ala Ile Gln
 1              5              10              15
Leu Glu Ala Glu Val Gly Asp Ile Ala Ala Asn Leu Ala Arg Ile Glu
      20              25              30
Ala Met Val Glu Glu Ala Ala Gly Lys Gly Ala Glu Leu Ile Ala Ile
      35              40              45
Pro Glu Phe Cys Thr Ser Arg Met Pro Phe Asp Ala Arg Val His Asp
      50              55              60
Ala Val Leu Pro Pro Asp Asn Phe Val Val Asp Ala Phe Arg Arg Met
      65              70              75              80
Ala Ala Thr His Asn Cys Arg Leu Gly Gly Ser Met Leu Ile Ala Asp
      85              90              95
Gly Gly Glu Ile Tyr Asn Arg Tyr His Phe Val Glu Pro Asp Gly Ser
      100             105             110
Val His Leu His Asp Lys Asp Leu Pro Thr Met Trp Glu Asn Ala Phe
      115             120             125
Tyr Thr Gly Gly Ser Asp Asp Gly Val Phe Asp Thr Gly Ile Gly Gly
      130             135             140
Val Gly Ala Ala Val Cys Trp Glu Leu Val Arg Thr Gly Thr Val Arg
      145             150             155             160
Arg Met Leu Gly Arg Val Asp Val Ala Met Thr Gly Thr His Trp Trp
      165             170             175
Thr Met Pro His Asn Trp Gly Ser Ala Val Ala Arg Thr Leu Ala Ala
      180             185             190
Met Thr Gln Tyr Asn Arg Tyr Met Ser Glu Asn Ala Pro Thr Glu Phe
      195             200             205
Ala Arg Arg Leu Gly Val Pro Val Leu Gln Ala Ser His Cys Gly Ser
      210             215             220
Phe Arg Thr Gly Phe Leu Leu Leu Pro Gly Ser Gly Arg Ala Leu Pro
      225             230             235             240

```

```

Tyr Asp Thr Glu Tyr Val Gly Ala Thr Gln Ile Val Asp Ala Asp Gly
      245                250                255
His Ile Leu Ala His Arg Arg Thr Gln Glu Gly Pro Gly Val Val Val
      260                265                270
Ala Asp Ile Thr Leu Gly Ala Arg Thr Pro Glu Leu Pro Leu Glu Asp
      275                280                285
Arg Phe Trp Ile Pro Glu Leu Pro Leu Phe Leu Lys Ala Tyr Trp His
      290                295                300
His Gln Asn Leu Cys Gly Lys Ser Tyr Tyr Arg Arg Val Gly Arg Asp
      305                310                315                320
Ala Gly Leu Ala Ala Glu Arg Ser Ala
      325                330

```

<210> 115

<211> 993

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 115

```

atgaaccaaa tcattaaagc ggcggcagtt caatgtagcc ctgtgttgta tagccaagcg      60
ggtacagtcg agaaaatctg tgacacgatt ttggagttgg ggcagcaagg tgtgcaattt      120
gccgtatttc ctgaaactgt tgtgccttat tacccttatt tttcttttgt gcaaccacgg      180
tttgccatgg gtaaagaaca tttaaagcta ttgcatgaat cggttgctcg gccatcggca      240
gcaacaactt taattggaca ggcattgcaa gaagcgaaca tgggtggttc tattggtatt      300
aatgagcgtg caggcggcac gatttataac gctcaattgt tgttgatgc ggatggttcg      360
attattcagc atcgccgtaa aattacccca acgtatcatg aacgtatggt gtgggggcaa      420
ggcgtatggc gtggtttacg tgcgatagat tctgctgtag gacgtattgg gtcgctggca      480
tggtgggagc attacaaccc tttggctcgg tttgctttga tggcggatgg tgagcaaatt      540
catgcggcga tgtttccggg atcactcgtg gggcagattt ttgcagatca gatcagtgcc      600
accattcagc accatgcttt agagtcgggc tgttttggg tgaatgccac agcatggcct      660
gacccagagc aacaacaaca aattatgcaa gatacaggct gtgaactcgg tccaatttcg      720
gggggatggt ttacggccat cgtttctcca gaaggcaaat tttgtctga accgatcaca      780
caaggcgaag gttatgtgat tgcgatttta gacttttcct taatcgaaaa acgtaaacgg      840
atgatggatt ctgttgggca ttatagtcgt ccagaattac tcagtttgtt gattgatcgt      900
cgtcctacct cagttttgca tgagttaaaa ctagagaatc catcgaataa cagcatcgaa      960
aaagtgtctg aatttgccga ggtacacgca tag                                     993

```

<210> 116

<211> 330

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 116

```

Met Asn Gln Ile Ile Lys Ala Ala Ala Val Gln Cys Ser Pro Val Leu
  1          5          10          15
Tyr Ser Gln Ala Gly Thr Val Lys Lys Ile Cys Asp Thr Ile Leu Glu
      20          25          30
Leu Gly Gln Gln Gly Val Gln Phe Ala Val Phe Pro Glu Thr Val Val
      35          40          45
Pro Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Pro Pro Phe Ala Met Gly
      50          55          60
Lys Glu His Leu Lys Leu Leu His Glu Ser Val Val Val Pro Ser Ala
      65          70          75          80
Ala Thr Thr Leu Ile Gly Gln Ala Cys Lys Glu Ala Asn Met Val Val
      85          90          95

```

```

Ser Ile Gly Ile Asn Glu Arg Ala Gly Gly Thr Ile Tyr Asn Ala Gln
      100      105      110
Leu Leu Phe Asp Ala Asp Gly Ser Ile Ile Gln His Arg Arg Lys Ile
      115      120      125
Thr Pro Thr Tyr His Glu Arg Met Val Trp Gly Gln Gly Asp Gly Ser
      130      135      140
Gly Leu Arg Ala Ile Asp Ser Ala Val Gly Arg Ile Gly Ser Leu Ala
      145      150      155      160
Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Phe Ala Leu Met Ala Asp
      165      170      175
Gly Glu Gln Ile His Ala Ala Met Phe Pro Gly Ser Leu Val Gly Gln
      180      185      190
Ile Phe Ala Asp Gln Ile Ser Ala Thr Ile Gln His His Ala Leu Glu
      195      200      205
Ser Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Pro Glu Gln
      210      215      220
Gln Gln Gln Ile Met Gln Asp Thr Gly Cys Glu Leu Gly Pro Ile Ser
      225      230      235      240
Gly Gly Cys Phe Thr Ala Ile Val Ser Pro Glu Gly Lys Phe Leu Ser
      245      250      255
Glu Pro Ile Thr Gln Gly Glu Gly Tyr Val Ile Ala Asp Leu Asp Phe
      260      265      270
Ser Leu Ile Glu Lys Arg Lys Arg Met Met Asp Ser Val Gly His Tyr
      275      280      285
Ser Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Arg Pro Thr Ser
      290      295      300
Val Leu His Glu Leu Lys Leu Glu Asn Pro Ser Asn Asn Ser Ile Glu
      305      310      315      320
Lys Val Ser Glu Phe Ala Glu Val His Ala
      325      330

```

<210> 117

<211> 957

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 117

```

atgactcaat ccaggataat tcgtgctgcg gcagcgcaga tcgctccgga ttgacaggtt      60
ccaggtaaca cgatcgacaa agtttgccgc accatcagcg aggcggccgc aaaaggcgta      120
cagattattg ttttccctga aaccttggtg ccttattacc cttacttctc ttacatttca      180
ccgcccattc aacagggcaa agaacatttg cggtgtatg accatgcagt ggtgtgcccc      240
ggctcggaaa ccgaggcaat ttcagctctt gccgcccaac acaatatggt ggtggttttg      300
ggtgtgaacg agcgcgatca cggcacactt tacaacgcac aaattatttt caacagcgac      360
ggaaagattc tgttgaagcg ccgaaaaaatt acaccaactt atcacgagcg gatggtgttg      420
gggcagggtg acgcttcagg cttgaaggtg gttgattccg cagtgggccc tgtgggtgca      480
ttggcctggt gggaacacta caacccttg gctcgtatt gtttgatggc ccagcacgaa      540
gaaattcact gtgcgcagtt tcccggttca ttggtggggc aagtttttgc cgaccaaatg      600
gaagtgacca ttcgtcacca cgcacttgag tcgggctgtt ttgtcatcaa cagcaccgct      660
tggttttctg aagaacaggt tcaaagtatt tcatccgaca gcgcattgca gaaagggtt      720
agaggcggtt gtttcacggc cattgtcagc cctgagggaa agctgttggtc tgagccgctc      780
accgagggtg agggcatggt gatcgccgac ctgcacatgg cgttggttac gaaacgcaaa      840
cgcattgatg attcagtggt ccattatgcg cgccccgagt tgttgagttt gctggttcgg      900
gatgaggctt caagcccat gaaaaaaatt cagggagttc aacatgctga gtactga      957

```

<210> 118

<211> 318

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 118

```

Met Thr Gln Ser Arg Ile Ile Arg Ala Ala Ala Ala Gln Ile Ala Pro
 1          5          10          15
Asp Leu Gln Val Pro Gly Asn Thr Ile Asp Lys Val Cys Arg Thr Ile
          20          25          30
Ser Glu Ala Ala Ala Lys Gly Val Gln Ile Ile Val Phe Pro Glu Thr
          35          40          45
Leu Val Pro Tyr Tyr Pro Tyr Phe Ser Tyr Ile Ser Pro Pro Ile Gln
          50          55          60
Gln Gly Lys Glu His Leu Arg Leu Tyr Asp His Ala Val Val Val Pro
65          70          75          80
Gly Ser Glu Thr Glu Ala Ile Ser Ala Leu Ala Ala Gln His Asn Met
          85          90          95
Val Val Val Leu Gly Val Asn Glu Arg Asp His Gly Thr Leu Tyr Asn
          100          105          110
Ala Gln Ile Ile Phe Asn Ser Asp Gly Lys Ile Leu Leu Lys Arg Arg
          115          120          125
Lys Ile Thr Pro Thr Tyr His Glu Arg Met Val Trp Gly Gln Gly Asp
          130          135          140
Ala Ser Gly Leu Lys Val Val Asp Ser Ala Val Gly Arg Val Gly Ala
145          150          155          160
Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Cys Leu Met
          165          170          175
Ala Gln His Glu Glu Ile His Cys Ala Gln Phe Pro Gly Ser Leu Val
          180          185          190
Gly Gln Val Phe Ala Asp Gln Met Glu Val Thr Ile Arg His His Ala
          195          200          205
Leu Glu Ser Gly Cys Phe Val Ile Asn Ser Thr Ala Trp Leu Ser Glu
          210          215          220
Glu Gln Val Gln Ser Ile Ser Ser Asp Ser Ala Leu Gln Lys Gly Leu
225          230          235          240
Arg Gly Gly Cys Phe Thr Ala Ile Val Ser Pro Glu Gly Lys Leu Leu
          245          250          255
Ala Glu Pro Leu Thr Glu Gly Glu Gly Met Val Ile Ala Asp Leu Asp
          260          265          270
Met Ala Leu Val Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His
          275          280          285
Tyr Ala Arg Pro Glu Leu Leu Ser Leu Leu Val Arg Asp Glu Ala Ser
          290          295          300
Ser Pro Met Lys Lys Ile Gln Gly Val Gln His Ala Glu Tyr
305          310          315

```

<210> 119

<211> 984

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 119

```

atggatacac tcaaagttgg attggttcag atggcccca tctggttgaa ccgggataaa      60
accctgatca aagttgagga ataatgacag aaagcaggca aacagggctg caacctggta      120
gcttttggtg aagcgctggt tcccggtac cccttctggg tggaacgcac agagggcgcc      180
agattcaatt ccaaagtcca gaaagaactc ttgcacatt acctgatca ggcggtgcag      240
atcgaagcgc gccaccttga tcctctccag gcattagccc aacaatacaa gatggctgtg      300
tacgtgggga cgattgaacg cccgcctgag cggagcggcc acagcctgta ctgctcccta      360

```

```

atatttatag acccagaagg cgagatcggc tcggttcacc gcaagttgat gcccacccat 420
gaggaacgcc tggctctggtc aactggcgat gggcacggcc tgccaacaca ttctctgggc 480
gcctttaccg ttggcggact caactgctgg gaaaactgga tgccgctctc ccgcacagct 540
ctttatgcca tgggagagga tcttcatggt gctgcctggc ccgggagtca gcgcaatact 600
tatgatataa ccaaattcat tgccaaggaa tctcgtcttt atgtgatctc cgtatccggg 660
atgatgaaaa aagaaaatat cctctctgaa attccccaca gccaattgat gctggaaaat 720
agcgaggata ttatggctga tggcggatcc tgtctggctg gaccagatgg agaattggatc 780
atcgagccca tcgtcggaga ggaaaccctg gtaactgctg aactatcaca tcagcgggtc 840
agagaagaaa gacagaattt cgaccaaca ggtcactaca gtcggcctga tgtgaccgcg 900
ctggtagtcg accgcaggcg ccagcagatc ctggagatca ccccgacga aaaaggaaga 960
tcggatgaaa atcaatccct ttaa 984

```

<210> 120

<211> 327

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 120

```

Met Asp Thr Leu Lys Val Gly Leu Val Gln Met Ala Pro Ile Trp Leu
1      5      10     15
Asn Arg Asp Lys Thr Leu Ile Lys Val Glu Glu Tyr Met Gln Lys Ala
20     25     30
Gly Lys Gln Gly Cys Asn Leu Val Ala Phe Gly Glu Ala Leu Val Pro
35     40     45
Gly Tyr Pro Phe Trp Val Glu Arg Thr Glu Gly Ala Arg Phe Asn Ser
50     55     60
Lys Val Gln Lys Glu Leu Phe Ala His Tyr Leu Asp Gln Ala Val Gln
65     70     75     80
Ile Glu Ala Gly His Leu Asp Pro Leu Gln Ala Leu Ala Gln Gln Tyr
85     90     95
Lys Met Ala Val Tyr Val Gly Thr Ile Glu Arg Pro Pro Glu Arg Ser
100    105    110
Gly His Ser Leu Tyr Cys Ser Leu Ile Phe Ile Asp Pro Glu Gly Glu
115    120    125
Ile Gly Ser Val His Arg Lys Leu Met Pro Thr His Glu Glu Arg Leu
130    135    140
Val Trp Ser Thr Gly Asp Gly His Gly Leu Arg Thr His Ser Leu Gly
145    150    155    160
Ala Phe Thr Val Gly Leu Asn Cys Trp Glu Asn Trp Met Pro Leu
165    170    175
Ser Arg Thr Ala Leu Tyr Ala Met Gly Glu Asp Leu His Val Ala Ala
180    185    190
Trp Pro Gly Ser Gln Arg Asn Thr Tyr Asp Ile Thr Lys Phe Ile Ala
195    200    205
Lys Glu Ser Arg Ser Tyr Val Ile Ser Val Ser Gly Met Met Lys Lys
210    215    220
Glu Asn Ile Leu Ser Glu Ile Pro His Ser Gln Leu Met Leu Glu Asn
225    230    235    240
Ser Glu Asp Ile Met Ala Asp Gly Gly Ser Cys Leu Ala Gly Pro Asp
245    250    255
Gly Glu Trp Ile Ile Glu Pro Ile Val Gly Glu Glu Thr Leu Val Thr
260    265    270
Ala Glu Leu Ser His Gln Arg Val Arg Glu Glu Arg Gln Asn Phe Asp
275    280    285
Pro Thr Gly His Tyr Ser Arg Pro Asp Val Thr Arg Leu Val Val Asp
290    295    300
Arg Arg Arg Gln Gln Ile Leu Glu Ile Thr Pro Asp Glu Lys Gly Arg
305    310    315    320

```


Ser Asp Glu Asn Gln Ser Leu
325

<210> 121
<211> 1158
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 121
atgagcaaaa aagttctagg cggcagagaa aaagtaaaag ttgcagtagt tcaggctgcg 60
cccgttttca tggacaagga gaagacgatt gaaaaggctt gcaagctaata aaaagaagcg 120
gggagaaatc gagccgagct catagcgttc tcagagtcatt tcatccccgt ctatcctgca 180
tactataccg tcggctatga aacccttct caagaatgga gagattacgt gattgcgcta 240
caggataact ccgtgctgat tccgagcgag gataccgagg tactcggaca ggctgcaaag 300
gaggcagggg cttatgcagt aataggatgc agcgagatgg acgaccgtcc gggaagccga 360
acagtttaca acacgctcct cttcatcggc aaagacggca aggtcatggg aaggcataga 420
aaactcaaac ccacgttcac ggagagaata tactggggag agggagatgc tggagacata 480
aagggttttg ataccgagat cggcaggatc ggaggcctcg tatgctggga gaaccatatg 540
actctagtca gggccgcgat gatacacagg ggagaggagt ttcatatcgc ggtctggcgc 600
ggaaactgga agggcgcgga aaacaagctt ctccaagcag ataatagccc agggagcgcc 660
ctctgcaacc ttcaatctct cattaagta caccgctttg aggcgggggc gtttgtgctg 720
agcgtttgag gctttttgac gccagaggat ttcccggaaa ggtggcatta tataagggat 780
ggttaaccata ttaactgcga ctgggcactg ggcggaagct caatcgtaaa tcccgcggcg 840
cggtatctcg tcgagcctaa ctttgagaag gatgcaatcc tctatgcgga ttgttatgca 900
aaccagataa aagcagtaaa agcggttttt gattcccttg gccactattc ccgctgggat 960
attgcccaac tggcgataag gcaggaagcc tggaatccag aggtttcttt gatcgattcc 1020
tcttcgactg aagttgagct tccggcagac gagcttcgaa ggatttcgga gaagtttgaa 1080
gtaactgcgg ataagttgga atctttgctt gaggaaattg gaaagattaa aaagcccagg 1140
aaacaagccg gttcctaa 1158

<210> 122
<211> 385
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 122
Met Ser Lys Lys Val Leu Gly Gly Arg Glu Lys Val Lys Val Ala Val
1 5 10 15
Val Gln Ala Ala Pro Val Phe Met Asp Lys Glu Lys Thr Ile Glu Lys
20 25 30
Ala Cys Lys Leu Ile Lys Glu Ala Gly Arg Asn Arg Ala Glu Leu Ile
35 40 45
Ala Phe Ser Glu Ser Phe Ile Pro Val Tyr Pro Ala Tyr Tyr Thr Val
50 55 60
Gly Tyr Glu Thr Pro Ser Gln Glu Trp Arg Asp Tyr Val Ile Ala Leu
65 70 75 80
Gln Asp Asn Ser Val Leu Ile Pro Ser Glu Asp Thr Glu Val Leu Gly
85 90 95
Gln Ala Ala Lys Glu Ala Gly Ala Tyr Ala Val Ile Gly Cys Ser Glu
100 105 110
Met Asp Asp Arg Pro Gly Ser Arg Thr Val Tyr Asn Thr Leu Leu Phe
115 120 125
Ile Gly Lys Asp Gly Lys Val Met Gly Arg His Arg Lys Leu Lys Pro
130 135 140
Thr Phe Thr Glu Arg Ile Tyr Trp Gly Glu Gly Asp Ala Gly Asp Ile

145 150 155 160
 Lys Val Phe Asp Thr Glu Ile Gly Arg Ile Gly Gly Leu Val Cys Trp
 165 170 175
 Glu Asn His Met Thr Leu Val Arg Ala Ala Met Ile His Arg Gly Glu
 180 185 190
 Glu Phe His Ile Ala Val Trp Pro Gly Asn Trp Lys Gly Ala Glu Asn
 195 200 205
 Lys Leu Leu Gln Ala Asp Asn Ser Pro Gly Gly Ala Leu Cys Asn Leu
 210 215 220
 Gln Ser Leu Ile Lys Val His Ala Phe Glu Ala Gly Ala Phe Val Leu
 225 230 235 240
 Ser Ala Cys Gly Phe Leu Thr Pro Glu Asp Phe Pro Glu Arg Trp His
 245 250 255
 Tyr Ile Arg Asp Gly Asn His Ile Asn Cys Asp Trp Ala Leu Gly Gly
 260 265 270
 Ser Ser Ile Val Asn Pro Ala Gly Arg Tyr Leu Val Glu Pro Asn Phe
 275 280 285
 Glu Lys Asp Ala Ile Leu Tyr Ala Asp Cys Tyr Ala Asn Gln Ile Lys
 290 295 300
 Ala Val Lys Ala Val Phe Asp Ser Leu Gly His Tyr Ser Arg Trp Asp
 305 310 315 320
 Ile Ala Gln Leu Ala Ile Arg Gln Glu Ala Trp Asn Pro Glu Val Ser
 325 330 335
 Leu Ile Asp Ser Ser Ser Thr Glu Val Glu Leu Pro Ala Asp Glu Leu
 340 345 350
 Arg Arg Ile Ser Glu Lys Phe Glu Val Thr Ala Asp Lys Leu Glu Ser
 355 360 365
 Leu Leu Glu Glu Ile Gly Lys Ile Lys Lys Pro Arg Lys Gln Ala Gly
 370 375 380
 Ser
 385

<210> 123

<211> 990

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 123

atgtcaactt tcaagatcgc taccgtgcag agtgcaccag tatattatgga ccgcgaagct 60
 accattgaca agacttgcca gctgatcgcc gaagcagcac aagatgacga cgttcgcccta 120
 gtggctcttcc ccgaggcctt tatccccacc tatccggact gggatatggcg tatccctccc 180
 ggacagcacc agatgcttgc cgacctgtac ggggagtgtc tcgagcagtc ggtgacgata 240
 cccagtcttg ctaccgagcg gctctgtcag gctgcaaaga aagcgggctt ttatgtagct 300
 gtgggcctta acgaacgcaa tacagaggcc agcaacgcta ccctgtacaa caccctgctc 360
 tacattgacg ccgagggcaa cttgctaggt aagcaccgaa agctgggtacc gaccgctccc 420
 gaacgcatgg tctgggcaca gggagatggc agtacccttg aggtctacga gacctccttc 480
 ggaaaactca gcgactaat ctgttgggag aactacatgc ctctcgctcg ttatgccctg 540
 tatgcctggg gagtacagct ctatttggct cctacttggg atcgaggcga gccctggctt 600
 tccactctgc ggcacattgc caaggaagga cgagtatacg tggtcggctg ctctatcgcc 660
 ttacgtaagg aagacatccc cgaccgattc gaattcaagg cgaagtacta cgcagaggca 720
 ggagagtggg taaacaaagg tgacagcgtc atcgctcggtc ccgatggcga gctcatcgcc 780
 gggcctctac ataaggaaca ggggatactc tatgctgagc tggacacaag gcagatgcac 840
 gccccaagt ggaacctgga tgtagccgga cactacgcgc gcccgacgt gtttcggctg 900
 accgtgagca aggatggcca tccgatgctc ggcgttgccc aagggcccaa gcatgagccg 960
 caagataaga ccgaagtatt agagggctag 990

<210> 124

<211> 329

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 124

```

Met Ser Thr Phe Lys Ile Ala Thr Val Gln Ser Ala Pro Val Phe Met
 1          5          10          15
Asp Arg Glu Ala Thr Ile Asp Lys Thr Cys Glu Leu Ile Ala Glu Ala
 20          25          30
Ala Gln Asp Asp Val Arg Leu Val Val Phe Pro Glu Ala Phe Ile
 35          40          45
Pro Thr Tyr Pro Asp Trp Val Trp Arg Ile Pro Pro Gly Gln His Gln
 50          55          60
Met Leu Ala Asp Leu Tyr Gly Glu Leu Leu Glu Gln Ser Val Thr Ile
 65          70          75          80
Pro Ser Leu Ala Thr Glu Arg Leu Cys Gln Ala Ala Lys Lys Ala Gly
 85          90          95
Val Tyr Val Ala Val Gly Leu Asn Glu Arg Asn Thr Glu Ala Ser Asn
100          105          110
Ala Thr Leu Tyr Asn Thr Leu Leu Tyr Ile Asp Ala Glu Gly Asn Leu
115          120          125
Leu Gly Lys His Arg Lys Leu Val Pro Thr Ala Pro Glu Arg Met Val
130          135          140
Trp Ala Gln Gly Asp Gly Ser Thr Leu Glu Val Tyr Glu Thr Ser Phe
145          150          155          160
Gly Lys Leu Ser Gly Leu Ile Cys Trp Glu Asn Tyr Met Pro Leu Ala
165          170          175
Arg Tyr Ala Leu Tyr Ala Trp Gly Val Gln Leu Tyr Leu Ala Pro Thr
180          185          190
Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Leu Arg His Ile Ala Lys
195          200          205
Glu Gly Arg Val Tyr Val Val Gly Cys Ser Ile Ala Leu Arg Lys Glu
210          215          220
Asp Ile Pro Asp Arg Phe Glu Phe Lys Ala Lys Tyr Tyr Ala Glu Ala
225          230          235          240
Gly Glu Trp Ile Asn Lys Gly Asp Ser Val Ile Val Gly Pro Asp Gly
245          250          255
Glu Leu Ile Ala Gly Pro Leu His Lys Glu Gln Gly Ile Leu Tyr Ala
260          265          270
Glu Leu Asp Thr Arg Gln Met His Ala Pro Lys Trp Asn Leu Asp Val
275          280          285
Ala Gly His Tyr Ala Arg Pro Asp Val Phe Arg Leu Thr Val Ser Lys
290          295          300
Asp Gly His Pro Met Leu Gly Val Ala Gln Gly Pro Lys His Glu Pro
305          310          315          320
Gln Asp Lys Thr Glu Val Leu Glu Gly
325

```

<210> 125

<211> 1050

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 125

```

atgacaactg taaaaaagac ggtacgcgca gcagcgatcc agatcgacc tgacctcgac      60
agtgcaggcg gtacgctgga caaggtttgc acggccattc aaaaggcggc ggcacaaggc      120

```

```

gcgagctgg tggtttttcc cgaaaccttc ttgccctact atccttactt ttcattcgtg 180
cgcccgccct tcgcatccgg ccggaacac ttgctgctat atgaacgcgc agtggcggtg 240
ccaggcccg taccgatgc cgtctctgcc gtcgcgcgca gccacggcgt ggtggtggtg 300
ctcggcgta atgaacgcga ccatggcacg ctgtacaaca cccaactggt gttcgacgcg 360
aatggcgaac tgggtgtgaa acgcagaaaa atcacgccga cttatcacga gcggatgatc 420
tggggtcaag gcgacggcag cggactcaaa gtagtgcaaa cggcggtcgg ccggctagggc 480
gcgctagcct gttgggaaca ctacaacca ctggcccggt atgcattgat ggcgcaacac 540
gaagaaatcc attgcgcca gtttccggg tccatggtcg ggcaaatatt cgccgaccag 600
atggaagtga cgatacgcca tcacgctctc gagtcggctt gcttcgtggt gaatgccaca 660
ggctggctga ccgatgcgca aatcacatcg atcacgccg accccgcgct acaaaaggca 720
ttacgtggcg gttgctgcac cgccatcgtc tcgccgaag gtgtgctcct ggcagagccg 780
ctacgcagcg gcgaaggcat ggtgatcgcc gatctcgata tggcactcat caccaaacgc 840
aaacggatga tggattcggg cgccactat gcgcggcccg aattgttaag cctgcttgtc 900
gacgaccggc gcaaggtacc ggtatccgcg ctatttgccg acagcaaccc tgccaacggg 960
cacacagttt tcaccccatc cgacatacca acccttgggg gcgcacatca tgcaaacagt 1020
taccaaaccg aaccagcaac tgatcactga 1050

```

<210> 126

<211> 349

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 126

```

Met Thr Thr Val Lys Lys Thr Val Arg Ala Ala Ala Ile Gln Ile Ala
1          5          10          15
Pro Asp Leu Asp Ser Ala Gly Gly Thr Leu Asp Lys Val Cys Thr Ala
20        25        30
Ile Gln Lys Ala Ala Ala Gln Gly Ala Glu Leu Val Val Phe Pro Glu
35        40        45
Thr Phe Leu Pro Tyr Tyr Pro Tyr Phe Ser Phe Val Arg Pro Pro Phe
50        55        60
Ala Ser Gly Pro Glu His Leu Leu Leu Tyr Glu Arg Ala Val Ala Val
65        70        75        80
Pro Gly Pro Val Thr Asp Ala Val Ser Ala Val Ala Arg Ser His Gly
85        90        95
Val Val Val Val Leu Gly Val Asn Glu Arg Asp His Gly Thr Leu Tyr
100       105       110
Asn Thr Gln Leu Val Phe Asp Ala Asn Gly Glu Leu Val Leu Lys Arg
115       120       125
Arg Lys Ile Thr Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly
130       135       140
Asp Gly Ser Gly Leu Lys Val Val Gln Thr Ala Val Gly Arg Leu Gly
145       150       155       160
Ala Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu
165       170       175
Met Ala Gln His Glu Glu Ile His Cys Ala Gln Phe Pro Gly Ser Met
180       185       190
Val Gly Gln Ile Phe Ala Asp Gln Met Glu Val Thr Ile Arg His His
195       200       205
Ala Leu Glu Ser Ala Cys Phe Val Val Asn Ala Thr Gly Trp Leu Thr
210       215       220
Asp Ala Gln Ile Thr Ser Ile Thr Pro Asp Pro Ala Leu Gln Lys Ala
225       230       235       240
Leu Arg Gly Gly Cys Thr Ala Ile Val Ser Pro Glu Gly Val Leu
245       250       255
Leu Ala Glu Pro Leu Arg Ser Gly Glu Gly Met Val Ile Ala Asp Leu
260       265       270
Asp Met Ala Leu Ile Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly

```

```

      275      280      285
His Tyr Ala Arg Pro Glu Leu Leu Ser Leu Leu Val Asp Asp Arg Arg
      290      295      300
Lys Val Pro Val Ser Ala Leu Phe Ala Asp Ser Asn Pro Ala Asn Gly
305      310      315      320
His Thr Val Phe Thr Pro Ser Asp Ile Pro Thr Leu Gly Ser Ala His
      325      330      335
His Ala Asn Ser Tyr Gln Thr Glu Pro Ala Thr Asp His
      340      345

```

<210> 127
 <211> 1005
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 127
atgatatgcac ggaagacaat aagggcggcg gcggtgcaga tagcgctgt gatggaagat      60
cggaaggcga cgaccgacaa ggtgtgcgcc tacattcagg aagcaggcga gaatggagcc      120
gaaattgtgg tgtttcctga aaccttcatt cccaattatc cctatttctc ttttgtaaaa      180
cctcccggtg tggcaggtaa ggatcacctt accttgtatg accaagcggg ggaaatccct      240
agccctacta ccgaccaagt ggggtctatg gccaaaaaat ggggaatcgt agtggtgttg      300
ggcgtgaacg aaagaagcca cggcactttg tacaatgccc aaattgtctt tgacgctact      360
gggtgatatt tattggtgag acgcaaaatc acccctacct atcatgaacg gatgatctgg      420
ggacagggag atggcagtgg attaaaagca gtagacacag ctgtgggaag agtgggcgct      480
ttggcgtggt gggaacacta taatccactt gcgcgctacg cccttatggt agaccatgag      540
gaaattcatt gcagccaatt ccctggctct atggtcggcc ccattttcgg tgaccagata      600
gaagtgcaga ttcgccacca tgcgttgga tgggtgtgt ttgtcatcaa ttccacaggt      660
tggctgtttg aagagcaaat ccaagccatc accgatgac cgaaactgca caaagcattg      720
aaagacggct gtatgaccgc cattatttct cccgaaggcg tgcatttgac caaacctta      780
acagaaggcg aaggcatcat ctacgcctat ctggacatga aactcataga caagcggaaa      840
cggatgatgg actcggtagg acactatgca cgtccagagt tgctctcttt gcatatcaac      900
aatgcagagc aaaaaccagc cgtttacacc tctcctctta ccaaacgga aaccaagaa      960
gacgtaaaaa gctatgatcg caacaaagaa cagcttatcg tctga      1005

```

<210> 128
 <211> 334
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 128
Met Ile Ala Arg Lys Thr Ile Arg Ala Ala Val Gln Ile Ala Pro
 1      5      10      15
Val Met Glu Asp Arg Lys Ala Thr Thr Asp Lys Val Cys Ala Tyr Ile
      20      25      30
Gln Glu Ala Gly Glu Asn Gly Ala Glu Ile Val Val Phe Pro Glu Thr
      35      40      45
Phe Ile Pro Asn Tyr Pro Tyr Phe Ser Phe Val Lys Pro Pro Val Leu
      50      55      60
Ala Gly Lys Asp His Leu Thr Leu Tyr Asp Gln Ala Val Glu Ile Pro
      65      70      75      80
Ser Pro Thr Thr Asp Gln Val Gly Ser Met Ala Lys Lys Trp Gly Ile
      85      90      95
Val Val Val Leu Gly Val Asn Glu Arg Ser His Gly Thr Leu Tyr Asn
      100      105      110
Ala Gln Ile Val Phe Asp Ala Thr Gly Asp Ile Val Leu Val Arg Arg

```

```

      115      120      125
Lys Ile Thr Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly Asp
      130      135      140
Gly Ser Gly Leu Lys Ala Val Asp Thr Ala Val Gly Arg Val Gly Ala
      145      150      155      160
Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met
      165      170      175
Val Asp His Glu Glu Ile His Cys Ser Gln Phe Pro Gly Ser Met Val
      180      185      190
Gly Pro Ile Phe Gly Asp Gln Ile Glu Val Thr Ile Arg His His Ala
      195      200      205
Leu Glu Ser Gly Cys Phe Val Ile Asn Ser Thr Gly Trp Leu Phe Glu
      210      215      220
Glu Gln Ile Gln Ala Ile Thr Asp Asp Pro Lys Leu His Lys Ala Leu
      225      230      235      240
Lys Asp Gly Cys Met Thr Ala Ile Ile Ser Pro Glu Gly Val His Leu
      245      250      255
Thr Lys Pro Leu Thr Glu Gly Glu Gly Ile Ile Tyr Ala Tyr Leu Asp
      260      265      270
Met Lys Leu Ile Asp Lys Arg Lys Arg Met Met Asp Ser Val Gly His
      275      280      285
Tyr Ala Arg Pro Glu Leu Leu Ser Leu His Ile Asn Asn Ala Glu Gln
      290      295      300
Lys Pro Ala Val Tyr Thr Ser Pro Leu Thr Lys Thr Glu Thr Lys Glu
      305      310      315      320
Asp Val Lys Ser Tyr Asp Arg Asn Lys Glu Gln Leu Ile Val
      325      330

```

<210> 129
 <211> 1011
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 129
atgtcagaaa agcgaattat taaagcggct gcagttcaaa tcacaccaga ttttgaatcg      60
catgatggaa ccgtaaagaa ggtttgtaat gtaattgatg aagcgggtgc taaaggtgta      120
cagatcattg tattccctga aacctttatt ccatattacc catatttttc tttcatcact      180
ccaccagtga ctgctggcgc ggagcatttg cggctctatg aaaaaagtgt cgtgatacct      240
ggtcccgtta ctcaagccat ttccgaacgt gcacgcatga ataatatggt tgttgacttt      300
ggtgtaaatg agcgtgataa cggcagtcta tataacaccc agattatttt tgatgctacc      360
ggtgagatgc ttctgaagag aagaaaaatc acacctacct atcatgagcg catgatttgg      420
gggcaaggag atgcttcagg cctgaaggtc gtcgatacgg ctattgggcg agtcggagca      480
ttggcatgct gggagcacta taaccctttg gctagataca gcctcatgac acagcatgaa      540
gaaattcact gtgctcaatt tccaggctcc atggttggtc agatcttcgc agatcaaattg      600
gatgtcacga ttcgatcatc tgccttgagg tcaggttgct tcgtcatcaa ctccactggc      660
tggttaactg atgatcagat caaatctatc accgacgatc ccaaaatgca gaaagcttta      720
agaggtgggt gcaacacggc cattatttct ccagaaggga atcattttaac cgagcctttg      780
cgagaagggt aaggcatggt gattgctgat cttgatatgg cactcatcac caaacgaaaa      840
agaatgatgg actcagttgg ccactacgcc agaccagaac tgttgagctt agcgatcaat      900
gatgtccgg ctactccttc attccagatg aacgaacatc gtcttaaatc agtgcaatta      960
cctatcgtag aggagcttaa aaatgacaac aagcttagca gtggacagta a      1011

```

<210> 130
 <211> 336
 <212> PRT
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 130

```

Met Ser Glu Lys Arg Ile Ile Lys Ala Ala Ala Val Gln Ile Thr Pro
 1          5          10          15
Asp Phe Glu Ser His Asp Gly Thr Val Lys Lys Val Cys Asn Val Ile
      20          25          30
Asp Glu Ala Gly Ala Lys Gly Val Gln Ile Ile Val Phe Pro Glu Thr
      35          40          45
Phe Ile Pro Tyr Tyr Pro Tyr Phe Ser Phe Ile Thr Pro Pro Val Thr
      50          55          60
Ala Gly Ala Glu His Leu Arg Leu Tyr Glu Lys Ser Val Val Ile Pro
      65          70          75          80
Gly Pro Val Thr Gln Ala Ile Ser Glu Arg Ala Arg Met Asn Asn Met
      85          90          95
Val Val Val Leu Gly Val Asn Glu Arg Asp Asn Gly Ser Leu Tyr Asn
      100          105          110
Thr Gln Ile Ile Phe Asp Ala Thr Gly Glu Met Leu Leu Lys Arg Arg
      115          120          125
Lys Ile Thr Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly Asp
      130          135          140
Ala Ser Gly Leu Lys Val Val Asp Thr Ala Ile Gly Arg Val Gly Ala
      145          150          155          160
Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ser Leu Met
      165          170          175
Thr Gln His Glu Glu Ile His Cys Ala Gln Phe Pro Gly Ser Met Val
      180          185          190
Gly Gln Ile Phe Ala Asp Gln Met Asp Val Thr Ile Arg His His Ala
      195          200          205
Leu Glu Ser Gly Cys Phe Val Ile Asn Ser Thr Gly Trp Leu Thr Asp
      210          215          220
Asp Gln Ile Lys Ser Ile Thr Asp Asp Pro Lys Met Gln Lys Ala Leu
      225          230          235          240
Arg Gly Gly Cys Asn Thr Ala Ile Ile Ser Pro Glu Gly Asn His Leu
      245          250          255
Thr Glu Pro Leu Arg Glu Gly Glu Gly Met Val Ile Ala Asp Leu Asp
      260          265          270
Met Ala Leu Ile Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His
      275          280          285
Tyr Ala Arg Pro Glu Leu Leu Ser Leu Ala Ile Asn Asp Ala Pro Ala
      290          295          300
Thr Pro Ser Phe Gln Met Asn Glu His Arg Leu Lys Ser Val Gln Leu
      305          310          315          320
Pro Ile Ala Glu Glu Leu Lys Asn Asp Asn Lys Leu Ser Ser Gly Gln
      325          330          335

```

<210> 131

<211> 1011

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 131

```

atgtcagaaa agcgaattat taaagcggct gcagttcaaa tcacaccaga ttttgaatcg      60
catgatggaa ccgtaaaagaa ggtttgtaat gtaattgatg aagcgggtgc taaagggtgta      120
cagatcattg tattccctga aacctttatt ccatattacc catatttttc tttcatcact      180
ccaccagtga ctgctggcgc ggagcatttg cggtctatg aaaaaagtgt cgtgatacct      240
gtcccggtta ctcaagacat ttccgaacgt gcacgcatga ataatatggt tgttgtactt      300
ggtgtaaatg agcgtgataa cggcagtcta tataacaccc agattatttt tgatgctacc      360

```

```

ggtgagatgc ttctgaagag aagaaaaatc acacctacct atcatgagcg catgatttgg 420
gggcaaggag atgcttcagg cctgaagggtc gtcgatacgg ctattgggag agtcggagca 480
ttggcatgct gggagcacta taaccctttg gctagataca gcctcatgac acagcatgaa 540
gaaattcact gtgctcaatt tccaggctcc atgggttggtc agatcttcgc agatcaaatg 600
gatgtcacga ttcgtcatca tgccttgagg tcagggttgc tgcgtcatcaa ctccactggc 660
tggttaactg atgatcagat caaatctatc accgacgac ccaaaatgca gaaagcttta 720
agaggtggtt gcaacacggc cattatttct ccagaaggga atcattttaac cgagcctttg 780
cgagaagggt aaggcatggt gattgctgat cttgatatgg cactcatcac caaacgaaaa 840
agaatgatgg actcagttgg ccactacgcc agaccagaac tgttgagctt agcgatcaat 900
gatgtccgg ctactccttc attccagatg aacgaacatc gtcttaaatc agtgcaatta 960
cctatcgagc aggagcttaa aaatgacaac aagcttagca gtggacagta a 1011

```

<210> 132

<211> 336

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 132

```

Met Ser Glu Lys Arg Ile Ile Lys Ala Ala Val Gln Ile Thr Pro
1          5          10          15
Asp Phe Glu Ser His Asp Gly Thr Val Lys Lys Val Cys Asn Val Ile
20        25        30
Asp Glu Ala Gly Ala Lys Gly Val Gln Ile Ile Val Phe Pro Glu Thr
35        40        45
Phe Ile Pro Tyr Tyr Pro Tyr Phe Ser Phe Ile Thr Pro Pro Val Thr
50        55        60
Ala Gly Ala Glu His Leu Arg Leu Tyr Glu Lys Ser Val Val Ile Pro
65        70        75        80
Gly Pro Val Thr Gln Asp Ile Ser Glu Arg Ala Arg Met Asn Asn Met
85        90        95
Val Val Val Leu Gly Val Asn Glu Arg Asp Asn Gly Ser Leu Tyr Asn
100       105       110
Thr Gln Ile Ile Phe Asp Ala Thr Gly Glu Met Leu Leu Lys Arg Arg
115       120       125
Lys Ile Thr Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly Asp
130       135       140
Ala Ser Gly Leu Lys Val Val Asp Thr Ala Ile Gly Arg Val Gly Ala
145       150       155       160
Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ser Leu Met
165       170       175
Thr Gln His Glu Glu Ile His Cys Ala Gln Phe Pro Gly Ser Met Val
180       185       190
Gly Gln Ile Phe Ala Asp Gln Met Asp Val Thr Ile Arg His His Ala
195       200       205
Leu Glu Ser Gly Cys Phe Val Ile Asn Ser Thr Gly Trp Leu Thr Asp
210       215       220
Asp Gln Ile Lys Ser Ile Thr Asp Asp Pro Lys Met Gln Lys Ala Leu
225       230       235       240
Arg Gly Gly Cys Asn Thr Ala Ile Ile Ser Pro Glu Gly Asn His Leu
245       250       255
Thr Glu Pro Leu Arg Glu Gly Glu Gly Met Val Ile Ala Asp Leu Asp
260       265       270
Met Ala Leu Ile Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His
275       280       285
Tyr Ala Arg Pro Glu Leu Leu Ser Leu Ala Ile Asn Asp Ala Pro Ala
290       295       300
Thr Pro Ser Phe Gln Met Asn Glu His Arg Leu Lys Ser Val Gln Leu
305       310       315       320

```


Pro Ile Ala Glu Glu Leu Lys Asn Asp Asn Lys Leu Ser Ser Gly Gln
 325 330 335

<210> 133
 <211> 1026
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 133
 atgtcgacca agcggatcgt acgcgccgct gccgttcagc tggcaccgga tctggagcgg 60
 ccggagggca cactggagaa ggtttgcgcg gccatcgaca aggcggcggg ggacggtgtg 120
 cagctcatcg tcttcccga gaccttcgta cgtactacc cgtacttctc ttctgtgcgt 180
 gcgccgggtc cgatgggtgc cgagcacatg cggttatacg agcgcgcggg agcggtgccc 240
 ggtccagtaa cggccaccgt ggcggagcgg gcaaaagcgc acgcgatggt cgtcgtgctg 300
 ggtgtaaacg agcgcgatca cggctcactg tataacgcgc aactgatctt cgacgagacc 360
 ggccgtctcg tctcaaacg ccgcaagatc actccgacct atcacgagcg catggtgtgg 420
 gggcaggggc acggcagcgg ccttaagggt gtagacaccg gtatcggcag gatcggagcc 480
 ctgcctgctg gggagcacta caaccgctc gcgcgctatg cgctcatggc gcagcacgaa 540
 gagattcatt gcgcgcagtt tccgggctcg atggtggggc cgatcttcgc ggatcagatc 600
 gaggtcacga tccgccatca cgcgctggag tcgggctgct tcgtcgtcaa tgcgaccggc 660
 tggctgacac ccgaacagat cgcgtcgatc acaccggacg cgggtctgca aaaggcaatc 720
 agcggggggt gcaacaccgc gatcatctcg ccggaggggc tgcacctggc ccgcccgttg 780
 cgagaagggt agggcatggt cgtggccgac ctgcacatgg cgctcatcac caaacgcaaa 840
 cgcatgatgg attcgtggg tcaactacgt cgcccggagt tgctcagcct gcgcatcgat 900
 agccgcgccg cttcgccgat gtcgtcacia atggaaatac ccgggagcct gcatgaaatc 960
 accagccacg atgtccagcc agcaactgat gaccgagctc cagtcctccg gcttgaggtt 1020
 ggctga 1026

<210> 134
 <211> 341
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 134
 Met Ser Thr Lys Arg Ile Val Arg Ala Ala Val Gln Leu Ala Pro
 1 5 10 15
 Asp Leu Glu Arg Pro Glu Gly Thr Leu Glu Lys Val Cys Ala Ala Ile
 20 25 30
 Asp Lys Ala Ala Gly Asp Gly Val Gln Leu Ile Val Phe Pro Glu Thr
 35 40 45
 Phe Val Pro Tyr Tyr Pro Tyr Phe Ser Phe Val Arg Ala Pro Val Ala
 50 55 60
 Met Gly Ala Glu His Met Arg Leu Tyr Glu Arg Ala Val Ala Val Pro
 65 70 75 80
 Gly Pro Val Thr Ala Thr Val Ala Glu Arg Ala Lys Ala His Ala Met
 85 90 95
 Val Val Val Leu Gly Val Asn Glu Arg Asp His Gly Ser Leu Tyr Asn
 100 105 110
 Ala Gln Leu Ile Phe Asp Glu Thr Gly Arg Leu Val Leu Lys Arg Arg
 115 120 125
 Lys Ile Thr Pro Thr Tyr His Glu Arg Met Val Trp Gly Gln Gly Asp
 130 135 140
 Gly Ser Gly Leu Lys Val Val Asp Thr Gly Ile Gly Arg Ile Gly Ala
 145 150 155 160
 Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met

```

      165      170      175
Ala Gln His Glu Ile His Cys Ala Gln Phe Pro Gly Ser Met Val
      180      185      190
Gly Pro Ile Phe Ala Asp Gln Ile Glu Val Thr Ile Arg His His Ala
      195      200      205
Leu Glu Ser Gly Cys Phe Val Val Asn Ala Thr Gly Trp Leu Thr Pro
      210      215      220
Glu Gln Ile Ala Ser Ile Thr Pro Asp Ala Gly Leu Gln Lys Ala Ile
      225      230      235
Ser Gly Gly Cys Asn Thr Ala Ile Ile Ser Pro Glu Gly Val His Leu
      245      250      255
Ala Pro Pro Leu Arg Glu Gly Glu Gly Met Val Val Ala Asp Leu Asp
      260      265      270
Met Ala Leu Ile Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His
      275      280      285
Tyr Ala Arg Pro Glu Leu Leu Ser Leu Arg Ile Asp Ser Arg Ala Ala
      290      295      300
Ser Pro Met Ser Ser Gln Met Glu Ile Pro Gly Ser Leu His Glu Ile
      305      310      315
Thr Ser His Asp Val Gln Pro Ala Thr Asp Asp Arg Ala Pro Val Leu
      325      330      335
Arg Leu Glu Val Gly
      340

```

<210> 135

<211> 1011

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 135

```

atgtcagaca agcgaatcat taaagcggct gcagttcaaa tcactcctga ctttgactca      60
gcagatggaa ccgttaagaa agtgtgcaag gtaatcgatg aagcaggtgc aaagggagtt      120
caaattattg tattcccgga aaccttcac cttactacc catacttttc attcattaca      180
cctccagtcg ctgctggcgc tgagcattta aagctttatg agaaaagtgt cgtgatacct      240
ggcccgggta cccaagcgat tgccgagcga gccagggtta atcagatggt tgcgtgctt      300
ggtgtcaacg agcgagataa cggtagcctc tacaacacac aattgatctt tgataccaac      360
ggcgaactgc tacttaaaag aagaaaaatc acccctacct accatgaacg tatgatctgg      420
gggcaagggt atgcatcagg tctcaaagta gttgaaacag agatcgcccg agtaggtgcc      480
ttggcttggt gggaacacta caaccctctg gccagatatg cactcatgac acagcatgaa      540
gaaattcact gtgcgcaatt cccaggctct atggttgccc agatatttgc cgatcagatg      600
gatgtcacta tccgacatca cgccttagag tcaggctgct tcgtcatcaa cgccactggc      660
tggctcaccg acgcgcaaat ccaatcgatt actgatgacc caaaaatgca aaaagcatta      720
cgtggcggct gcaacacagc catcatctcc cccgaagggg tgcaactaac agagccacta      780
cgtgaaggag aaggcatggt gattgccaat cttgatatgg cactcatcac aaaacgaaaa      840
agaatgatgg attcggtagg ccattattca agaccagaat tattaagcct ggcaattaac      900
gacaaaccag caactacaac attttcaatg actgaggggc gtactcaaac agagccattt      960
cgaatcgag aggagttgaa aaatgacgac aagcttagca ctggaaacta a      1011

```

<210> 136

<211> 336

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 136

Met Ser Asp Lys Arg Ile Ile Lys Ala Ala Val Gln Ile Thr Pro

1	5	10	15
Asp Phe Asp	Ser Ala Asp Gly Thr	Val Lys Lys Val Cys Lys Val Ile	
	20	25	30
Asp Glu Ala	Gly Ala Lys Gly Val	Gln Ile Ile Val Phe Pro Glu Thr	
	35	40	45
Phe Ile Pro	Tyr Tyr Pro Tyr Phe Ser Phe Ile Thr	Pro Pro Val Thr	
	50	55	60
Ala Gly Ala	Glu His Leu Lys Leu Tyr Glu Lys Ser Val Val Ile Pro		
	65	70	75
Gly Pro Val	Thr Gln Ala Ile Ala Glu Arg Ala Arg Val Asn Gln Met		
	85	90	95
Val Val Val	Leu Gly Val Asn Glu Arg Asp Asn Gly Ser Leu Tyr Asn		
	100	105	110
Thr Gln Leu	Ile Phe Asp Thr Asn Gly Glu Leu Leu Leu Lys Arg Arg		
	115	120	125
Lys Ile Thr	Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly Asp		
	130	135	140
Ala Ser Gly	Leu Lys Val Val Glu Thr Glu Ile Ala Arg Val Gly Ala		
	145	150	155
Leu Ala Cys	Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met		
	165	170	175
Thr Gln His	Glu Glu Ile His Cys Ala Gln Phe Pro Gly Ser Met Val		
	180	185	190
Gly Gln Ile	Phe Ala Asp Gln Met Asp Val Thr Ile Arg His His Ala		
	195	200	205
Leu Glu Ser	Gly Cys Phe Val Ile Asn Ala Thr Gly Trp Leu Thr Asp		
	210	215	220
Ala Gln Ile	Gln Ser Ile Thr Asp Asp Pro Lys Met Gln Lys Ala Leu		
	225	230	235
Arg Gly Gly	Cys Asn Thr Ala Ile Ile Ser Pro Glu Gly Val His Leu		
	245	250	255
Thr Glu Pro	Leu Arg Glu Gly Glu Gly Met Val Ile Ala Asn Leu Asp		
	260	265	270
Met Ala Leu	Ile Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His		
	275	280	285
Tyr Ser Arg	Pro Glu Leu Leu Ser Leu Ala Ile Asn Asp Lys Pro Ala		
	290	295	300
Thr Thr Thr	Phe Ser Met Thr Glu Gly Arg Thr Gln Thr Glu Pro Phe		
	305	310	315
Arg Ile Ala	Glu Glu Leu Lys Asn Asp Asp Lys Leu Ser Thr Gly Asn		
	325	330	335

<210> 137

<211> 978

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 137

atggctattg	tcaaggccgc	ggcgggtgcag	atcagtcagg	tgctctacag	tcgcgccggc	60
acagtggaca	aggtcgctgc	gaagatccgc	gagctgggcc	gacgaggggg	cgagttcgcc	120
gtcttccccc	agaccgtcat	tccctactat	ccctacttct	ctttcgtgca	gccccctac	180
accagggcca	ccgaacacct	gcgcctgctc	gaggaatcgg	tgaccgtgcc	ctccgccgaa	240
accgacgcga	tcgccaaggc	cgctcgcgag	gccggcatgg	tcgtctccat	cggcgtcaac	300
gagcgcgacg	gcggaaccat	ctacaacacc	caactcctct	tcgacgccga	cggcactctc	360
atccagcgcc	gccgcaagat	cacccccacc	tatcacgaac	gcattggtctg	ggggcaggga	420
gacgggtcag	gtctgcgcgc	cgctcgacagt	gcggtcggcc	gcacgggcca	gctcgccctgc	480
tgggagcact	accagccact	ggcccggtac	gccctcatcg	ctgacggcga	gcagatccac	540
gcgcgcgatgt	accccggcgc	cttcgggcgc	gatctgttctg	ccgagcagat	cgaggtcaac	600

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atccgccagc acgccctgga atccgccagc ttcgtcgtca acgccaccgc ctggctcgac 660
gccgatcagc aggccagat cgccaaggac accggaggcc cgggtcccgc cttctccggt 720
ggcttcttca ccgccatcgt cgaccccgaa ggccgtatca tcggcgaccc cctcaccagc 780
ggcgaaggcg aagtgatcgc cgacctcgat ctgctcttca tcaaccgccg caagcgccctc 840
atggacgcca gtggacacta ccagccgccc gaaattctta gcttcacatt gaccggtgca 900
ccggcgccctt atgtcaagag cgcggcgtgc cggggaaccc cgggtacgac cgtggccgag 960
gagggacggt ccgcttag

```

<210> 138

<211> 325

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 138

```

Met Ala Ile Val Lys Ala Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
1      5      10      15
Ser Arg Ala Gly Thr Val Asp Lys Val Val Ala Lys Ile Arg Glu Leu
20     25     30
Gly Arg Arg Gly Val Glu Phe Ala Val Phe Pro Glu Thr Val Ile Pro
35     40     45
Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Pro Pro Tyr Thr Gln Ala Thr
50     55     60
Glu His Leu Arg Leu Leu Glu Glu Ser Val Thr Val Pro Ser Ala Glu
65     70     75     80
Thr Asp Ala Ile Ala Lys Ala Ala Arg Glu Ala Gly Met Val Val Ser
85     90     95
Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Ile Tyr Asn Thr Gln Leu
100    105    110
Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln Arg Arg Arg Lys Ile Thr
115    120    125
Pro Thr Tyr His Glu Arg Met Val Trp Gly Gln Gly Asp Gly Ser Gly
130    135    140
Leu Arg Ala Val Asp Ser Ala Val Gly Arg Ile Gly Gln Leu Ala Cys
145    150    155    160
Trp Glu His Tyr Gln Pro Leu Ala Arg Tyr Ala Leu Ile Ala Asp Gly
165    170    175    180
Glu Gln Ile His Ala Ala Met Tyr Pro Gly Ala Phe Gly Gly Asp Leu
185    190
Phe Ala Glu Gln Ile Glu Val Asn Ile Arg Gln His Ala Leu Glu Ser
195    200    205
Ala Ser Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp Gln Gln
210    215    220
Ala Gln Ile Ala Lys Asp Thr Gly Gly Pro Val Pro Ala Phe Ser Gly
225    230    235    240
Gly Phe Phe Thr Ala Ile Val Asp Pro Glu Gly Arg Ile Ile Gly Asp
245    250    255
Pro Leu Thr Ser Gly Glu Gly Glu Val Ile Ala Asp Leu Asp Leu Ala
260    265    270
Leu Ile Asn Arg Arg Lys Arg Leu Met Asp Ala Ser Gly His Tyr Gln
275    280    285
Pro Pro Glu Ile Leu Ser Phe Thr Leu Thr Gly Ala Pro Ala Pro Tyr
290    295    300
Val Lys Ser Ala Ala Cys Arg Gly Thr Pro Gly Thr Thr Val Ala Glu
305    310    315    320
Glu Gly Arg Ser Ala
325

```

<210> 139

<211> 999
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 139
 atgaaaacaa cggttaccgt tgcctgcgtt caggccgccc ccgtatttat ggatttagaa 60
 ggcaccgtag ataaaacaat caccctcatc tctgaagccg cacagaaagg cgcggagctc 120
 atcgcttttc cggagacctg gatacccggt tacccgtggt tcttatggct gaactcgccc 180
 gccacaaata tgcccctggt ttatcagtat catcagaact ctctggtgct ggacagtacc 240
 caggcgaagc gaattgcgga tgcggcacgg cagaataaca tcaactgtcgc tctgggcttc 300
 agcgaacgcg atcatggaag cctctatatc gcacagtggc tgattggcag cgacggggag 360
 accattggca tccggcgcaa gctcaaggcc acgcacgtgg agcgtacgct gttcggcgaa 420
 agcgacggct cctccctgac cacctgggag acacctctgg gtaacgtcgg ggccctctgc 480
 tgctgggagc acctgcagcc gctgtcccgc tatgcaatgt attcccagca tgaggagatc 540
 cacatcgctg cctggcccag tttcagtctc tacaccagtg caacggccgc actgggtcct 600
 gacgtcaata cggcggtctc acgcctctat gccgcggagg ggcagtgtct cgtgatagcc 660
 ccgtgtgccg tggtttctga tgaaatgatt gatttactct gtcctgatga tgaccggaga 720
 gcgttactca gtgccggagg gggacatgcc cgtatttacg gcccgacgg aagagaactc 780
 gtcacccctc tcggggaaaa tgaggaagga ctgcttatcg ctgagctcga ctctgctgcg 840
 attacctttg ccaaactggc ggcagaccgg gttggccact attcccgtcc tgacgtgacc 900
 cgctcctttt ttaatccttc agccaacaag actgtgatta aacgacattc gcctcctgag 960
 ttaattgccg agcagactgc agaagaagag gaggagtag 999

<210> 140
 <211> 332
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 140
 Met Lys Thr Thr Val Thr Val Ala Cys Val Gln Ala Ala Pro Val Phe
 1 5 10 15
 Met Asp Leu Glu Gly Thr Val Asp Lys Thr Ile Thr Leu Ile Ser Glu
 20 25 30
 Ala Ala Gln Lys Gly Ala Glu Leu Ile Ala Phe Pro Glu Thr Trp Ile
 35 40 45
 Pro Gly Tyr Pro Trp Phe Leu Trp Leu Asn Ser Pro Ala Thr Asn Met
 50 55 60
 Pro Leu Val Tyr Gln Tyr His Gln Asn Ser Leu Val Leu Asp Ser Thr
 65 70 75 80
 Gln Ala Lys Arg Ile Ala Asp Ala Ala Arg Gln Asn Asn Ile Thr Val
 85 90 95
 Ala Leu Gly Phe Ser Glu Arg Asp His Gly Ser Leu Tyr Ile Ala Gln
 100 105 110
 Trp Leu Ile Gly Ser Asp Gly Glu Thr Ile Gly Ile Arg Arg Lys Leu
 115 120 125
 Lys Ala Thr His Val Glu Arg Thr Leu Phe Gly Glu Ser Asp Gly Ser
 130 135 140
 Ser Leu Thr Thr Trp Glu Thr Pro Leu Gly Asn Val Gly Ala Leu Cys
 145 150 155 160
 Cys Trp Glu His Leu Gln Pro Leu Ser Arg Tyr Ala Met Tyr Ser Gln
 165 170 175
 His Glu Glu Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu Tyr Thr
 180 185 190
 Ser Ala Thr Ala Ala Leu Gly Pro Asp Val Asn Thr Ala Ala Ser Arg
 195 200 205

```

Leu Tyr Ala Ala Glu Gly Gln Cys Phe Val Ile Ala Pro Cys Ala Val
 210                215                220
Val Ser Asp Glu Met Ile Asp Leu Leu Cys Pro Asp Asp Asp Arg Arg
225                230                235                240
Ala Leu Leu Ser Ala Gly Gly Gly His Ala Arg Ile Tyr Gly Pro Asp
 245                250                255
Gly Arg Glu Leu Val Thr Pro Leu Gly Glu Asn Glu Glu Gly Leu Leu
 260                265                270
Ile Ala Glu Leu Asp Ser Ala Ala Ile Thr Phe Ala Lys Leu Ala Ala
 275                280                285
Asp Pro Val Gly His Tyr Ser Arg Pro Asp Val Thr Arg Leu Leu Phe
 290                295                300
Asn Pro Ser Ala Asn Lys Thr Val Ile Lys Arg His Ser Pro Pro Glu
305                310                315                320
Leu Ile Ala Glu Gln Thr Ala Glu Glu Glu Glu
 325                330

```

<210> 141
 <211> 1026
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 141
atggtgttca aggcagcgac tgttcatgca gctccggtat tcatggacaa ggaagcgtcg      60
atagataagg ctatcgacct catcaagaag gccggtcagg aagggattaa gcttctgggt      120
tttccggaag cgtttattcc gggctatccg tattttatcg aatgctatcc gccgcttgcg      180
caggtggaag cgctcgccca gtacactgac gcttccgtgg agatcgacgg cccggaagtc      240
acccggcttc agcaggtagc caaggcgga ggcgttgtag tcgtcatggg catcagcgaa      300
cgaatggctg agacccgaac ctgcttcaac tcgcaggtgt tcattgacgt cgacggcacg      360
ctgctcggcg tgcacgcaa gctgcagccg acttatgccg agcgcaaggt atgggcacag      420
ggcggtgggt atacgctgag gacctacaag agctcgcttg gcgtgctcgg cggtcttgcc      480
tgctgggagc acacgatgaa cctcgcgcgg caggccctga tcatgcagag cgagcagatc      540
catgcggctg catggcccgg actatcgacg atgcgaggtt tcgagcccgt ggccgatatc      600
cagatcgacg ccatgatgaa gactcacgcg cttaccgcac agtgctgggt gctttcggcc      660
ggcaatcccg tcgaccggac ctgcctcgac tggatggaaa agaacatcgg accgcaggat      720
tacgtcaccg agggcgcgcg atggagcgcc gttatccatc cgttcaacag ctatctcggc      780
ggccctcaca cgggccttga ggaaaagctg gtcgtcgcgg agatcaatct ggacgatctc      840
aagttcgtca aagtctggct cgacagcaaa gggcaactat ctcggccgga aatcctgaaa      900
cttggcgctc accaaaagca gatttggcct gatgaacatt tgctggcgcg gcaggatgtg      960
accgagttgc tgaggcgga tatcatcgaa tacccttgc aactgttgca agaccgcgcg      1020
caatag                                           1026

```

<210> 142
 <211> 341
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 142
Met Val Phe Lys Ala Ala Thr Val His Ala Ala Pro Val Phe Met Asp
 1                5                10                15
Lys Glu Ala Ser Ile Asp Lys Ala Ile Asp Leu Ile Lys Lys Ala Gly
 20                25                30
Gln Glu Gly Ile Lys Leu Leu Val Phe Pro Glu Thr Phe Ile Pro Gly
 35                40                45
Tyr Pro Tyr Phe Ile Glu Cys Tyr Pro Pro Leu Ala Gln Val Glu Ala

```

50	55	60
Leu Ala Gln Tyr Thr Asp	Ala Ser Val Glu Ile Asp	Gly Pro Glu Val
65	70	75
Thr Arg Leu Gln Gln Val	Ala Lys Ala Ala Gly	Val Ala Val Val Met
85	90	95
Gly Ile Ser Glu Arg Met	Ala Glu Thr Arg Thr	Cys Phe Asn Ser Gln
100	105	110
Val Phe Ile Asp Val Asp	Gly Thr Leu Leu Gly	Val His Arg Lys Leu
115	120	125
Gln Pro Thr Tyr Ala Glu	Arg Lys Val Trp Ala	Gln Gly Gly Gly Tyr
130	135	140
Thr Leu Arg Thr Tyr Lys	Ser Ser Leu Gly Val	Leu Gly Gly Leu Ala
145	150	155
Cys Trp Glu His Thr Met	Asn Leu Ala Arg Gln	Ala Leu Ile Met Gln
165	170	175
Ser Glu Gln Ile His Ala	Ala Ala Trp Pro	Gly Leu Ser Thr Met Arg
180	185	190
Gly Phe Glu Pro Val Ala	Asp Ile Gln Ile Asp	Ala Met Met Lys Thr
195	200	205
His Ala Leu Thr Ala Gln	Cys Trp Val Leu Ser	Ala Gly Asn Pro Val
210	215	220
Asp Arg Thr Cys Leu Asp	Trp Met Glu Lys Asn	Ile Gly Pro Gln Asp
225	230	235
Tyr Val Thr Glu Gly Gly	Gly Trp Ser Ala Val	Ile His Pro Phe Asn
245	250	255
Ser Tyr Leu Gly Gly Pro	His Thr Gly Leu Glu	Glu Lys Leu Val Val
260	265	270
Gly Glu Ile Asn Leu Asp	Asp Leu Lys Phe Val	Lys Val Trp Leu Asp
275	280	285
Ser Lys Gly His Tyr Ala	Arg Pro Glu Ile Leu	Lys Leu Gly Val Asn
290	295	300
Gln Lys Gln Ile Trp Pro	Asp Glu His Leu Leu	Ala Arg Gln Asp Val
305	310	315
Thr Glu Leu Leu Glu Ala	Asp Ile Ile Glu Tyr	Pro Leu Gln Leu Leu
325	330	335
Gln Asp Arg Ala Gln		
340		

<210> 143

<211> 1122

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 143

atgacgatca	ttgcaggcgc	ggttcatgcg	gcgccggtat	tcatggatgt	cgatgccact	60
atcgacaagg	catgcgaaat	cattcgcaag	gcaggcaaag	acggaatcga	gcttctcgtc	120
ttccctgagg	ttttcgtacc	cggtacccc	tacttcatcg	agtgtatcc	gaccttgaac	180
caaaccgctg	cgctggccgc	ctatacggat	gcctcgatcg	aggttccagg	cccggaaagtc	240
cggcgcttgc	aggtggccgc	acatcaggcc	ggcgtgatgg	ttgtgatggg	cgtgagcgag	300
cgtctgcgcg	gatctcgcac	ctgcttcaac	agccagggtg	tcatcgaccg	tgacggcacc	360
ttgctgggcg	tgcaccgcaa	actccagccg	acctatgtcg	agcgcacgtg	ctggggccag	420
ggcggcgggac	acaccctcaa	ggtattcgac	agcacactgg	gcaaggtggg	cggactggcc	480
tgctgggagc	acacgatgaa	cctcgcgcg	catgcgttga	tcgcccaggg	tatccagatc	540
catgccgcgg	cctggcctgg	gctttcgaca	atggccgggt	tcgaagcggt	ggctgacgtc	600
cagatcgacg	cgatgatgaa	aactcatgcg	ttgagcgcg	aatgctttgt	cgtatcggcc	660
gcaaaccctg	tgatcagac	ctgcctggag	tgatggaga	aacacctcgg	cccgcagcaa	720
ctcgttaccg	ccggcgagg	ctggtcggca	atcgtccatc	ctttctgtgg	ttatatcgcc	780
gccctcaca	ccggtgccga	ggagaaggtt	ctggtaggcg	aaatcaatct	ggacgacctc	840

```

aagcaggtca aggtatgggt tgattccgca gggtcattatg cgcgcccgga agtcgtgcaa      900
ttgcgcgacg ccctggagag ccgtggcaat tatcgcgttg cgctgacccg cgacgccgac      960
accttcgtgc cgctggaaga ccgcgtgcgc tttgcgcgcc agcagaacgc cgacctcttc     1020
atctcgatcc acgcgcgacgc caacgccaac cacgatgcgc gcggggctgg cttcacttcg     1080
aagggttgaac acctttccac gggcatttta ccaggcgatt ga                        1122

```

<210> 144

<211> 373

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 144

```

Met Thr Ile Ile Ala Gly Ala Val His Ala Ala Pro Val Phe Met Asp
 1          5          10          15
Val Asp Ala Thr Ile Asp Lys Ala Cys Glu Ile Ile Arg Lys Ala Gly
      20          25          30
Lys Asp Gly Ile Glu Leu Leu Val Phe Pro Glu Val Phe Val Pro Gly
      35          40          45
Tyr Pro Tyr Phe Ile Glu Cys Tyr Pro Thr Leu Asn Gln Thr Ala Ala
      50          55          60
Leu Ala Ala Tyr Thr Asp Ala Ser Ile Glu Val Pro Gly Pro Glu Val
      65          70          75          80
Arg Arg Leu Gln Val Ala Ala His Gln Ala Gly Val Met Val Val Met
      85          90          95
Gly Val Ser Glu Arg Leu Arg Gly Ser Arg Thr Cys Phe Asn Ser Gln
      100          105          110
Val Phe Ile Asp Arg Asp Gly Thr Leu Leu Gly Val His Arg Lys Leu
      115          120          125
Gln Pro Thr Tyr Val Glu Arg Ile Val Trp Gly Gln Gly Gly His
      130          135          140
Thr Leu Lys Val Phe Asp Ser Thr Leu Gly Lys Val Gly Gly Leu Ala
      145          150          155          160
Cys Trp Glu His Thr Met Asn Leu Ala Arg His Ala Leu Ile Ala Gln
      165          170          175
Gly Ile Gln Ile His Ala Ala Ala Trp Pro Gly Leu Ser Thr Met Ala
      180          185          190
Gly Phe Glu Ala Val Ala Asp Val Gln Ile Asp Ala Met Met Lys Thr
      195          200          205
His Ala Leu Ser Ala Gln Cys Phe Val Val Ser Ala Ala Asn Pro Val
      210          215          220
Asp Gln Thr Cys Leu Glu Trp Met Glu Lys His Leu Gly Pro Gln Gln
      225          230          235          240
Leu Val Thr Ala Gly Gly Gly Trp Ser Ala Ile Val His Pro Phe Cys
      245          250          255
Gly Tyr Ile Ala Ala Pro His Thr Gly Ala Glu Glu Lys Val Leu Val
      260          265          270
Gly Glu Ile Asn Leu Asp Asp Leu Lys Gln Val Lys Val Trp Val Asp
      275          280          285
Ser Ala Gly His Tyr Ala Arg Pro Glu Val Val Gln Leu Arg Asp Ala
      290          295          300
Leu Glu Ser Arg Gly Asn Tyr Arg Val Ala Leu Thr Arg Asp Ala Asp
      305          310          315          320
Thr Phe Val Pro Leu Glu Asp Arg Val Arg Phe Ala Arg Gln Gln Asn
      325          330          335
Ala Asp Leu Phe Ile Ser Ile His Ala Asp Ala Asn Ala Asn His Asp
      340          345          350
Ala Arg Gly Ala Gly Phe Thr Ser Lys Val Glu Asn Leu Ser Thr Gly
      355          360          365

```


Ile Leu Pro Gly Asp
370

<210> 145
<211> 1014
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 145
atgggcatca cccacccgaa ctacaaggtc gcagtgggtcc aggctgcgcc ggtctggttg 60
aacctcgagg caacgggtcga gaagacaatc aggtatatatg aagaggcggc caaggctgga 120
gcgaagctga tagcgtttcc ggaaacctgg attccgggct atccatggca catttggtac 180
ggaacgcccc catgggcaat cggttaagggc ttcgtccagc gctatttcga caactcgctc 240
agctatgaca gcccgcctcgc gcggcagatc gctgacgcgc cagcaaagag caagatcacg 300
gttggtctcg gcctctccga gcgcgacggt ggaagcctat acatcgcgca atgggtgac 360
ggaccagatg gcgagaccat cgcgaaagcgc cgcaagctgc gtccgaccca cgtcgagcgc 420
acgggtgttcg gtgacgggtga cggcagccac atcgccgtgc atgaccgatc cgatctgggc 480
cggctcgggg cggttggtcgtg ctgggagcac gtgcagccgt tgacgaaatt cgcgatgtac 540
gcgcagaacg agcaggttca cgtggcagca tggccgagct tctcgatgta cgaacccttt 600
gcgcattgcgc tgggttgagg gacgaacaac gcggtcagca aggtctacgc ggtcgaggga 660
tcgtgcttcg tgctcgctcc ctgtgccgtt atttcgcaag cgatgggtga cgagatgtgc 720
gacactcccc acaagcgcgga gcttggtcac gccggcggcg gccacgcggt gatttacggc 780
cctgacggaa gcccgcctcgc agaaaagctc ggggaaaacg aagaggggct tctctacgcg 840
acggtaaatc ttgctgcgat cgggggtgcc aagaatgccg cggatccggc cgggcactat 900
tcgcgtccgg acgttctaag gctgctattc aacaagagcc cggcccgaag agtggagcat 960
tttgcgtgc cgcacgagca gctcgagatc ggggcaggcc cgtctggcga ctga 1014

<210> 146
<211> 337
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 146
Met Gly Ile Thr His Pro Asn Tyr Lys Val Ala Val Val Gln Ala Ala
1 5 10 15
Pro Val Trp Leu Asn Leu Glu Ala Thr Val Glu Lys Thr Ile Arg Tyr
20 25 30
Ile Glu Glu Ala Ala Lys Ala Gly Ala Lys Leu Ile Ala Phe Pro Glu
35 40 45
Thr Trp Ile Pro Gly Tyr Pro Trp His Ile Trp Ile Gly Thr Pro Ala
50 55 60
Trp Ala Ile Gly Lys Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
65 70 75 80
Ser Tyr Asp Ser Pro Leu Ala Arg Gln Ile Ala Asp Ala Ala Lys
85 90 95
Ser Lys Ile Thr Val Val Leu Gly Leu Ser Glu Arg Asp Gly Gly Ser
100 105 110
Leu Tyr Ile Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
115 120 125
Lys Arg Arg Lys Leu Arg Pro Thr His Val Glu Arg Thr Val Phe Gly
130 135 140
Asp Gly Asp Gly Ser His Ile Ala Val His Asp Arg Ser Asp Leu Gly
145 150 155 160
Arg Leu Gly Ala Leu Cys Cys Trp Glu His Val Gln Pro Leu Thr Lys
165 170 175

Phe Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ala Trp Pro
 180 185 190
 Ser Phe Ser Met Tyr Glu Pro Phe Ala His Ala Leu Gly Trp Glu Thr
 195 200 205
 Asn Asn Ala Val Ser Lys Val Tyr Ala Val Glu Gly Ser Cys Phe Val
 210 215 220
 Leu Ala Pro Cys Ala Val Ile Ser Gln Ala Met Val Asp Glu Met Cys
 225 230 235 240
 Asp Thr Pro Asp Lys Arg Glu Leu Val His Ala Gly Gly Gly His Ala
 245 250 255
 Val Ile Tyr Gly Pro Asp Gly Ser Pro Leu Ala Glu Lys Leu Gly Glu
 260 265 270
 Asn Glu Glu Gly Leu Leu Tyr Ala Thr Val Asn Leu Ala Ala Ile Gly
 275 280 285
 Val Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
 290 295 300
 Val Leu Arg Leu Leu Phe Asn Lys Ser Pro Ala Arg Arg Val Glu His
 305 310 315 320
 Phe Ala Leu Pro His Glu Gln Leu Glu Ile Gly Ala Gly Pro Ser Gly
 325 330 335
 Asp

<210> 147
 <211> 1098
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 147
 atgacccagc acgagaccac tgcccggagg ctggcagctg tgcattgccgc gcctgtgttc 60
 atggacaccg acgcgaccat cgacaagggt atcggtctcg tcgaacaggc cggccgcgaa 120
 ggcatcgaa tcctgggtgtt ccccgagacc ttcgtgcctg gttacccta ctggatcgag 180
 tgctatccgc cgctgcagca ggtggccgcc aacgcgcagt acacggacgc ctccgtcgag 240
 gtgcctggtc cggagatcaa gcgggtgcag gcggcctgtg cccgcgctgg cgtcgaagtc 300
 gtcctcggcg tcagcgagcg actcaggggt accaggacat gcttcaactc ccaggtgttc 360
 atcgacgcg acgggagcct gtcggcggtg caccgcaagc tgcagccgac gtacgtggag 420
 cgcatcggtg gggcccaggg cggaggcgcg accctgtcgg tgttcggctc ccgctccggc 480
 cggatcggcg gtctggcctg ctgggagcac acgatgaacc tggctcgtaa ggcaactgctt 540
 gagcaggagc agcagatcca cgcggcggtg tggcctgccc tgtcgacgat ggcgggggttc 600
 gagaccgtcg cggacgcccc gatcgaggcc atgatgaaga cccatgcgct cacggcacag 660
 gtgttcgtca tctgcgcgtc caaccgggtg gacggcactt gcctggaatg gatgcgggac 720
 aacctcgggtg aacagaagtt cgtgaccgcc ggaggggggt ggtccgcggt catccacccc 780
 ttcaactcct tcctcggcgg gccgcatacc ggtttggagg agaagctcgt cagcgcgacg 840
 atcgacttct ccgacatccg cttggtcaag gcctgggttg attcgaaggg gcactacgcg 900
 cggcccaggg tcctgcgact cgcggtcgac cgcaagccac tgtggcacga cgagtgcgag 960
 gtgccgggac aggcgcaggt acgcacccgc gctgcttctc tggcagtgca ggagcaccgg 1020
 gtggtgctgc ctacgggggc ggcgcggccc gctccgcaag actgggacac ctctgcggcg 1080
 caggagctga cttcctga 1098

<210> 148
 <211> 365
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 148

```

Met Thr Gln His Glu Thr Thr Ala Arg Arg Leu Ala Ala Val His Ala
 1          5          10          15
Ala Pro Val Phe Met Asp Thr Asp Ala Thr Ile Asp Lys Val Ile Gly
          20          25          30
Phe Val Glu Gln Ala Gly Arg Glu Gly Ile Glu Leu Leu Val Phe Pro
          35          40          45
Glu Thr Phe Val Pro Gly Tyr Pro Tyr Trp Ile Glu Cys Tyr Pro Pro
          50          55          60
Leu Gln Gln Val Ala Ala Asn Ala Gln Tyr Thr Asp Ala Ser Val Glu
65          70          75          80
Val Pro Gly Pro Glu Ile Lys Arg Val Gln Ala Ala Cys Ala Arg Ala
          85          90          95
Gly Val Glu Val Val Leu Gly Val Ser Glu Arg Leu Arg Gly Thr Arg
          100          105          110
Thr Cys Phe Asn Ser Gln Val Phe Ile Asp Ala Asp Gly Ser Leu Leu
          115          120          125
Gly Val His Arg Lys Leu Gln Pro Thr Tyr Val Glu Arg Ile Val Trp
          130          135          140
Ala Gln Gly Gly Gly Ala Thr Leu Ser Val Phe Gly Ser Arg Ser Gly
145          150          155          160
Arg Ile Gly Gly Leu Ala Cys Trp Glu His Thr Met Asn Leu Ala Arg
          165          170          175
Gln Ala Leu Leu Glu Gln Glu Gln Ile His Ala Ala Ala Trp Pro
          180          185          190
Ala Leu Ser Thr Met Ala Gly Phe Glu Thr Val Ala Asp Ala Gln Ile
          195          200          205
Glu Ala Met Met Lys Thr His Ala Leu Thr Ala Gln Val Phe Val Ile
          210          215          220
Cys Ala Ser Asn Pro Val Asp Gly Thr Cys Leu Glu Trp Met Arg Asp
225          230          235          240
Asn Leu Gly Glu Gln Lys Phe Val Thr Ala Gly Gly Gly Trp Ser Ala
          245          250          255
Val Ile His Pro Phe Asn Ser Phe Leu Gly Gly Pro His Thr Gly Leu
          260          265          270
Glu Glu Lys Leu Val Ser Ala Thr Ile Asp Phe Ser Asp Ile Arg Leu
          275          280          285
Val Lys Ala Trp Val Asp Ser Lys Gly His Tyr Ala Arg Pro Glu Val
          290          295          300
Leu Arg Leu Ala Val Asp Arg Lys Pro Leu Trp His Asp Glu Cys Glu
305          310          315          320
Val Pro Gly Gln Ala Gln Val Arg Thr Arg Ala Ala Ser Leu Ala Val
          325          330          335
Gln Glu His Pro Val Val Leu Pro Gln Gly Ala Ala Arg Pro Ala Pro
          340          345          350
Gln Asp Trp Asp Thr Ser Ala Ala Gln Glu Leu Thr Ser
          355          360          365

```

<210> 149

<211> 942

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 149

```

atgacgaagc ttgagaagggt ggtcgcggcg gcggtccagg cgacgccgga gttcctcgac      60
cgcgaggcga ccgtcgagaa ggccgtgcgg ctgatcaagg aagcggccgg ggagggcgcc      120
ggcctgatcg tgttccccga gacgttcac cgcacgtacc cggactgggt ctggcgcgcg      180
ccggcctggg acggcccatc cgcggacctg tacgcaatgc tgctggagaa cgcggtggag      240
atccccgggc cggtgacgga gaccctgggg aaggcggcga agcaggccaa ggccttcgtg      300

```

```

tcgatgggcg tcaacgagcg cgagccgggc ggcgggacga tctacaacac gcaggtcacg 360
ttcggaccgg acgggagcgt gctcggcaag caccgcaagc tgatgccgac cggcggcgag 420
cgctgtgtgt gggggatggg cgacgggtcg atgctccagg tctatgacac gccgttcggc 480
cgcctgggcg ggctgatctg ctgggagaac tacatgccgc tcgcgcgcta ctcgatgtac 540
gccaaagggcg tggacgtcta cgttgcgccc acgtgggaca acagcgacat gtgggtggcg 600
acgctccgcc acatcgccaa ggaggggccc ctgtacgtga tcggcgtggc gccgctgctg 660
cgcggttcgg acgtccccga cgacgtgccg gggaaggccc agctgtgggg cggcgatgac 720
gactggatgt cgcgcggcct ctccaccatc gtcgcgccgg gcggcgaggt gctggccggg 780
ccgctgacgg aggaggaagg catcctctac gcggagatcg acccggcgag agcccgttcg 840
tcacggcacc agttcgatcc ggtggggcac tactcgcgcc ccgacgtgtt tcggctcgtc 900
gtggacgagt cgcccaagcc ccagacgtcc ggcccgggct ag 942

```

<210> 150

<211> 313

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 150

```

Met Thr Lys Leu Glu Lys Val Val Ala Ala Ala Val Gln Ala Thr Pro
 1          5          10          15
Glu Phe Leu Asp Arg Glu Ala Thr Val Glu Lys Ala Val Arg Leu Ile
 20          25          30
Lys Glu Ala Ala Gly Glu Gly Ala Gly Leu Ile Val Phe Pro Glu Thr
 35          40          45
Phe Ile Pro Thr Tyr Pro Asp Trp Val Trp Arg Ala Pro Ala Trp Asp
 50          55          60
Gly Pro Ser Ala Asp Leu Tyr Ala Met Leu Leu Glu Asn Ala Val Glu
 65          70          75          80
Ile Pro Gly Pro Val Thr Glu Thr Leu Gly Lys Ala Ala Lys Gln Ala
 85          90          95
Lys Ala Phe Val Ser Met Gly Val Asn Glu Arg Glu Pro Gly Gly Gly
100          105          110
Thr Ile Tyr Asn Thr Gln Val Thr Phe Gly Pro Asp Gly Ser Val Leu
115          120          125
Gly Lys His Arg Lys Leu Met Pro Thr Gly Gly Glu Arg Leu Val Trp
130          135          140
Gly Met Gly Asp Gly Ser Met Leu Gln Val Tyr Asp Thr Pro Phe Gly
145          150          155          160
Arg Leu Gly Gly Leu Ile Cys Trp Glu Asn Tyr Met Pro Leu Ala Arg
165          170          175
Tyr Ser Met Tyr Ala Lys Gly Val Asp Val Tyr Val Ala Pro Thr Trp
180          185          190
Asp Asn Ser Asp Met Trp Val Ala Thr Leu Arg His Ile Ala Lys Glu
195          200          205
Gly Arg Leu Tyr Val Ile Gly Val Ala Pro Leu Leu Arg Gly Ser Asp
210          215          220
Val Pro Asp Asp Val Pro Gly Lys Ala Glu Leu Trp Gly Gly Asp Asp
225          230          235          240
Asp Trp Met Ser Arg Gly Phe Ser Thr Ile Val Ala Pro Gly Gly Glu
245          250          255
Val Leu Ala Gly Pro Leu Thr Glu Glu Gly Ile Leu Tyr Ala Glu
260          265          270
Ile Asp Pro Ala Arg Ala Arg Ser Ser Arg His Gln Phe Asp Pro Val
275          280          285
Gly His Tyr Ser Arg Pro Asp Val Phe Arg Leu Val Val Asp Glu Ser
290          295          300
Pro Lys Pro Gln Thr Ser Gly Pro Gly
305          310

```

<210> 151
 <211> 993
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 151
 atgagagtcg ttaaagccgc cgcggtccaa ctgaaaccag tcctttatag ccgtgagggg 60
 acagtcgata acgtcgtcaa gaagatccac gagctgggcc aacaaggagt gcagttcgca 120
 acgttcccgc aaaccgtggt gccttactat ccgtactttt cgatcgtgca gtccggctat 180
 caaatccttg ccggcgggtga gttcctaaag ctgcttgatc agtcagtgc cgtgccatct 240
 cttgccaccg aagcgatcgc cgaggcctgc aggcaagcgg gcgtcgttgt ctccatcggc 300
 gtcaacgagc gtgacggggg aactctgtac aatacgcaac ttctctttga tgccgacggc 360
 acgttgattc aaagacgacg caagatcacg cccacccatt acgagcgcac ggtctggggc 420
 cagggcgatg gctcagggtt acggcgggtt gacagcaagg tcgcgcgcac tggccaactg 480
 gcttggtttg agcactacaa cccgcttgcc cgttacgcca tgatggccga tggcgagcaa 540
 atccactctg cgatgttccc gggctccatg ttcggcgatg cgttttcaga gaaggtggaa 600
 atcaacgtaa ggcagcatgc aatggagtct ggtgctttg tcgtctgcgc tacggcctgg 660
 ctggatgccg accaacaggc acaaatcatg aaggacacag gctgcgagat cgggccgatc 720
 tcgggcgggt gcttcaccgc tatcgtgaca cccgacggga cgctgatagg cgaacccatc 780
 cactcgggcg aaggcggttg tattgccgac ctgcatttca agctcatcga caagcggaag 840
 cacgtggtgg acacgcgcgg ccactacagc cggccagaat tgctcagcct cctaattgat 900
 cggactccca cggcacacat acacgaacgg aacgagcaac cgaagtcggc cgttgagcaa 960
 gactcgaga atgtattcac cgctattgct taa 993

<210> 152
 <211> 330
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 152
 Met Arg Val Val Lys Ala Ala Ala Val Gln Leu Lys Pro Val Leu Tyr
 1 5 10 15
 Ser Arg Glu Gly Thr Val Asp Asn Val Val Lys Lys Ile His Glu Leu
 20 25 30
 Gly Gln Gln Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
 35 40 45
 Tyr Tyr Pro Tyr Phe Ser Ile Val Gln Ser Gly Tyr Gln Ile Leu Ala
 50 55 60
 Gly Gly Glu Phe Leu Lys Leu Leu Asp Gln Ser Val Thr Val Pro Ser
 65 70 75 80
 Leu Ala Thr Glu Ala Ile Gly Glu Ala Cys Arg Gln Ala Gly Val Val
 85 90 95
 Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn Thr
 100 105 110
 Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln Arg Arg Arg Lys
 115 120 125
 Ile Thr Pro Thr His Tyr Glu Arg Met Val Trp Gly Gln Gly Asp Gly
 130 135 140
 Ser Gly Leu Arg Ala Val Asp Ser Lys Val Ala Arg Ile Gly Gln Leu
 145 150 155 160
 Ala Cys Phe Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Met Met Ala
 165 170 175
 Asp Gly Glu Gln Ile His Ser Ala Met Phe Pro Gly Ser Met Phe Gly
 180 185 190

```

Asp Ala Phe Ser Glu Lys Val Glu Ile Asn Val Arg Gln His Ala Met
      195                200                205
Glu Ser Gly Cys Phe Val Val Cys Ala Thr Ala Trp Leu Asp Ala Asp
      210                215                220
Gln Gln Ala Gln Ile Met Lys Asp Thr Gly Cys Glu Ile Gly Pro Ile
225      230                235                240
Ser Gly Gly Cys Phe Thr Ala Ile Val Thr Pro Asp Gly Thr Leu Ile
      245                250                255
Gly Glu Pro Ile His Ser Gly Glu Gly Val Cys Ile Ala Asp Leu Asp
      260                265                270
Phe Lys Leu Ile Asp Lys Arg Lys His Val Val Asp Thr Arg Gly His
      275                280                285
Tyr Ser Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro Thr
      290                295                300
Ala His Ile His Glu Arg Asn Glu Gln Pro Lys Ser Ala Val Glu Gln
305      310                315                320
Asp Ser Gln Asn Val Phe Thr Ala Ile Ala
      325                330

```

<210> 153
 <211> 1074
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 153
atgccaaacg caagaaagat tgttgagacc gtggcccaag ttgcacagga attcttcgac      60
actgaagcga atctcggtaa agcgatagcg gcgattcaca atgctgcgaa gcaaggcgca      120
gatatcgctc tcttcgccga atgctatttg ggccaatata catattgggc gcaattttac      180
gacaactctg ccaagaacta ttccaagggt tggacggccc tgtacgacgg tgcgatcact      240
gtgggtggcg atgaatgccg ggctattgct gctgcggcta gacagtccaa gattcatgtc      300
gtcatggggt gcaatgagct atccgaccga gccggcgcg caacgttata caacagcctc      360
ttgtttttcg accgaaaggg cgagttgatc ggtcgacacc ggaattgatg gccgtcgatg      420
cacgagcggg tgatccatgg cacaggcgac ggaagagact tgaatgttta cgataccgat      480
atcggtatgt tgggtgggtt gatttgcttg gagcaccata tgcgctctc gaagtatgcc      540
atggcgacta tgggtgaaga agttcatgtt gcaagctggc ctgggatgtg gcgcgaggga      600
gacgcggaac tcggtgagag gatggtcgaa gcggatcttg gggcgccgtt tgtttgtgac      660
gccgaatttg cgatccgaga atatgcggca gagacaggaa atttcgttct aagcgcgtct      720
ggatattttc cgaaggacaa tatatccgat gagtggcgcg aagcgattcc aaaccttcaa      780
gcgcagtggg ctgtgggagg gagttctatc gtggcaccgg ggggctccta tctgggtccca      840
ccactcatta atgaggagaa gatcctctgc gccgaactcg atttcaatct caggcgtctt      900
tggaagcctt ggatcgatcc gattggtcac tattcgctc ccgatgttta tagcctgcaa      960
ctgcataacg ttgctgggag tgagtattcc tatcaggccg tagatttgaa gcgcacgcca     1020
aagccccaat cgctgtgggt agatgcgtcc gaggaagacg gtgcgctgaa ttga      1074

```

<210> 154
 <211> 357
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 154
Met Pro Asn Ala Arg Lys Ile Val Gly Ala Val Ala Gln Val Ala Gln
      1           5           10           15
Glu Phe Phe Asp Thr Glu Ala Asn Leu Gly Lys Ala Ile Ala Ala Ile
      20           25           30
His Asn Ala Ala Lys Gln Gly Ala Asp Ile Val Val Phe Ala Glu Cys

```

<400> 155						
atgggcatcg	aacatccgaa	atacaagggtg	gccgtggtgc	aggccgcgcc	ggcctggctc	60
gatctcgacg	gctcgatcaa	gaagggcgatt	gcgctgatcg	aggaagcggc	cgccaagggc	120
gctaagctga	tcgctttccc	cgaaaccttc	attcccggtg	atccctggga	catctggctg	180
gactcgccga	cctgggcgat	cgggcgcggc	ttgtgcagc	gctacttcga	taactcgctg	240
gcctacgcga	gccccgaagc	cgaaaagctg	cgcgccgcgg	tcaagaaggc	caagctcact	300
gccgtgattg	gcctgtcgga	gcgcgacggc	ggcagcctct	atatagcgca	atggctgatt	360
ggccctgatg	gcgagaccat	cgaaaaacgc	agaaaagctgc	ggccaacgca	cgcggaacgc	420
accgtttttg	gcgaggggtga	cggcagcgac	cttgccgtgc	acgaccggcc	cggaatcggg	480
cggctgggag	cgctgtgtgc	ctgggagcac	ctgcaacgcg	tttcgaatac	cgcgctgtat	540
gcgcgaacg	aacaggtcca	tgtcgcgtca	tggccagact	tctcgtctca	gcaccccttc	600

```

gcgccggcgc tcggcgccga ggtcaacaat gcggcttccc gcgtctacgc ggtcgagggc 660
tcgtgcttcg tgctggcgcc gtgcgccacg gtttcgcaag ccatgatcga cgagctgtgt 720
gaccggcccg acaagcatgc gctgttgacg gccggtggcg gacacgccgc gatttacggc 780
ccggacggca gctcgatcgc ggagaagctg ccgcaggacg cggagggcct gttgatcgcc 840
gagatcgatc tcggggcgat cgggggtgccc aagaatgcag ccgaccggcg cggtcattat 900
tcgcggccgg acgtgacgag actcctgctg aacaagaacc ggatgcgaag ggtcgaggag 960
tttgcgctgc cggtcgatcc ggtcgcaacg accgaggagg agcaagtcgc gacgccgtcg 1020
aggcccagcc aggccgcgta a 1041

```

<210> 156
 <211> 346
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 156
 Met Gly Ile Glu His Pro Lys Tyr Lys Val Ala Val Val Gln Ala Ala
 1 5 10 15
 Pro Ala Trp Leu Asp Leu Asp Gly Ser Ile Lys Lys Ala Ile Ala Leu
 20 25 30
 Ile Glu Glu Ala Ala Ala Lys Gly Ala Lys Leu Ile Ala Phe Pro Glu
 35 40 45
 Thr Phe Ile Pro Gly Tyr Pro Trp His Ile Trp Leu Asp Ser Pro Ala
 50 55 60
 Trp Ala Ile Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
 65 70 75 80
 Ala Tyr Asp Ser Pro Gln Ala Glu Lys Leu Arg Ala Ala Val Lys Lys
 85 90 95
 Ala Lys Leu Thr Ala Val Ile Gly Leu Ser Glu Arg Asp Gly Gly Ser
 100 105 110
 Leu Tyr Ile Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
 115 120 125
 Lys Arg Arg Lys Leu Arg Pro Thr His Ala Glu Arg Thr Val Phe Gly
 130 135 140
 Glu Gly Asp Gly Ser Asp Leu Ala Val His Asp Arg Pro Gly Ile Gly
 145 150 155 160
 Arg Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys
 165 170 175
 Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ser Trp Pro
 180 185 190
 Ser Phe Ser Leu Tyr Asp Pro Phe Ala Pro Ala Leu Gly Ala Glu Val
 195 200 205
 Asn Asn Ala Ala Ser Arg Val Tyr Ala Val Glu Gly Ser Cys Phe Val
 210 215 220
 Leu Ala Pro Cys Ala Thr Val Ser Gln Ala Met Ile Asp Glu Leu Cys
 225 230 235 240
 Asp Arg Pro Asp Lys His Ala Leu Leu His Ala Gly Gly Gly His Ala
 245 250 255
 Ala Ile Tyr Gly Pro Asp Gly Ser Ser Ile Ala Glu Lys Leu Pro Gln
 260 265 270
 Asp Ala Glu Gly Leu Leu Ile Ala Glu Ile Asp Leu Gly Ala Ile Gly
 275 280 285
 Val Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
 290 295 300
 Val Thr Arg Leu Leu Leu Asn Lys Asn Arg Met Arg Arg Val Glu Glu
 305 310 315 320
 Phe Ala Leu Pro Val Asp Pro Val Ala Thr Thr Glu Glu Glu Gln Val
 325 330 335
 Ala Thr Pro Ser Arg Pro Ser Gln Ala Ala

340

345

<210> 157

<211> 1011

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 157

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atgagagtcg ttaaagctgc tgcgggtccaa ctgagtcctcg tgctgtatag ccgtgagggg 60
acagtagaaa aggtcggttcg gaagatccac gagcttggcg atcaaggagt cgagttcgcc 120
acgttcccg agaccgtagt gccctactat ccgtacttct cggccgtcca gacgccgatt 180
cagaacatgc acggcccggg gcacctgaag ttgctcgagc aatcggtgac cgtcccgtcg 240
cccgccaccg acgcgatcgg cgacgcctgc cgccacgccg gcgtcgctcg ctcgatcggc 300
gtcaacgaac gcgatggcgg cagcatctac aacacgcagc tcctgttcga cgccgacggc 360
accttgatcc agcgcggcgg aaagatcacg ccgaccttct acgaacgaat ggtctgggga 420
caggggtgacg gttcggggct gcgcgcctgc gacagccgcg taggacgcat cggccagctc 480
gcctgtttcg agcactacaa cccgctggcg cgctacgcca tgatggccga cggcgagcag 540
attcactccg cgatgtaccg cggctccatc tttggagacg cattcgcgca gaaaatcgag 600
atcaacatcc gccagcacgc gctcgagtcg ggtgcgttcg tcgtcaacgc caccgcctgg 660
ctcgatgccg accagcaggg gcggatcatg aaggataccg gctgcaccat cgaaccgatc 720
tcgggcgggt gcttcaccgc catcgtcacc ccggacggga ccctgctggg cgaagcgata 780
cgttcggggg agggagtggt ggtcgccgat ctcgacttca cgctgatcga caggcgcaag 840
caagtgatgg actctcgtgg tcactacagt cggccggagt tgctcagcct tctgatcgac 900
cgcacacca cgcacacct acacgaacgc gaagcgcacc ccagagcaag tgaggactgg 960
caaggttccg agagtctgcg cgccatgcag gcctcggcac cgaaggtctg a 1011

```

<210> 158

<211> 336

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 158

```

Met Arg Val Val Lys Ala Ala Ala Val Gln Leu Ser Pro Val Leu Tyr
 1           5           10           15
Ser Arg Glu Gly Thr Val Glu Lys Val Val Arg Lys Ile His Glu Leu
 20           25           30
Gly Asp Gln Gly Val Glu Phe Ala Thr Phe Pro Glu Thr Val Val Pro
 35           40           45
Tyr Tyr Pro Tyr Phe Ser Ala Val Gln Thr Pro Ile Gln Asn Met His
 50           55           60
Gly Pro Glu His Leu Lys Leu Leu Glu Gln Ser Val Thr Val Pro Ser
 65           70           75           80
Pro Ala Thr Asp Ala Ile Gly Asp Ala Cys Arg His Ala Gly Val Val
 85           90           95
Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Ile Tyr Asn Thr
100           105           110
Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln Arg Arg Arg Lys
115           120           125
Ile Thr Pro Thr Phe Tyr Glu Arg Met Val Trp Gly Gln Gly Asp Gly
130           135           140
Ser Gly Leu Arg Ala Val Asp Ser Arg Val Gly Arg Ile Gly Gln Leu
145           150           155           160
Ala Cys Phe Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Met Met Ala
165           170           175
Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Ile Phe Gly

```

	180		185		190										
Asp	Ala	Phe	Ala	Gln	Lys	Ile	Glu	Ile	Asn	Ile	Arg	Gln	His	Ala	Leu
	195						200					205			
Glu	Ser	Gly	Ala	Phe	Val	Val	Asn	Ala	Thr	Ala	Trp	Leu	Asp	Ala	Asp
	210					215					220				
Gln	Gln	Ala	Arg	Ile	Met	Lys	Asp	Thr	Gly	Cys	Thr	Ile	Glu	Pro	Ile
225					230					235				240	
Ser	Gly	Gly	Cys	Phe	Thr	Ala	Ile	Val	Thr	Pro	Asp	Gly	Thr	Leu	Leu
			245						250					255	
Gly	Glu	Ala	Ile	Arg	Ser	Gly	Glu	Gly	Val	Val	Val	Ala	Asp	Leu	Asp
		260						265					270		
Phe	Thr	Leu	Ile	Asp	Arg	Arg	Lys	Gln	Val	Met	Asp	Ser	Arg	Gly	His
	275						280					285			
Tyr	Ser	Arg	Pro	Glu	Leu	Leu	Ser	Leu	Leu	Ile	Asp	Arg	Thr	Pro	Thr
	290					295					300				
Ala	His	Leu	His	Glu	Arg	Glu	Ala	His	Pro	Arg	Ala	Ser	Glu	Asp	Trp
305				310						315				320	
Gln	Gly	Ser	Glu	Ser	Leu	Arg	Ala	Met	Gln	Ala	Ser	Ala	Pro	Lys	Val
			325					330						335	

<210> 159

<211> 930

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 159

atgtcatcaa	ccgtgacggt	tgccattatt	caggcagcac	ccgtgtatta	tgacctgcct	60
gccacgctgg	acaaagccgc	caaactggtg	gcggatgcgg	cggcacaggg	cgcaacgctg	120
attgtcttcg	gcgagacatg	gtttccgggg	tatccggcat	ggctggatta	ctgcccacat	180
gtcgcgctgt	ggaatcatcc	cccgaccaag	caggatattg	agcgcctgca	tcgcaacagc	240
atcgtgtgtc	caagcaagga	actcgatttt	ctgggggcgc	tggcacgcaa	gcatcagggtg	300
gtgctgggtg	tgagcattaa	tgaacgtgtg	gagcaggggc	cggggcatgg	cacgctgtat	360
aacacgctgc	tcacgattga	cgccgatggc	acgctggcaa	atcatcatcg	caaactgatg	420
ccgacctata	ccgagcgcat	ggtgtggggc	atgggcgacg	gggtgggggt	gcaagcggtg	480
gatactgccg	tcgggcgcgt	aggcggctta	atctgctggg	aacactggat	gccgttggca	540
cgccagacca	tgacatcatg	cgccgaacag	attcataatt	ccgtcttccc	aaccgtccat	600
gagatgcacc	agattgccag	ccgccagtat	gcctttgaag	ggcggacgtt	tgtgctgacc	660
gttggcggca	ttcttgccgc	acaggacttg	cccgcggaac	tggaacgccc	cgccgatttg	720
ccgcccacgc	agcttgtcca	gcgcggcggc	agcgccatta	tcgcgcggga	tggtcggtat	780
ctggcggggtc	cagtctataa	tgaggaaacc	atcctgaccg	caacgctgga	tttgggcgag	840
atcatccgcg	agagcatgac	gctggatgtc	accggacatt	atgcccgccc	ggatgttttt	900
gacctgaccg	tgaagcgcag	ccgaccatga				930

<210> 160

<211> 309

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 160

Met	Ser	Ser	Thr	Val	Thr	Val	Ala	Ile	Ile	Gln	Ala	Ala	Pro	Val	Tyr
1			5					10					15		
Tyr	Asp	Leu	Pro	Ala	Thr	Leu	Asp	Lys	Ala	Ala	Lys	Leu	Val	Ala	Asp
		20					25					30			
Ala	Ala	Ala	Gln	Gly	Ala	Thr	Leu	Ile	Val	Phe	Gly	Glu	Thr	Trp	Phe
	35						40					45			

Pro Gly Tyr Pro Ala Trp Leu Asp Tyr Cys Pro Asn Val Ala Leu Trp
 50 55 60
 Asn His Pro Pro Thr Lys Gln Val Phe Glu Arg Leu His Arg Asn Ser
 65 70 75 80
 Ile Ala Val Pro Ser Lys Glu Leu Asp Phe Leu Gly Ala Leu Ala Arg
 85 90 95
 Lys His Gln Val Val Leu Val Leu Ser Ile Asn Glu Arg Val Glu Gln
 100 105 110
 Gly Ala Gly His Gly Thr Leu Tyr Asn Thr Leu Leu Thr Ile Asp Ala
 115 120 125
 Asp Gly Thr Leu Ala Asn His His Arg Lys Leu Met Pro Thr Tyr Thr
 130 135 140
 Glu Arg Met Val Trp Gly Met Gly Asp Gly Val Gly Leu Gln Ala Val
 145 150 155 160
 Asp Thr Ala Val Gly Arg Val Gly Gly Leu Ile Cys Trp Glu His Trp
 165 170 175
 Met Pro Leu Ala Arg Gln Thr Met His Ile Ser Gly Glu Gln Ile His
 180 185 190
 Ile Ser Val Phe Pro Thr Val His Glu Met His Gln Ile Ala Ser Arg
 195 200 205
 Gln Tyr Ala Phe Glu Gly Arg Thr Phe Val Leu Thr Val Gly Gly Ile
 210 215 220
 Leu Ala Ala Gln Asp Leu Pro Ala Glu Leu Glu Arg Pro Ala Asp Leu
 225 230 235 240
 Pro Pro Thr Gln Leu Val Gln Arg Gly Gly Ser Ala Ile Ile Ala Pro
 245 250 255
 Asp Gly Arg Tyr Leu Ala Gly Pro Val Tyr Asn Glu Glu Thr Ile Leu
 260 265 270
 Thr Ala Thr Leu Asp Leu Gly Glu Ile Ile Arg Glu Ser Met Thr Leu
 275 280 285
 Asp Val Thr Gly His Tyr Ala Arg Pro Asp Val Phe Asp Leu Thr Val
 290 295 300
 Lys Arg Ser Arg Pro
 305

<210> 161
 <211> 1008
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 161
 atgaccacca tccgcgcgcg cgccgtgcag tttagcccg tgctgtactc gcgccaggcc 60
 accgtcgaca agctgtgccg caccctgctg gaactgggccc gcgaaggggt gcagttcgcg 120
 gtattcccgg aaaccgtggt gccgtactac ccatattttt ccttcgtgca gccaccgttc 180
 gccatgggca aacaacacct gttgctgctc gagcaatccg tcaactgtgcc ctctgacgtc 240
 acccggcaga tcggtgaggg ctgccgggaa gcggggatcg tcgccagcat cggcgtcaac 300
 gaacgcgacg gcggcactat ttataacgcg cagtgtgctg tcgatgccga cggcagcctg 360
 attcagcagc ggcgcaagat caccgccgacc tatcacgaac gcatggtctg ggggcagggc 420
 gatggttccg gcctgcgcgc cgtggacagt gcggtggggc gtatcggttc cctggcctgc 480
 tgggaacatt acaacccctt ggcgcgctac gcgctgatgg ccgatggcga acagattcat 540
 gtggcgatgt ttcccggctc cctggtcggc gacatctttg ccgagcagat cgaagtcacc 600
 atccgccacc acgcccctgga aagcggctgc ttcgtggtca acgccacggc ttggctggat 660
 gccgaccagc agggccggat catgcaggac accggctgcg agttggggcc gatttcggc 720
 ggctgtttta ccgcgatcat ttcccggag ggcaagggtc tcggcgagcc gctgcgcagc 780
 ggcaaggggg tgggtcattg tgacctgcac ctggccctga tcgacaagcg caaacgcgat 840
 atggattcgg tcggtcacta cagccgcccg gaactgctca gcctgcttat cgaccgcagc 900
 ccgaccgccc acgtgcatga acttgccgcc gcgttaatc ctgccaggga gtctgatcca 960
 ctagtgcga cctgcaggcg cgcgagctcc agcttttgtt ccctttag 1008

<210> 162
 <211> 335
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 162
 Met Thr Thr Ile Arg Ala Ala Ala Val Gln Phe Ser Pro Val Leu Tyr
 1 5 10 15
 Ser Arg Gln Ala Thr Val Asp Lys Leu Cys Arg Thr Leu Leu Glu Leu
 20 25 30
 Gly Arg Glu Gly Val Gln Phe Ala Val Phe Pro Glu Thr Val Val Pro
 35 40 45
 Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Pro Pro Phe Ala Met Gly Lys
 50 55 60
 Gln His Leu Leu Leu Leu Glu Gln Ser Val Thr Val Pro Ser Asp Val
 65 70 75 80
 Thr Arg Gln Ile Gly Glu Ala Cys Arg Glu Ala Gly Ile Val Ala Ser
 85 90 95
 Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Ile Tyr Asn Ala Gln Leu
 100 105 110
 Leu Phe Asp Ala Asp Gly Ser Leu Ile Gln Gln Arg Arg Lys Ile Thr
 115 120 125
 Pro Thr Tyr His Glu Arg Met Val Trp Gly Gln Gly Asp Gly Ser Gly
 130 135 140
 Leu Arg Ala Val Asp Ser Ala Val Gly Arg Ile Gly Ser Leu Ala Cys
 145 150 155 160
 Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met Ala Asp Gly
 165 170 175
 Glu Gln Ile His Val Ala Met Phe Pro Gly Ser Leu Val Gly Asp Ile
 180 185 190
 Phe Ala Glu Gln Ile Glu Val Thr Ile Arg His His Ala Leu Glu Ser
 195 200 205
 Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp Gln Gln
 210 215 220
 Gly Arg Ile Met Gln Asp Thr Gly Cys Glu Leu Gly Pro Ile Ser Gly
 225 230 235 240
 Gly Cys Phe Thr Ala Ile Ile Ser Pro Glu Gly Lys Val Leu Gly Glu
 245 250 255
 Pro Leu Arg Ser Gly Glu Gly Val Val Ile Ala Asp Leu Asp Leu Ala
 260 265 270
 Leu Ile Asp Lys Arg Lys Arg Met Met Asp Ser Val Gly His Tyr Ser
 275 280 285
 Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Ser Pro Thr Ala His
 290 295 300
 Val His Glu Leu Ala Ala Ala Leu Asn Pro Ala Arg Glu Ser Asp Pro
 305 310 315 320
 Leu Val Ser Thr Cys Arg Arg Ala Ser Ser Ser Phe Cys Ser Leu
 325 330 335

<210> 163
 <211> 978
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 163

```

gtgaccatca tcaaagccgc cgcagtgcag atcagccccg tgctttacag ccgggaagcc      60
accgtcgaaa aggtcgttcg cgagaccgcg gaactcggcc agaagggcgt gcagttcgca      120
acgtttccgg aaaccgtggg gccgtactac ccatacttct ccgccgtcca gacgggcatc      180
gaactgctgt ccggcaaaga gcacctgcga ctgctggagc aggccgtgac tgttccttcc      240
cccgccactg atgcgattgc ccaggcggca cgcgaggccg gcatgggtgg gtatgatcggc      300
gtcaacgagc gtgacggcgg caccatctac aacacgcagc tgctctttga tgccgacggc      360
acgctggtgc agcgccgccc caagatcacg ccgacgcatt tcgagcgcat ggtgtggggc      420
caggggcagc gttcgggcct gcgcgcagtg gataccaagg tcggccgcat tggccagctg      480
gcctgcttcg agcacaacaa ccgctcgcg cgctacgcaa tgatggccga tggcgagcag      540
atccattcct ccatgtaccc gggctccgcc ttcggcgacg gattcgcgca gcgatggag      600
atcaacattc gccaacacgc cctggagtcg ggttgcttcg tggatgaatgc caccgcgtgg      660
ctcgacgccc accagcaggc gcagatcatg aaggacacgg gctgcgccat cgggccgcatc      720
tctggcggct gcttcacgac catcgtcacg ccggacggca tgctgatcgg cgaaccctc      780
cgcgagggcg agggcgagat catcgccgac ctcgatttca ccctgatcga ccgccgcaag      840
ctgctgatgg actcggtcgg ccaactacaac cgtccggagc tgctgagcct gctgatcgac      900
cgcacacccc cggcgaaactt ccatgagcgc agtacgcac ccgccgtcga tgccgccagc      960
ggcctcgaaa tcctctaa

```

<210> 164

<211> 325

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 164

```

Val Thr Ile Ile Lys Ala Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
1      5      10      15
Ser Arg Glu Ala Thr Val Glu Lys Val Val Arg Glu Thr Arg Glu Leu
20     25     30
Gly Gln Lys Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
35     40     45
Tyr Tyr Pro Tyr Phe Ser Ala Val Gln Thr Gly Ile Glu Leu Leu Ser
50     55     60
Gly Lys Glu His Leu Arg Leu Leu Glu Gln Ala Val Thr Val Pro Ser
65     70     75     80
Pro Ala Thr Asp Ala Ile Ala Gln Ala Ala Arg Glu Ala Gly Met Val
85     90     95
Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Ile Tyr Asn Thr
100    105    110
Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Val Gln Arg Arg Lys
115    120    125
Ile Thr Pro Thr His Phe Glu Arg Met Val Trp Gly Gln Gly Asp Gly
130    135    140
Ser Gly Leu Arg Ala Val Asp Thr Lys Val Gly Arg Ile Gly Gln Leu
145    150    155    160
Ala Cys Phe Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Met Met Ala
165    170    175
Asp Gly Glu Gln Ile His Ser Ser Met Tyr Pro Gly Ser Ala Phe Gly
180    185    190
Asp Gly Phe Ala Gln Arg Met Glu Ile Asn Ile Arg Gln His Ala Leu
195    200    205
Glu Ser Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp
210    215    220
Gln Gln Ala Gln Ile Met Lys Asp Thr Gly Cys Ala Ile Gly Pro Ile
225    230    235    240
Ser Gly Gly Cys Phe Thr Thr Ile Val Thr Pro Asp Gly Met Leu Ile
245    250    255
Gly Glu Pro Leu Arg Glu Gly Glu Gly Glu Ile Ile Ala Asp Leu Asp

```

```

                260                265                270
Phe Thr Leu Ile Asp Arg Arg Lys Leu Leu Met Asp Ser Val Gly His
                275                280                285
Tyr Asn Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro Ala
                290                295                300
Ala Asn Phe His Glu Arg Ser Thr His Pro Ala Val Asp Ala Ala Ser
305                310                315                320
Gly Leu Glu Ile Leu
                325

```

<210> 165
 <211> 1008
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 165
atggccaatt tcaaattcaa ggcggcgcg gtgcaggccg cgcccgcctt cctcgatctc      60
gaggctagca tcgccaagtc gatcgccctg atcgaacaag ccgcccgcga cggcgccaag      120
ctgatcgctt ttcccgaagt cttcattccc ggctaccctt ggcacatctg gctcgacagt      180
cccgccctgg cgatcgggcg cggcttcgtc tcgcgctatt tcgagaactc gctggactac      240
aacagccccg aggcgagcg cctcaggctc gccgtcaaga aggcgggcct gacggcgggtg      300
atcgccctct ccgagcgcg cggcggcgag ctctacatcg cgcaatggat catcgccct      360
gacggcgaga ccgttgcgaa acggcgtaag ctccggccga cccattgcga gcgcacggtc      420
tatggagaag gcgacggcag cgacctcgcg gtccacgacg tatctggcat cggccgtctc      480
ggcgcgctct gctgctggga gcatatccag ccgctgtcga aattcgcgat gtattcgcaa      540
aatgagcaag tgcacgtcgc gtcctggccg agcttctcgc tctacgaccc gttcgcgccc      600
gcgctggggc ccgaggtcaa caacgcagcc tcgcggtatc atcggttcga aggtcatgc      660
ttcgtcattg cgccctgcgc gaccgtttcg cctgcaatga tcgaggaact gtgcgacgcg      720
ccaaacaaac atgcgcttct gcacgcgggc ggcggcttcg cgcgcatcta tgggcgggac      780
ggcgcttcga tcgccgagac gctgccgcca gatcaggaag gcttgatcta cgccgacatc      840
gacctaccg cgatcgcggt cgccaaggcc gccgcgcatc ccgcccggca ttattcgcg      900
cccgacgtca cgcgctgct cttcaacaag aagcccgtc ggcgagtcga aacttttgct      960
ttgcccgctc atgcgcccgc gccggagacg cagaccgccc cgagctga      1008

```

<210> 166
 <211> 335
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 166
Met Ala Asn Phe Lys Phe Lys Ala Ala Ala Val Gln Ala Ala Pro Ala
  1                5                10                15
Phe Leu Asp Leu Glu Ala Ser Ile Ala Lys Ser Ile Ala Leu Ile Glu
                20                25                30
Gln Ala Ala Ala Asn Gly Ala Lys Leu Ile Ala Phe Pro Glu Val Phe
                35                40                45
Ile Pro Gly Tyr Pro Trp His Ile Trp Leu Asp Ser Pro Ala Trp Ala
                50                55                60
Ile Gly Arg Gly Phe Val Ser Arg Tyr Phe Glu Asn Ser Leu Asp Tyr
65                70                75                80
Asn Ser Pro Glu Ala Glu Arg Leu Arg Leu Ala Val Lys Lys Ala Gly
                85                90                95
Leu Thr Ala Val Ile Gly Leu Ser Glu Arg Asp Gly Gly Ser Leu Tyr
                100                105                110
Ile Ala Gln Trp Ile Ile Gly Pro Asp Gly Glu Thr Val Ala Lys Arg

```

```

      115      120      125
Arg Lys Leu Arg Pro Thr His Cys Glu Arg Thr Val Tyr Gly Glu Gly
  130      135      140
Asp Gly Ser Asp Leu Ala Val His Asp Val Ser Gly Ile Gly Arg Leu
  145      150      155      160
Gly Ala Leu Cys Cys Trp Glu His Ile Gln Pro Leu Ser Lys Phe Ala
      165      170      175
Met Tyr Ser Gln Asn Glu Gln Val His Val Ala Ser Trp Pro Ser Phe
      180      185      190
Ser Leu Tyr Asp Pro Phe Ala Pro Ala Leu Gly Ala Glu Val Asn Asn
      195      200      205
Ala Ala Ser Arg Ile Tyr Ala Val Glu Gly Ser Cys Phe Val Ile Ala
      210      215      220
Pro Cys Ala Thr Val Ser Pro Ala Met Ile Glu Glu Leu Cys Asp Ala
      225      230      235      240
Pro Asn Lys His Ala Leu Leu His Ala Gly Gly Gly Phe Ala Arg Ile
      245      250      255
Tyr Gly Pro Asp Gly Ala Ser Ile Ala Glu Thr Leu Pro Pro Asp Gln
      260      265      270
Glu Gly Leu Ile Tyr Ala Asp Ile Asp Leu Thr Ala Ile Gly Val Ala
      275      280      285
Lys Ala Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val Thr
      290      295      300
Arg Leu Leu Phe Asn Lys Lys Pro Ala Arg Arg Val Glu Thr Phe Ala
      305      310      315      320
Leu Pro Val Asp Ala Pro Ala Pro Glu Thr Gln Thr Ala Ala Ser
      325      330      335

```

<210> 167

<211> 1017

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 167

```

atgggtattg aacatccgaa gtacagggtt gccgtggtgc aggccgcacc ggcctggctc      60
gatcttgacg cgtcgatcga caagtcgacg gcgctgatcg aggaggctgc ccagaaaggc      120
gccaaagctga tcgcattccc cgaggccttc atccccggct acccctggca tatctggatg      180
gactcgcccg cctgggcgat tggccgcggt tttgtgcagc gctacttcga caattcgctg      240
gcctatgaca gcccgcaggc cgagaagctg cgcgcggccg tgcgcaaggc aaaactcacg      300
gccgtgatcg gcttgtcgga gcgtgacggc gccagccttt atctcgaca atggctgatc      360
ggccccgacg gcgagaccat cgcaaaacgg cgcaagctgc ggccgacaca tgccgagcgc      420
actgtgtacg gcgagggcga cggcagcgac cttgcggtcc acaatcgtcc ggacatcggc      480
aggctcggtg cgctctgctg ctgggagcat cttcagccac tgcgaaata cgcgatgtac      540
gcgcagaacg agcagggtgca cgtcgcggcc tggccgagct tttcgctcta cgatcccttc      600
gccgtggcgc tcggcgccga ggtgaacaac gcggcctccc gcgtctatgc ggtcgaaggc      660
tcttgcttcg tgctggcgcc gtgcgcgaca gtctcgcaag ccatgatcga cgagctctgc      720
gatcggccgg acaagcacgc gctgctgcat gtcggcggcg gctttgccgc gatctacggg      780
cccgcaggca gccagatcgg cgacaagctc gccccgacc aggagggcct gttgatcgcc      840
gagatcgatc tcggcgccat aggtgtcgcc aagaacgccg cggatcccgc cgggcactat      900
tcgcggcccg acgtgacgcg gctgttgctc aacaagaaac cgtacaagcg cgtcgaacag      960
ttctcgccgc cgtcggaggc ggttgaaccc acggatatcg cggcggcggc aagctga      1017

```

<210> 168

<211> 338

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 168

```

Met Gly Ile Glu His Pro Lys Tyr Arg Val Ala Val Val Gln Ala Ala
 1           5           10           15
Pro Ala Trp Leu Asp Leu Asp Ala Ser Ile Asp Lys Ser Ile Ala Leu
      20           25           30
Ile Glu Glu Ala Ala Gln Lys Gly Ala Lys Leu Ile Ala Phe Pro Glu
      35           40           45
Ala Phe Ile Pro Gly Tyr Pro Trp His Ile Trp Met Asp Ser Pro Ala
      50           55           60
Trp Ala Ile Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
      65           70           75           80
Ala Tyr Asp Ser Pro Gln Ala Glu Lys Leu Arg Ala Ala Val Arg Lys
      85           90           95
Ala Lys Leu Thr Ala Val Ile Gly Leu Ser Glu Arg Asp Gly Gly Ser
      100          105          110
Leu Tyr Leu Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
      115          120          125
Lys Arg Arg Lys Leu Arg Pro Thr His Ala Glu Arg Thr Val Tyr Gly
      130          135          140
Glu Gly Asp Gly Ser Asp Leu Ala Val His Asn Arg Pro Asp Ile Gly
      145          150          155          160
Arg Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys
      165          170          175
Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ala Trp Pro
      180          185          190
Ser Phe Ser Leu Tyr Asp Pro Phe Ala Val Ala Leu Gly Ala Glu Val
      195          200          205
Asn Asn Ala Ala Ser Arg Val Tyr Ala Val Glu Gly Ser Cys Phe Val
      210          215          220
Leu Ala Pro Cys Ala Thr Val Ser Gln Ala Met Ile Asp Glu Leu Cys
      225          230          235          240
Asp Arg Pro Asp Lys His Ala Leu Leu His Val Gly Gly Gly Phe Ala
      245          250          255
Ala Ile Tyr Gly Pro Asp Gly Ser Gln Ile Gly Asp Lys Leu Ala Pro
      260          265          270
Asp Gln Glu Gly Leu Leu Ile Ala Glu Ile Asp Leu Gly Ala Ile Gly
      275          280          285
Val Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
      290          295          300
Val Thr Arg Leu Leu Leu Asn Lys Lys Pro Tyr Lys Arg Val Glu Gln
      305          310          315          320
Phe Ser Pro Pro Ser Glu Ala Val Glu Pro Thr Asp Ile Ala Ala Ala
      325          330          335
Ala Ser

```

<210> 169

<211> 1077

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 169

```

atggccctca cccatccgaa attgaaagtc gccgccgtgc aggcagctcc cgcgttcctc      60
gatgtcgatg ccgcagtgga caaagcgggtg cggctaatacg acgaagcggc agcaaacggc      120
tccagtctgg tggcattccc cgagacctgg atccccggct atccgttttg gatctggctt      180
ggctcgccgg cctgggcaat catgcgcggg tttgtgtctc gctatttcga taattcgctc      240

```



```

agctatgaca gccggcaggc agagcgcttg cgcgacgccg cgaagcgcca caaactgacc 300
gtcgtcatgg gcctgtccga gcgcgccggc ggtagccttt acatcgcgca gtggatcatt 360
ggtcccaatg gcgagaccgt cgcacagcgg cgcaagctca agcccaccca tgcggagcgc 420
accgtcttcg gcgaggggtga cggcagccac ctggcgggtac acaatcttcc aatcgagcgg 480
ctcgggtgcg tgtgctgctg ggagcacctc cagccgctct ccaaatacgc gatgtacgcc 540
cagaacgaag agatccacgt ggcggcatgg ccgtccttct cgctctacga cccgtttgcg 600
cacgcgctcg gcgcggaagt caacaacgca gcgagccaga tctacgcggg tgaaggttcc 660
tgctttgtcg tcgcgccatg tcgggtgatc tcgcaggaaa tgatcgatct tatgtgcat 720
acccccgaca agcatcagct tattcacgtc ggtggcgggt tcaccgtgat ctatggccc 780
gacgggtgcg gcacgcggca caagctcgcg ccagatcagg aaggcattgt ctatgccgac 840
atcgatctcg gcatgatccc gatcgcgaaa gctgccgccg atcctgccgg ccactatgag 900
cgaccgcagc ttaccgcctc tctgttcaac aatcgctccc ccaatcgggt ggaaaccctc 960
gtgctccccg ttgatcaggt ccgtgacatc gatgcacgtg tggaggccgc ggcacctcag 1020
gcgcgaccag caaccgggaa cgaggatccc gccgcaaagc ctatggccgc cgaatga 1077

```

<210> 170

<211> 358

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 170

```

Met Ala Leu Thr His Pro Lys Leu Lys Val Ala Ala Val Gln Ala Ala
 1          5          10          15
Pro Ala Phe Leu Asp Val Asp Ala Ala Val Asp Lys Ala Val Arg Leu
 20          25          30
Ile Asp Glu Ala Ala Ala Asn Gly Ser Ser Leu Val Ala Phe Pro Glu
 35          40          45
Thr Trp Ile Pro Gly Tyr Pro Phe Trp Ile Trp Leu Gly Ser Pro Ala
 50          55          60
Trp Ala Ile Met Arg Gly Phe Val Ser Arg Tyr Phe Asp Asn Ser Leu
 65          70          75          80
Ser Tyr Asp Ser Arg Gln Ala Glu Arg Leu Arg Asp Ala Ala Lys Arg
 85          90          95
His Lys Leu Thr Val Val Met Gly Leu Ser Glu Arg Ala Gly Gly Ser
100          105          110
Leu Tyr Ile Ala Gln Trp Ile Ile Gly Pro Asn Gly Glu Thr Val Ala
115          120          125
Gln Arg Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly
130          135          140
Glu Gly Asp Gly Ser His Leu Ala Val His Asn Leu Pro Ile Gly Arg
145          150          155          160
Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr
165          170          175
Ala Met Tyr Ala Gln Asn Glu Glu Ile His Val Ala Ala Trp Pro Ser
180          185          190
Phe Ser Leu Tyr Asp Pro Phe Ala His Ala Leu Gly Ala Glu Val Asn
195          200          205
Asn Ala Ala Ser Gln Ile Tyr Ala Val Glu Gly Ser Cys Phe Val Val
210          215          220
Ala Pro Cys Ala Val Ile Ser Gln Glu Met Ile Asp Leu Met Cys Asp
225          230          235          240
Thr Pro Asp Lys His Gln Leu Ile His Val Gly Gly Gly Phe Thr Val
245          250          255
Ile Tyr Gly Pro Asp Gly Ala Arg Ile Gly Asp Lys Leu Ala Pro Asp
260          265          270
Gln Glu Gly Ile Val Tyr Ala Asp Ile Asp Leu Gly Met Ile Pro Ile
275          280          285
Ala Lys Ala Ala Ala Asp Pro Ala Gly His Tyr Ala Arg Pro Asp Val

```

```

      290              295              300
Thr Arg Leu Leu Phe Asn Asn Arg Pro Ala Asn Arg Val Glu Thr Leu
305              310              315              320
Val Leu Pro Val Asp Gln Val Arg Asp Ile Asp Ala Arg Val Glu Ala
      325              330              335
Ala Ala Pro Gln Ala Arg Pro Ala Thr Gly Asn Glu Asp Pro Ala Ala
      340              345              350
Lys Pro Met Ala Ala Glu
      355

```

<210> 171
 <211> 1011
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 171
atgactaagg gaacagtga agtcgcggcg gcgcaggtca cccccgtgtt catggatcgt      60
aaagccacga tcgtcaaggc ctgcgacacg atcgccgagg cgggcaagaa cggcgcgcg      120
ctggtggtgt tcccggagac gtttgttctt ggctaccggg actgggtctg gacggcgacg      180
gctgggacgc atcgcgatat ccaccaggcg atgtacgcgg aactgctgga ccaggctgtc      240
tcgattccga gcccggcgac ggacgccctc tgccgtgctg caaagaaggc gggcgtctac      300
gtcgtcatcg gcgtcaatga gctgagtggg ccggggcgaa gcctgtacaa cacgctgatc      360
tacatcgatg acgaaggcga gatcatgggc cgccaccgca agctggtccc cacgatgggc      420
gagcgccctg tctgggcacc cggcgacggc agcacgctgg aggcgtacga gacatcgatc      480
ggcaggctgg gcggactgat ctgctgggag aactacatgc cgctggcccg ctacgccatg      540
tacgcctggg gcgtgcagat ctacgtcggc ccgacgtggg acagctcggg cgggtgggtt      600
ggcagcatgc agcacatcgc ccgcgaaggg cggacggcgg tgatcggctg ctgcatggcg      660
atccgtcgca gcgacatccc ggacaagtac gagttcaaga agctgtaccc gccgagcaag      720
agcaaagacg aagaatgggt gaacgatggc aacagcgtca tcgtcgcacc cgggtggacga      780
atactcgccg ggccggtcgc caaagaggag acgatcctct acgccgatct ggaccgcgca      840
gccgagcgcg gttcaaaagt ctcgttagat gtggcagggc actacgcgcg gccggacgtc      900
ttccagctga cgggtgaatc cggtccggca gaactggtga atgtggccgg tgatatcgca      960
ccggcaacca acggcaaaagt caaaacaccg gcgaaattac gccgcaagta a      1011

```

<210> 172
 <211> 336
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 172
Met Thr Lys Gly Thr Val Lys Val Ala Ala Ala Gln Val Thr Pro Val
1              5              10              15
Phe Met Asp Arg Lys Ala Thr Ile Val Lys Ala Cys Asp Thr Ile Ala
      20              25              30
Glu Ala Gly Lys Asn Gly Ala Arg Leu Val Val Phe Pro Glu Thr Phe
      35              40              45
Val Pro Gly Tyr Pro Asp Trp Val Trp Thr Ala Thr Ala Gly Thr His
      50              55              60
Arg Asp Ile His Gln Ala Met Tyr Ala Glu Leu Leu Asp Gln Ala Val
      65              70              75              80
Ser Ile Pro Ser Pro Ala Thr Asp Ala Leu Cys Arg Ala Ala Lys Lys
      85              90              95
Ala Gly Val Tyr Val Val Ile Gly Val Asn Glu Leu Ser Gly Pro Gly
      100             105             110
Gly Ser Leu Tyr Asn Thr Leu Ile Tyr Ile Asp Asp Glu Gly Glu Ile

```

115	120	125
Met Gly Arg His Arg Lys Leu Val Pro Thr Met Gly Glu Arg Leu Val		
130	135	140
Trp Ala Pro Gly Asp Gly Ser Thr Leu Glu Ala Tyr Glu Thr Ser Ile		
145	150	155
Gly Arg Leu Gly Gly Leu Ile Cys Trp Glu Asn Tyr Met Pro Leu Ala		
165	170	175
Arg Tyr Ala Met Tyr Ala Trp Gly Val Gln Ile Tyr Val Ala Pro Thr		
180	185	190
Trp Asp Ser Ser Asp Gly Trp Val Gly Ser Met Gln His Ile Ala Arg		
195	200	205
Glu Gly Arg Thr Ala Val Ile Gly Cys Cys Met Ala Ile Arg Arg Ser		
210	215	220
Asp Ile Pro Asp Lys Tyr Glu Phe Lys Lys Leu Tyr Pro Pro Ser Lys		
225	230	235
Ser Lys Asp Glu Glu Trp Val Asn Asp Gly Asn Ser Val Ile Val Ala		
245	250	255
Pro Gly Gly Arg Ile Leu Ala Gly Pro Val Ala Lys Glu Glu Thr Ile		
260	265	270
Leu Tyr Ala Asp Leu Asp Pro Ala Ala Glu Arg Gly Ser Lys Phe Ser		
275	280	285
Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Gln Leu Thr		
290	295	300
Val Asn Arg Gly Pro Ala Glu Leu Val Asn Val Ala Gly Asp Ile Ala		
305	310	315
Pro Ala Thr Asn Gly Lys Val Lys Thr Pro Ala Lys Leu Arg Arg Lys		
325	330	335

<210> 173

<211> 993

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 173

atgaaagttg ttaaagccgc cgcagtcctaa ctgagtcctcg tcctctatatag ccgcgagggga	60
acgggtcgaga gggtcgttcg gaagatccac gagcttgccc ggcaggggggt acagttcgcc	120
accttcccgg agaccgtagt gccttactac ccgtactttt ccttcgtcca gacgccctta	180
cagattatag ccggacctga gcatctaaag ctgctcgacc aggcagtgac cgtgcccgtcc	240
cctgccaccg acgctatcag cgaggctgcc aggcaggcgg gagttgtgggt gtccatagggc	300
gtcaacgagc gtgacggcgg aaccctgtac aacacgcagc tgctcttcga tgccgatggc	360
gccttgatcc agcgccggcg caagattacg cccactcatt tcgagcgcat gatctggggc	420
cagggcgacg ggtcgggcct gcgcgctgtc gacagcaagg tcggtcgcat tggccagctc	480
gcatgctggg agcacaacaa cccctggcg cgctacgca tgatagccga cggcgagcag	540
atccattcgg caatgtatcc gggctccatg ttcggcgacc cgtttgcccc gaagacggaa	600
atcaatatcc ggcagcatgc attggagtct gcgtgcttcg tcgtgtgcgc cacggcctgg	660
ctggacgccg atcagcaggc gcaaactctgc aaggacactg gctgcgacat cggcccgatc	720
tcgggcggtt gcttcaccgc gatcgtggcg cctgatggaa ccttgctggg cgagcccatc	780
cgctcggggc aaggcatggt catcgtcgac ctcgacttca cgctcatcga caagcgcaag	840
caggtgatgg actcgcgcg ccaactacaac cggccggaat tgctcagtct cctgatcgac	900
cgcacacca ctgcgcatgt tcacgaccgc gctgtgcgcc ccgagtcagc cgcggagcaa	960
cgttcggagg aacttctcgc tacggctgtc taa	993

<210> 174

<211> 330

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 174

```

Met Lys Val Val Lys Ala Ala Ala Val Gln Leu Ser Pro Val Leu Tyr
 1      5      10      15
Ser Arg Glu Gly Thr Val Glu Arg Val Val Arg Lys Ile His Glu Leu
 20      25      30
Gly Arg Gln Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
 35      40      45
Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Thr Pro Leu Gln Ile Ile Ala
 50      55      60
Gly Pro Glu His Leu Lys Leu Leu Asp Gln Ala Val Thr Val Pro Ser
 65      70      75      80
Pro Ala Thr Asp Ala Ile Ser Glu Ala Ala Arg Gln Ala Gly Val Val
 85      90      95
Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn Thr
 100     105     110
Gln Leu Leu Phe Asp Ala Asp Gly Ala Leu Ile Gln Arg Arg Arg Lys
 115     120     125
Ile Thr Pro Thr His Phe Glu Arg Met Ile Trp Gly Gln Gly Asp Gly
 130     135     140
Ser Gly Leu Arg Ala Val Asp Ser Lys Val Gly Arg Ile Gly Gln Leu
 145     150     155     160
Ala Cys Trp Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Met Ile Ala
 165     170     175
Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Met Phe Gly
 180     185     190
Asp Pro Phe Ala Gln Lys Thr Glu Ile Asn Ile Arg Gln His Ala Leu
 195     200     205
Glu Ser Ala Cys Phe Val Val Cys Ala Thr Ala Trp Leu Asp Ala Asp
 210     215     220
Gln Gln Ala Gln Ile Cys Lys Asp Thr Gly Cys Asp Ile Gly Pro Ile
 225     230     235     240
Ser Gly Gly Cys Phe Thr Ala Ile Val Ala Pro Asp Gly Thr Leu Leu
 245     250     255
Gly Glu Pro Ile Arg Ser Gly Glu Gly Met Val Ile Val Asp Leu Asp
 260     265     270
Phe Thr Leu Ile Asp Lys Arg Lys Gln Val Met Asp Ser Arg Gly His
 275     280     285
Tyr Asn Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro Thr
 290     295     300
Ala His Val His Asp Arg Ala Val Arg Pro Glu Ser Ala Ala Glu Gln
 305     310     315     320
Arg Ser Glu Glu Leu Leu Ala Thr Ala Val
 325     330

```

<210> 175

<211> 945

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 175

```

atgaccacct acgggcagtt tagacttgcc gcgatcaatg ccgcgcctgt ctacttcgac      60
agggaagcat ccaccgaaaa agcttgccgg ctcattctcg aagcgggggc atcagggggc      120
acgctggcgg cgtttgcgga gacgtggcct cccggctatc cattccacat ctggagggaa      180
gttccgactg ctctccgagt ggaatacatc gctaatagcc tcgagattcc cagcccaacg      240
accgaccgat tgtgcgcggc ggctcgtcag gcgaacatcg atgttgtgat cggcgttgtc      300
gaactggatg cgcagacaca cgggacggtc tactgtacgc tcttgttcat tggcagcgat      360

```

```

ggctcaattc tgggacgtca tcgaaagatt aaaccgactt tcgtggagcg aaccgcatgg 420
ggggaaggtg acggcagcag cctgatcgtc tacgagcgcc cgtatggcaa gatcagtgg 480
ctgtgttgct gggaacacaa tatggttctg ccgggctacg cgctgatggc gcaggggacg 540
cagattcata tcgccgcatg gcccggtctg gaaagcactc gccatctgct cttatcaaga 600
gcattcgctt ctcaggcagc ggcgtatgtg attgatgtag gcgctatcgt caatcgtgac 660
gaccttcggg aagattacca ggctttgatt gctggaagct actggggcgg aagttgcatc 720
atcaaccagc aaggcgaggt catcgctggt ccagcgaaat cggagaccat tctggttgca 780
gattgctcaa ccgagcagat ctttagctca aaagtgtctt gtgatgtggg cgggcattat 840
tctgcgccgg atatttttca gtcctatgtc aatcgaaagc catatcaacg tatcgtcgag 900
acgaacaacc cacacccgcg tccgattgag ttcgattacc gttga 945

```

<210> 176

<211> 314

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 176

```

Met Thr Thr Tyr Gly Gln Phe Arg Leu Ala Ala Ile Asn Ala Ala Pro
1      5      10      15
Val Tyr Phe Asp Arg Glu Ala Ser Thr Glu Lys Ala Cys Arg Leu Ile
20     25     30
Leu Glu Ala Gly Ala Ser Gly Ala Thr Leu Ala Ala Phe Gly Glu Thr
35     40     45
Trp Leu Pro Gly Tyr Pro Phe His Ile Trp Arg Glu Val Pro Thr Ala
50     55     60
Leu Arg Val Glu Tyr Ile Ala Asn Ala Val Glu Ile Pro Ser Pro Thr
65     70     75     80
Thr Asp Arg Leu Cys Ala Ala Ala Arg Gln Ala Asn Ile Asp Val Val
85     90     95
Ile Gly Val Val Glu Leu Asp Ala Gln Thr His Gly Thr Val Tyr Cys
100    105    110
Thr Leu Leu Phe Ile Gly Ser Asp Gly Ser Ile Leu Gly Arg His Arg
115    120    125
Lys Ile Lys Pro Thr Phe Val Glu Arg Thr Ala Trp Gly Glu Gly Asp
130    135    140
Gly Ser Ser Leu Ile Val Tyr Glu Arg Pro Tyr Gly Lys Ile Ser Gly
145    150    155    160
Leu Cys Cys Trp Glu His Asn Met Val Leu Pro Gly Tyr Ala Leu Met
165    170    175
Ala Gln Gly Thr Gln Ile His Ile Ala Ala Trp Pro Gly Trp Glu Ser
180    185    190
Thr Arg His Leu Leu Leu Ser Arg Ala Phe Ala Ser Gln Ala Ala Ala
195    200    205
Tyr Val Ile Asp Val Gly Ala Ile Val Asn Arg Asp Asp Leu Arg Glu
210    215    220
Asp Tyr Gln Ala Leu Ile Ala Gly Ser Tyr Trp Gly Gly Ser Cys Ile
225    230    235    240
Ile Asn Pro Glu Gly Glu Val Ile Ala Gly Pro Ala Lys Ser Glu Thr
245    250    255
Ile Leu Val Ala Asp Cys Ser Thr Glu Gln Ile Phe Ser Ser Lys Val
260    265    270
Leu Cys Asp Val Gly Gly His Tyr Ser Arg Pro Asp Ile Phe Gln Leu
275    280    285
His Val Asn Arg Lys Pro Tyr Gln Arg Ile Val Glu Thr Asn Asn Pro
290    295    300
His Pro Ala Pro Ile Glu Phe Asp Tyr Arg
305    310

```

<210> 177
 <211> 948
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 177
 atggactcac ttaccggttg tctcgcgcaa atcgcgcccc tttggttgaa tcgggcgggg 60
 acgttggtcaa agatgttgga acaggttcga gcgcggaag aggcgggctg tcagcttggt 120
 gtgtttggtg aggcgttgct ccccggttat ccattttgga tcgaactgac gaacggcgca 180
 gtcttcaatt cgccgatgca aaaggaaatc cacgcgcact acatggatca agctgtgcag 240
 atcgaagcag ggcatcttga tccattgtgc ggcgcgga aagcgcacgg catcaccgtg 300
 gtcgcgggca tcatcgagcg tccgttggtat cgcgcgggac atagtttata tgcgagtctg 360
 gtgtatatcg atttgaacgg tgtcatccaa tcggtgcac gcaaactgat gccacacctat 420
 gaagaacgac tcacctggtc gcctggcgat ggtcatgggt tacgcgtgca tacactgggc 480
 gcttttacgg ttggcaaaact caattgttg gaaaactgga tgccgctgcc gcgcgcggct 540
 ctgtatgcgc aaggcgaaga tctgcacggt gctgtctggc ccgggtccgt gcgcaacaca 600
 caggatatta cgcgctttat cgcaatggag tcgcgatcgt ttgtcgtttc ggtttcgagt 660
 ttgatgcgca agagtgactt cccacaagat acgcctcacc tctccgccat tcttgaatct 720
 gcacccgatc cactcgccaa cggaggttcg tgtctggctg gacctgacgg taaatggatc 780
 gttgaaccgg ttgcgatga agagaagttg atcgtcgcca ccattgacca tgcccgtgta 840
 cgtgaagaac gccagaactt tgatccatcc ggtcattaca gccgaccaga tgtgacacaa 900
 ttgagagtca accgccagcg acaaagcggt atcgcttttg atgagtag 948

<210> 178
 <211> 315
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 178
 Met Asp Ser Leu Thr Val Gly Leu Ala Gln Ile Ala Pro Val Trp Leu
 1 5 10 15
 Asn Arg Ala Gly Thr Leu Ser Lys Met Leu Glu Gln Val Arg Ala Ala
 20 25 30
 Lys Glu Ala Gly Cys Gln Leu Val Phe Gly Glu Ala Leu Leu Pro
 35 40 45
 Gly Tyr Pro Phe Trp Ile Glu Leu Thr Asn Gly Ala Val Phe Asn Ser
 50 55 60
 Pro Met Gln Lys Glu Ile His Ala His Tyr Met Asp Gln Ala Val Gln
 65 70 75 80
 Ile Glu Ala Gly His Leu Asp Pro Leu Cys Gly Ala Ala Lys Ala His
 85 90 95
 Gly Ile Thr Val Val Ala Gly Ile Ile Glu Arg Pro Leu Asp Arg Gly
 100 105 110
 Gly His Ser Leu Tyr Ala Ser Leu Val Tyr Ile Asp Leu Asn Gly Val
 115 120 125
 Ile Gln Ser Val His Arg Lys Leu Met Pro Thr Tyr Glu Glu Arg Leu
 130 135 140
 Thr Trp Ser Pro Gly Asp Gly His Gly Leu Arg Val His Thr Leu Gly
 145 150 155 160
 Ala Phe Thr Val Gly Lys Leu Asn Cys Trp Glu Asn Trp Met Pro Leu
 165 170 175
 Pro Arg Ala Ala Leu Tyr Ala Gln Gly Glu Asp Leu His Val Ala Val
 180 185 190
 Trp Pro Gly Ser Val Arg Asn Thr Gln Asp Ile Thr Arg Phe Ile Ala
 195 200 205

Met Glu Ser Arg Ser Phe Val Val Ser Val Ser Ser Leu Met Arg Lys
 210 215 220
 Ser Asp Phe Pro Gln Asp Thr Pro His Leu Ser Ala Ile Leu Glu Ser
 225 230 235 240
 Ala Pro Asp Pro Leu Ala Asn Gly Gly Ser Cys Leu Ala Gly Pro Asp
 245 250 255
 Gly Lys Trp Ile Val Glu Pro Val Ala Asp Glu Glu Lys Leu Ile Val
 260 265 270
 Ala Thr Ile Asp His Ala Arg Val Arg Glu Glu Arg Gln Asn Phe Asp
 275 280 285
 Pro Ser Gly His Tyr Ser Arg Pro Asp Val Thr Gln Leu Arg Val Asn
 290 295 300
 Arg Gln Arg Gln Ser Val Ile Ala Phe Asp Glu
 305 310 315

<210> 179

<211> 915

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 179

atgaccacca	aagcagccat	cattcaggcg	cgccccatat	actacgatct	ggcggcgtgt	60
gtcgataagg	cgcttgccct	catcaccgag	gcggcggcac	gcggcgcgaa	catcgtcacg	120
ctcggcgaga	cgtggctgcc	gggctatccc	gcgtggctgg	atgtgtgctg	cgagatgggg	180
ctgtgggata	acgcgcgcac	caaaagccgtc	tttcagcggc	tccatgccaa	cagcgtcacc	240
atccccggcg	cggagatcag	ccagtctctg	gacatcgccc	gccgccttag	catcgtgctg	300
gtgctcagcg	tcaacgagcg	cgtccgcaac	accttggtca	acaccctgct	cacgattgac	360
gagcgcggcg	acatccgcaa	ccaccaccgc	aagctgatgc	cgacctacac	tgagcgcac	420
gtctgggggc	agggcgacgg	cgcgggctta	caggcggctg	agacggcaac	cgggcgcgtc	480
ggcgggctga	tctgctggga	acactggatg	ccgtgggcac	ggcaggcgct	gcacaacgcc	540
ggggagcaaa	ttcacgtttc	ggctttcccg	accgtcaacg	acccgcgcca	ccaagtccgc	600
agccgccagt	acgttttcga	ggggcgctgc	ttcgtgctga	ccgccggcag	catccagcgc	660
gccgacgacc	taccgcccga	actgaccgtc	aaggcgggca	tcgcgcggga	tgatctgggt	720
cagggcgcg	gcagcgccat	catcgcccg	gacatgcgct	acctcgccgg	accctgcttc	780
gacgagga	ccatcctcta	cgccgacctc	gacctgagcg	agacgatccg	cgagagcatg	840
acgctggacg	tgagcgggca	ttactcgcg	cccgcacgtg	tcaccttcga	ggttaatcgg	900
cagcggaaaa	tttag					915

<210> 180

<211> 304

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 180

Met Thr Thr Lys Ala Ala Ile Ile Gln Ala Arg Pro Ile Tyr Tyr Asp	
1 5 10 15	
Leu Ala Ala Cys Val Asp Lys Ala Leu Ala Leu Ile Thr Glu Ala Ala	
20 25 30	
Ala Arg Gly Ala Asn Ile Val Thr Leu Gly Glu Thr Trp Leu Pro Gly	
35 40 45	
Tyr Pro Ala Trp Leu Asp Val Cys Val Glu Met Gly Leu Trp Asp His	
50 55 60	
Ala Pro Thr Lys Ala Val Phe Gln Arg Leu His Ala Asn Ser Val Thr	
65 70 75 80	
Ile Pro Gly Ala Glu Ile Ser Gln Phe Cys Asp Ile Ala Arg Arg Leu	

<220>

<223> Obtained from an environmental sample

<400> 182

```

Met Pro Lys Thr Val Arg Ala Ala Ala Val Gln Ile Ala Pro Asp Leu
 1          5          10          15
Thr Ser Arg Ala Gly Thr Val Glu Arg Val Leu Asn Ala Ile Ala Glu
          20          25          30
Ala Ser Asp Lys Gly Ala Glu Leu Ile Val Phe Pro Glu Thr Phe Val
          35          40          45
Pro Trp Tyr Pro Tyr Phe Ser Phe Val Leu Pro Pro Val Gln Gln Gly
          50          55          60
Pro Glu His Leu Arg Leu Tyr Glu Glu Ala Val Thr Val Pro Ser Ala
          65          70          75          80
Glu Thr Arg Ala Val Ala Asp Ala Ala Arg Lys Arg Asn Ala Val Ile
          85          90          95
Val Leu Gly Val Asn Glu Arg Asp His Gly Ser Leu Tyr Asn Thr Gln
          100          105          110
Leu Ile Phe Asp Ala Asp Gly Ser Leu Lys Leu Lys Arg Arg Lys Ile
          115          120          125
Thr Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly Asp Gly Ala
          130          135          140
Gly Leu Lys Val Val Glu Thr Ala Ile Gly Arg Met Gly Ala Leu Ala
          145          150          155          160
Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met Ala Gln
          165          170          175
His Glu Glu Ile His Ala Ser His Phe Pro Gly Ser Leu Val Gly Pro
          180          185          190
Ile Phe Gly Glu Gln Ile Glu Val Thr Met Arg His His Ala Leu Glu
          195          200          205
Ser Gly Cys Phe Val Val Asn Ala Thr Gly Trp Leu Ser Glu Glu Gln
          210          215          220
Ile Ala Ser Ile His Pro Asp Pro Ser Leu Gln Lys Gly Leu Arg Asp
          225          230          235          240
Gly Cys Met Thr Cys Ile Ile Thr Pro Glu Gly Arg His Val Val Pro
          245          250          255
Pro Leu Thr Ser Gly Glu Gly Ile Leu Ile Gly Asp Leu Asp Met Arg
          260          265          270
Leu Ile Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His Tyr Ala
          275          280          285
Arg Pro Glu Leu Leu His Leu Val His Asp Thr Thr Pro Ala Arg Ala
          290          295          300
Arg Glu Gln Val Gly Leu Ser Gly Asp Phe Ser Asp Ala Gly Gln Asp
          305          310          315          320
Lys Leu Phe Glu Glu Val Gln Asp Ala
          325

```

<210> 183

<211> 1002

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 183

```

atggctgagt cacgcattat tcgtgccgcc gccgccaga ttgcgccaga tctccatgag      60
gccagcaaaa cgctggcccg ggtgctggac gcgatcgatc aggcagccgc acagggggca      120
gagatcatcg tctttcccga gacctttgtg ccttattacc cctacttctc gtttatcacg      180
cccgcatga cgcgcggagc ggcccatctg aaattgtatg accaggcggg ggtggtgccc      240
ggcccgatca cccatgcggt ggccgaacgc gccgcctgc gcaacatcgt cgtggtgctg      300
ggggtgaatg aacgtgacca cggcacgctc tacaacaccc aactggtatt tgatgccagc      360

```

```

ggggaactgg tgctgaaacg ccgcaaaatc accccgacct atcacgaacg gatgatctgg 420
ggacagggag acggtgccgg attaaaggtg gtggactcgg cggttgggcg catcggggct 480
ttagcctgct gggagcacta caaccactg gcgcgctaca gcctgatgac tcagcacgag 540
gagatccatt gcagccagtt ccctggttca ctggtggggc cgatttttgc cgagcagatg 600
gacgtcacca ttcgccatca tgcactggag tccggttgct ttgtcatcaa tgccaccggc 660
tggtgaccg aggagcagat caacgagctg accagcgacc cggcggttaca aaaggggctg 720
cgtggtggct gcaacaccgc catcatctcg ccggaaggcc gccatctggt gccgccactg 780
accgaaggtg aggggatttt gattgccgat ctggacatgg ccctgatcac caaacgcaa 840
cgcatgatgg attctgtcgg ccactatgcc cgaccggaat tactcagcct gcgcctcgat 900
cgacgcctg cccgttatgt ggtggcgcgt gataatgagt ccgaaaccgg aggaggcaac 960
gatgcagaac gtaccgtcta cgcgccagca gctgatcact ga 1002

```

<210> 184
 <211> 333
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 184

```

Met Ala Glu Ser Arg Ile Ile Arg Ala Ala Ala Gln Ile Ala Pro
1          5          10          15
Asp Leu His Glu Ala Ser Lys Thr Leu Ala Arg Val Leu Asp Ala Ile
          20          25          30
Asp Gln Ala Ala Ala Gln Gly Ala Glu Ile Ile Val Phe Pro Glu Thr
          35          40          45
Phe Val Pro Tyr Tyr Pro Tyr Phe Ser Phe Ile Thr Pro Ala Met Thr
          50          55          60
Ala Gly Ala Ala His Leu Lys Leu Tyr Asp Gln Ala Val Val Val Pro
65          70          75          80
Gly Pro Ile Thr His Ala Val Gly Glu Arg Ala Arg Leu Arg Asn Ile
          85          90          95
Val Val Val Leu Gly Val Asn Glu Arg Asp His Gly Thr Leu Tyr Asn
          100         105         110
Thr Gln Leu Val Phe Asp Ala Ser Gly Glu Leu Val Leu Lys Arg Arg
          115         120         125
Lys Ile Thr Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly Asp
          130         135         140
Gly Ala Gly Leu Lys Val Val Asp Ser Ala Val Gly Arg Ile Gly Ala
145         150         155         160
Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ser Leu Met
          165         170         175
Thr Gln His Glu Glu Ile His Cys Ser Gln Phe Pro Gly Ser Leu Val
          180         185         190
Gly Pro Ile Phe Ala Glu Gln Met Asp Val Thr Ile Arg His His Ala
          195         200         205
Leu Glu Ser Gly Cys Phe Val Ile Asn Ala Thr Gly Trp Leu Thr Glu
210         215         220
Glu Gln Ile Asn Glu Leu Thr Ser Asp Pro Ala Leu Gln Lys Gly Leu
225         230         235         240
Arg Gly Gly Cys Asn Thr Ala Ile Ile Ser Pro Glu Gly Arg His Leu
          245         250         255
Val Pro Pro Leu Thr Glu Gly Glu Gly Ile Leu Ile Ala Asp Leu Asp
          260         265         270
Met Ala Leu Ile Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His
          275         280         285
Tyr Ala Arg Pro Glu Leu Leu Ser Leu Arg Leu Asp Ala Thr Pro Ala
290         295         300
Arg Tyr Val Val Ala Arg Asp Asn Glu Ser Glu Thr Gly Gly Gly Asn
305         310         315         320

```

Asp Ala Glu Arg Thr Val Tyr Ala Pro Ala Ala Asp His
325 330

<210> 185
<211> 1017
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 185
atgggcattg aacatccgaa atacaagggtc gcggtgggtgc aggcggccccc cgcttggttc 60
gatctcgacg gctcgggtcga taagtcgatc gcgctgatca aggaggcggc cgagaagggg 120
gcgaagctga tcgcctttcc cgaggccttc atccccggtt acccctggca tatctggatg 180
gactcgccgg cctgggcat cgcccgccgc ttctgtcagc gttatttcga caattcgctg 240
tcctatgaca gtccgcaggc cgagcggctg cgcgatgcgg tgaagaaggc gaagctcacc 300
ggcgtgttcg gactgtccga gcgcgacggc ggcagcctct acctcgcgca atggctgatc 360
gggcccgatg gcgagacat cgccaagcgc cgcaagctgc ggccgaccca cgccgaacgt 420
accgtctatg gcgaaggcga cggcagcgat cttgcccgtgc atgcgcgcgc cgacatcggc 480
cggatcggcg cgctctgctg ctgggagcat ctgcagccac tgtcgaaata cgcgatgtac 540
gcccagaacg aacagggtcca tgctgcagcc tggcccagct tctcgtgta cgaccccttc 600
gcgcggcgct taggggccga ggtcaacaac gcggcctccc gcgtctatgc ggtggaaggc 660
tcctgcttcg tgctcgcgcc gtgcgcgacg gtgtcgcagg cgatgatcga cgagctctgc 720
gaccggcccc acaagaacgc gctgctgcac gtcggcgggc gctttgccgc gatctatggc 780
cccgcggca gccagatcgg cgacaagctg gcgccggacc aggaggggct gctgatcgcc 840
gagatcgacc ttggcgccat cgggtgtcgc aagaacgccg ccgatcccgc cgggcactat 900
tcgcgtcccg acgtgacgcg gttgctgctc aacaagaagc gataccagcg cgtcgagcag 960
ttcgcgctgc cggtcgacac cgctcgagccg gcggatatcg gcgcagcggc gagctga 1017

<210> 186
<211> 338
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 186
Met Gly Ile Glu His Pro Lys Tyr Lys Val Ala Val Val Gln Ala Ala
1 5 10 15
Pro Ala Trp Leu Asp Leu Asp Gly Ser Val Asp Lys Ser Ile Ala Leu
20 25 30
Ile Lys Glu Ala Ala Glu Lys Gly Ala Lys Leu Ile Ala Phe Pro Glu
35 40 45
Ala Phe Ile Pro Gly Tyr Pro Trp His Ile Trp Met Asp Ser Pro Ala
50 55 60
Trp Ala Ile Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
65 70 75 80
Ser Tyr Asp Ser Pro Gln Ala Glu Arg Leu Arg Asp Ala Val Lys Lys
85 90 95
Ala Lys Leu Thr Ala Val Phe Gly Leu Ser Glu Arg Asp Gly Gly Ser
100 105 110
Leu Tyr Leu Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
115 120 125
Lys Arg Arg Lys Leu Arg Pro Thr His Ala Glu Arg Thr Val Tyr Gly
130 135 140
Glu Gly Asp Gly Ser Asp Leu Ala Val His Ala Arg Ala Asp Ile Gly
145 150 155 160
Arg Ile Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys
165 170 175

Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ala Trp Pro
 180 185 190
 Ser Phe Ser Leu Tyr Asp Pro Phe Ala Pro Ala Leu Gly Ala Glu Val
 195 200 205
 Asn Asn Ala Ala Ser Arg Val Tyr Ala Val Glu Gly Ser Cys Phe Val
 210 215 220
 Leu Ala Pro Cys Ala Thr Val Ser Gln Ala Met Ile Asp Glu Leu Cys
 225 230 235 240
 Asp Arg Pro Asp Lys Asn Ala Leu Leu His Val Gly Gly Gly Phe Ala
 245 250 255
 Ala Ile Tyr Gly Pro Asp Gly Ser Gln Ile Gly Asp Lys Leu Ala Pro
 260 265 270
 Asp Gln Glu Gly Leu Leu Ile Ala Glu Ile Asp Leu Gly Ala Ile Gly
 275 280 285
 Val Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
 290 295 300
 Val Thr Arg Leu Leu Leu Asn Lys Lys Arg Tyr Gln Arg Val Glu Gln
 305 310 315 320
 Phe Ala Leu Pro Val Asp Thr Val Glu Pro Ala Asp Ile Gly Ala Ala
 325 330 335
 Ala Ser

<210> 187
 <211> 1059
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 187
 atgggcatca atcatcccaa gtacaaagtg gccgtcgtgc aagcggcacc tgtctggctc 60
 gacctggatg gaacagtcga caagtgcatt cggctgatag gcgaggccgc tgagaagggg 120
 tgcaagctca ttgcatttcc cgagacgttc atcccggggg acccctggca catctggatg 180
 ggagctccgg cctggacgat cgggcgcgga ttcgtgcagc gatacttcga caattcgctt 240
 gcgtacgaca gtccgcaggc aaacaagctt cgcgcgcggt tgaagcgcgc cggagtgcacg 300
 gcagttctcg gcttgtcggg gcgcgcgga ggctccctgt acatcgccca gtggctcatc 360
 ggacctgatg gcgagaccat cgctcaacgg cgaaagctgc gccccacca tgcggagcgc 420
 accgtcttcg gcgagggcga tggcagcgat ttggcgggtg acagccgccc cgacatcggc 480
 cgactgggtg ccctttgctg ctgggaacat ctccagcctt tgaccaagta cgcgatgtac 540
 gcgcaagacg agcaagtgcg cgtcgtgca tggccgagct tctcgatgta cgagcctttc 600
 gcgcacgccc tgggtgggga gacgaacaac gcggtgagca aggtgtacgc ggtcgaaggt 660
 tcgtgctacg tcctggcccc ctgcgccatc atctctcagg cgatgggtgga cgaactcgtc 720
 gacagcgagg acaagaagcc gctggttcat gccgcggggg ggcattgcgtt gatctatggt 780
 cccgatggca ccctgcttac tcccaagctt gcagaagacg aggagggcct actgatcgcg 840
 gagatcgatc tgggggcaat cggggtcgcc aagaacgcgg cagaccccg cggccactac 900
 tcgcggcccc atgtcaccgc cctgctcttc aacaaccggc cggccaagcg cgtggagacg 960
 atgtcgtctc cggtcgacgc ggcagaagtc gtggagccgg cggacggagc gctcaatgcg 1020
 tccgagggac gccagcgaca gttcaagctg cccgcctag 1059

<210> 188
 <211> 352
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 188
 Met Gly Ile Asn His Pro Lys Tyr Lys Val Ala Val Val Gln Ala Ala

1	5	10	15
Pro Val Trp	Leu Asp Leu Asp Gly Thr	Val Asp Lys Cys	Ile Arg Leu
	20	25	30
Ile Gly Glu	Ala Ala Glu Lys Gly Cys	Lys Leu Ile	Ala Phe Pro Glu
	35	40	45
Thr Phe Ile	Pro Gly Tyr Pro Trp His	Ile Trp Met Gly	Ala Pro Ala
	50	55	60
Trp Thr Ile	Gly Arg Gly Phe Val Gln Arg	Tyr Phe Asp Asn Ser	Leu
	65	70	75
Ala Tyr Asp	Ser Pro Gln Ala Asn Lys	Leu Arg Ala Ala	Val Lys Arg
	85	90	95
Ala Gly Val	Thr Ala Val Leu Gly Leu Ser	Glu Arg Arg Gly	Gly Ser
	100	105	110
Leu Tyr Ile	Ala Gln Trp Leu Ile Gly	Pro Asp Gly Glu	Thr Ile Ala
	115	120	125
Gln Arg Arg	Lys Leu Arg Pro Thr His	Ala Glu Arg Thr	Val Phe Gly
	130	135	140
Glu Gly Asp	Gly Ser Asp Leu Ala Val His	Ser Arg Pro Asp	Ile Gly
	145	150	155
Arg Leu Gly	Ala Leu Cys Cys Trp Glu	His Leu Gln Pro	Leu Thr Lys
	165	170	175
Tyr Ala Met	Tyr Ala Gln Asp Glu Gln	Val His Val Ala	Ala Trp Pro
	180	185	190
Ser Phe Ser	Met Tyr Glu Pro Phe Ala	His Ala Leu Gly	Trp Glu Thr
	195	200	205
Asn Asn Ala	Val Ser Lys Val Tyr Ala	Val Glu Gly Ser	Cys Tyr Val
	210	215	220
Leu Ala Pro	Cys Ala Ile Ile Ser Gln	Ala Met Val Asp	Glu Leu Val
	225	230	235
Asp Ser Glu	Asp Lys Lys Pro Leu Val	His Ala Gly Gly	Gly His Ala
	245	250	255
Val Ile Tyr	Gly Pro Asp Gly Thr Leu	Leu Thr Pro Lys	Leu Ala Glu
	260	265	270
Asp Glu Glu	Gly Leu Leu Ile Ala Glu	Ile Asp Leu Gly	Ala Ile Gly
	275	280	285
Val Ala Lys	Asn Ala Ala Asp Pro	Ala Gly His Tyr	Ser Arg Pro Asp
	290	295	300
Val Thr Arg	Leu Leu Phe Asn Asn Arg	Pro Ala Lys Arg	Val Glu Thr
	305	310	315
Met Leu Leu	Pro Val Asp Ala Ala Glu	Val Val Glu Pro	Ala Asp Gly
	325	330	335
Ala Leu Asn	Ala Ser Glu Gly Arg Gln	Arg Gln Phe Lys	Leu Pro Ala
	340	345	350

<210> 189

<211> 1005

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 189

atgcaagaca	cgaaattcaa	agttgcagtc	gtccaggccg	cgccgggtatt	catggatgcg	60
ccagcctccg	tggccaaggc	gatcggtttc	atccaggagg	cgggcgccagc	cggggcgaag	120
ctgctggcgt	tcccggaggt	ctggattccg	ggctaccctt	ggtggctttg	gctcgggacg	180
ccggcgtggg	gaatgcagtt	tgtgccgcgc	tatcacgcca	attcgctgcg	tgctgatgga	240
cccgaatcc	tcgctctttg	tgccggccgc	gccgaagcga	agatcaacgt	cgtgatgggc	300
ttctccgaaa	tcgacggagg	aacgctctac	ctaagtcagg	ttttcatcag	cgatgcgggc	360
aagatcatct	tcaagcgccg	aaagctcaag	ccgaccacag	tcgaacgtac	gctatttggt	420
gaaggagatg	ggtctgattt	ccgagtcgtc	gacagcagcg	tcggggccct	cggagccctg	480

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tgctgtgccg aacacattca gccgttgtcg aaatacgcca tgtacgcgat gaacgagcaa 540
attcatgtgg cgctcgtggcc atctttcacg ctctatcgcg gcaaagccta cgctttgggt 600
catgaggtga atcttgccgc cagccaaatc tacgcgctcg aaggaggttg cttcgtcttg 660
catgccacgg caattaccgg tcaggatatg ttcgacatgc tttgcgacac tccggaaagg 720
gcggatttgc tgaatgcgga gggagcaaaag ccgggtggag gctattcgat gatttttggt 780
cccgatggtc agccgatgtg cgagcatctg ccgcaggaca aggaaggcat cctctatgcc 840
ggcgtagacc tgctgatgat tgcgatcgcc aaagcggcct acgatcctac ggggcactac 900
gcccgcggtg atgtcgtccg tctcatggtc aaccgcagcc cccgtcgcac gagcgtcagc 960
ttcagcgaag acgagaacgc ggcggtcact ttcaccgaga cctga 1005

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<210> 190
 <211> 334
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 190
Met Gln Asp Thr Lys Phe Lys Val Ala Val Val Gln Ala Ala Pro Val
1      5      10      15
Phe Met Asp Ala Pro Ala Ser Val Ala Lys Ala Ile Gly Phe Ile Gln
20     25     30
Glu Ala Gly Ala Ala Gly Ala Lys Leu Leu Ala Phe Pro Glu Val Trp
35     40     45
Ile Pro Gly Tyr Pro Trp Trp Leu Trp Leu Gly Thr Pro Ala Trp Gly
50     55     60
Met Gln Phe Val Pro Arg Tyr His Ala Asn Ser Leu Arg Ala Asp Gly
65     70     75     80
Pro Glu Ile Leu Ala Leu Cys Ala Ala Ala Glu Ala Lys Ile Asn
85     90     95
Val Val Met Gly Phe Ser Glu Ile Asp Gly Gly Thr Leu Tyr Leu Ser
100    105    110
Gln Val Phe Ile Ser Asp Ala Gly Lys Ile Ile Phe Lys Arg Arg Lys
115    120    125
Leu Lys Pro Thr His Val Glu Arg Thr Leu Phe Gly Glu Gly Asp Gly
130    135    140
Ser Asp Phe Arg Val Val Asp Ser Ser Val Gly Arg Leu Gly Ala Leu
145    150    155    160
Cys Cys Ala Glu His Ile Gln Pro Leu Ser Lys Tyr Ala Met Tyr Ala
165    170    175
Met Asn Glu Gln Ile His Val Ala Ser Trp Pro Ser Phe Thr Leu Tyr
180    185    190
Arg Gly Lys Ala Tyr Ala Leu Gly His Glu Val Asn Leu Ala Ala Ser
195    200    205
Gln Ile Tyr Ala Leu Glu Gly Gly Cys Phe Val Leu His Ala Thr Ala
210    215    220
Ile Thr Gly Gln Asp Met Phe Asp Met Leu Cys Asp Thr Pro Glu Arg
225    230    235    240
Ala Asp Leu Leu Asn Ala Glu Gly Ala Lys Pro Gly Gly Gly Tyr Ser
245    250    255
Met Ile Phe Gly Pro Asp Gly Gln Pro Met Cys Glu His Leu Pro Gln
260    265    270
Asp Lys Glu Gly Ile Leu Tyr Ala Gly Val Asp Leu Ser Met Ile Ala
275    280    285
Ile Ala Lys Ala Ala Tyr Asp Pro Thr Gly His Tyr Ala Arg Gly Asp
290    295    300
Val Val Arg Leu Met Val Asn Arg Ser Pro Arg Arg Thr Ser Val Ser
305    310    315    320
Phe Ser Glu Asp Glu Asn Ala Ala Val Thr Phe Thr Glu Thr
325    330

```

<210> 191
 <211> 945
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 191
 atgaaaaagt tagctgtggt tcaacgtgcg tcaggatttt tagataagca gcagagcatc 60
 gcgttggcgg tggaaagtat tcagtcctgct gcgaataatg gcgcagagct tggtgttttt 120
 acggaagcct ttattcctgg ttatcctgtc tggttatggc gtctgcgccc tggcaaagac 180
 tgggggacaa cagacagtct ttatcaacgc ttaataagca acgcggttga ttaagctca 240
 tcggatttgg atccgattta tgaagcggca aaacgtcatc acgtcacggt tgtatgcggc 300
 attaataaac gcgactccag cgtcagccga acaacgctat acaacactta catcacggtt 360
 tgtcatgagg gcaatctcat caatgttcat cgaaaactga tgccgaccaa cccagagaga 420
 atggtgtggt gctttggtga tgcgactgga ttaagggtag tagacactcc tgcggaagg 480
 attggctcac tcgtttgctg ggagaactac atgccgttgg cacgctatgc actttatgct 540
 cagggcgctc aaatttaccat tgcgcctact tatgacagtg gctcggactg gactgaaagc 600
 ttgcgccata tcgccagaga gggcagatgc tacgttgtcg gcagcggtaa cttgttgaga 660
 gccagcgacc tgctgatga tttccagaa aaagaaaccc tctatcctga taaagacgag 720
 tggattaacg gcggagactc taccgttacc gctcccggcg gtgaaacatt agttgctccg 780
 ctgcatgcag aggaagggcat actgtattgc gatattgata ctgataaagt ggcggcggct 840
 cggcgcttct tcgacgttgc aggccattac tctcgcccag acatatttac actcaacgta 900
 aatcgagcgc cgcaaacatc tctgcgtatc agggaagccg agtaa 945

<210> 192
 <211> 314
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 192
 Met Lys Lys Leu Ala Val Val Gln Arg Ala Ser Gly Phe Leu Asp Lys
 1 5 10 15
 Gln Gln Ser Ile Ala Leu Ala Val Glu Ser Ile Gln Ser Ala Ala Asn
 20 25 30
 Asn Gly Ala Glu Leu Val Val Phe Thr Glu Ala Phe Ile Pro Gly Tyr
 35 40 45
 Pro Val Trp Leu Trp Arg Leu Arg Pro Gly Lys Asp Trp Gly Thr Thr
 50 55 60
 Asp Ser Leu Tyr Gln Arg Leu Ile Ser Asn Ala Val Asp Leu Ser Ser
 65 70 75 80
 Ser Asp Leu Asp Pro Ile Tyr Glu Ala Ala Lys Arg His His Val Thr
 85 90 95
 Val Val Cys Gly Ile Asn Glu Arg Asp Ser Ser Val Ser Arg Thr Thr
 100 105 110
 Leu Tyr Asn Thr Tyr Ile Thr Val Cys His Glu Gly Asn Leu Ile Asn
 115 120 125
 Val His Arg Lys Leu Met Pro Thr Asn Pro Glu Arg Met Val Trp Gly
 130 135 140
 Phe Gly Asp Ala Thr Gly Leu Arg Val Val Asp Thr Pro Val Gly Arg
 145 150 155 160
 Ile Gly Ser Leu Val Cys Trp Glu Asn Tyr Met Pro Leu Ala Arg Tyr
 165 170 175
 Ala Leu Tyr Ala Gln Gly Val Glu Ile Tyr Ile Ala Pro Thr Tyr Asp
 180 185 190
 Ser Gly Ser Asp Trp Thr Glu Ser Leu Arg His Ile Ala Arg Glu Gly

```

      195              200              205
Arg Cys Tyr Val Val Gly Ser Gly Asn Leu Leu Arg Ala Ser Asp Leu
  210              215              220
Pro Asp Asp Phe Pro Glu Lys Glu Thr Leu Tyr Pro Asp Lys Asp Glu
  225              230              235              240
Trp Ile Asn Gly Gly Asp Ser Thr Val Ile Ala Pro Gly Gly Glu Thr
      245              250              255
Leu Val Ala Pro Leu His Ala Glu Glu Gly Ile Leu Tyr Cys Asp Ile
      260              265              270
Asp Thr Asp Lys Val Ala Ala Ala Arg Arg Ser Phe Asp Val Ala Gly
      275              280              285
His Tyr Ser Arg Pro Asp Ile Phe Thr Leu Asn Val Asn Arg Ala Pro
      290              295              300
Gln Thr Ser Leu Arg Ile Arg Glu Ala Glu
  305              310

```

<210> 193
 <211> 966
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 193
atgtcaaacg agaaccacaa ccaaacattc aaagttgccg cgggtgcaggc cacacctgta      60
ttcctcgatc gtgaagcgcac catcgacaaa gcttgtgagt tgattgctgc agccggcaat      120
gaaggagcgc ggctgggtgt cttcccggag gcattcatcc catcctaccc agattgggta      180
tgggcaatcc caccgggcga agaaggcgtg ctcaatgagt tgtacgcgga actgctctcc      240
aattcgggtca cgattcccag tgatgtgacg gatagactgt gccgagccgc gagacttgcc      300
aatgcctacg tagtgatggg gatgagcgaa cgcaatgccg aggccagtgg cgcaagcctg      360
tataacacgc tgttgtacat cgatgcgcag ggcgagattc tgggcaaaca tcgaaagctg      420
gtgccacacg gcggcgaaac gctgggtgtg gcgcagggcg atggcagcac gctgcaggtc      480
tacgatactc cactgggtaa actcggcggt ttgatttgtt gggagaatta tatgccgctg      540
ggccgctaca ccattgtacg atggggcaca caaatctatg ttgcggcgac atgggatcgc      600
gggcaaccct ggctctccac tttacggcat atcgccaaag aaggcagggt gtacgtgatc      660
ggctgctgta tcgtgatgcg caaagacgat atcccagatc gttaccgat gaagcagaag      720
ttttacgcgg aggccgatga gtggatcaac ataggggaca gcgcaatcgt caatcctgaa      780
gggcagttta gcgcggggcc ggtacgcaaa caggaagaga ttctctacgc ggaaattgat      840
ccgcgcatgg tgcaaggccc gaagtggatg ctcgacgtag cagggcacta cgcgaggccg      900
gacgtattcc agttgacggt gcatacggat gcgaggcaga tgatcaggtt ggaacacgat      960
gtttaa

```

<210> 194
 <211> 321
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 194
Met Ser Asn Glu Asn His Asn Gln Thr Phe Lys Val Ala Ala Val Gln
  1              5              10              15
Ala Thr Pro Val Phe Leu Asp Arg Glu Ala Thr Ile Asp Lys Ala Cys
      20              25              30
Glu Leu Ile Ala Ala Ala Gly Asn Glu Gly Ala Arg Leu Val Val Phe
      35              40              45
Pro Glu Ala Phe Ile Pro Ser Tyr Pro Asp Trp Val Trp Ala Ile Pro
      50              55              60
Pro Gly Glu Glu Gly Val Leu Asn Glu Leu Tyr Ala Glu Leu Leu Ser

```


65		70		75		80
Asn Ser Val Thr Ile Pro Ser Asp Val Thr Asp Arg Leu Cys Arg Ala						
	85		90			95
Ala Arg Leu Ala Asn Ala Tyr Val Val Met Gly Met Ser Glu Arg Asn						
	100		105			110
Ala Glu Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Ile Asp						
	115		120			125
Ala Gln Gly Glu Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly						
	130		135			140
Gly Glu Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Gln Val						
	145		150			155
Tyr Asp Thr Pro Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn						
	165		170			175
Tyr Met Pro Leu Ala Arg Tyr Thr Met Tyr Ala Trp Gly Thr Gln Ile						
	180		185			190
Tyr Val Ala Ala Thr Trp Asp Arg Gly Gln Pro Trp Leu Ser Thr Leu						
	195		200			205
Arg His Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys Ile						
	210		215			220
Val Met Arg Lys Asp Asp Ile Pro Asp Arg Tyr Pro Met Lys Gln Lys						
	225		230			235
Phe Tyr Ala Glu Ala Asp Glu Trp Ile Asn Ile Gly Asp Ser Ala Ile						
	245		250			255
Val Asn Pro Glu Gly Gln Phe Ser Ala Gly Pro Val Arg Lys Gln Glu						
	260		265			270
Glu Ile Leu Tyr Ala Glu Ile Asp Pro Arg Met Val Gln Gly Pro Lys						
	275		280			285
Trp Met Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Gln						
	290		295			300
Leu Thr Val His Thr Asp Ala Arg Gln Met Ile Arg Leu Glu His Asp						
	305		310			315
Val						320

<210> 195

<211> 993

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 195

atgaaagtcg tcaaagccgc cgcggtacag ttcagcccgg tgctctatag ccgtgaggca	60
accgtcgcca aggtcgtgca gaagatccac gaactcggcc agaaaaggcgt gcagttcgcc	120
accttcccgc aaacggctcgt gccttattac ccttactttg cggccgtcca gacgggcatac	180
gagcttctct cgggcaccga acatctgcgc ctgctcgaac aggctgtgac tgtcccgtcc	240
gctgctaccg acgcgatcgg cgaagccgcg cgaaggccg gcattggtcgt gtccattggc	300
gtcaatgagc gcgatggcgg cagcgtgtac aacgcacaac tgctcttcga tgccgacggg	360
acgctgatcc agcgccgcg caagatcacg ccgacgcatt tcgaacgcac gatctggggc	420
cagggagatg gctcgggctt gcgtgcagtc gacagcgccg tcggccgcgt cggccagctc	480
gcatgtttcg agcacaacaa cccgctcgcc cgctacgcaa tgatcgccga cggcgagcag	540
atccattcgg cgatgtaccc tggctcggcc tttggcgagg gcttcgcccc gcgtatggaa	600
atcaacatcc gccagcatgc gctcgagtcg gccgctttcg tcgtcaacgc aacagcgtgg	660
ctggacgccc accagcaggc gcaaatcatg aaggacaccg gttgtggaat cgggtccgatac	720
acggggcggt gcttcaccac gatcgtctct cctgacggca tgctgatggc cgagccgctt	780
cgctcgggtg aaggcgaagt gatcgtcgat ctcgacttca cgcagatcga ccgcccgaag	840
atgctgatgg actcggccgg ccaactacaac cgccctgaac tgctgagtcg gatgatcgac	900
cgtagccga cgcgcgatgt tcacgaacgc gcttcgcacc cgatgatcgt caacgaccag	960
ggttccgacg atctgcgcac ccaggctgca tga	993

<210> 196
 <211> 330
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 196
 Met Lys Val Val Lys Ala Ala Ala Val Gln Phe Ser Pro Val Leu Tyr
 1 5 10 15
 Ser Arg Glu Ala Thr Val Ala Lys Val Val Gln Lys Ile His Glu Leu
 20 25 30
 Gly Gln Lys Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
 35 40 45
 Tyr Tyr Pro Tyr Phe Ala Ala Val Gln Thr Gly Ile Glu Leu Leu Ser
 50 55 60
 Gly Thr Glu His Leu Arg Leu Leu Glu Gln Ala Val Thr Val Pro Ser
 65 70 75 80
 Ala Ala Thr Asp Ala Ile Gly Glu Ala Ala Arg Lys Ala Gly Met Val
 85 90 95
 Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn Ala
 100 105 110
 Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln Arg Arg Arg Lys
 115 120 125
 Ile Thr Pro Thr His Phe Glu Arg Met Ile Trp Gly Gln Gly Asp Gly
 130 135 140
 Ser Gly Leu Arg Ala Val Asp Ser Ala Val Gly Arg Val Gly Gln Leu
 145 150 155 160
 Ala Cys Phe Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Met Ile Ala
 165 170 175
 Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Ala Phe Gly
 180 185 190
 Glu Gly Phe Ala Gln Arg Met Glu Ile Asn Ile Arg Gln His Ala Leu
 195 200 205
 Glu Ser Ala Ala Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp
 210 215 220
 Gln Gln Ala Gln Ile Met Lys Asp Thr Gly Cys Gly Ile Gly Pro Ile
 225 230 235 240
 Thr Gly Gly Cys Phe Thr Thr Ile Val Ser Pro Asp Gly Met Leu Met
 245 250 255
 Ala Glu Pro Leu Arg Ser Gly Glu Gly Glu Val Ile Val Asp Leu Asp
 260 265 270
 Phe Thr Gln Ile Asp Arg Arg Lys Met Leu Met Asp Ser Ala Gly His
 275 280 285
 Tyr Asn Arg Pro Glu Leu Leu Ser Leu Met Ile Asp Arg Thr Pro Thr
 290 295 300
 Ala His Val His Glu Arg Ala Ser His Pro Met Ile Val Asn Asp Gln
 305 310 315 320
 Gly Ser Asp Asp Leu Arg Thr Gln Ala Ala
 325 330

<210> 197
 <211> 1017
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 197

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atgggcatcg aacatccaaa ataccgcgtt gccgccgtgc aggtgcgcc ggcctggctc      60
gacctcgatc gctcgatcga caaggctatt gcactgatcg aggaggccgc cgcgaacggc      120
gccagattga tcgattccc ggaggtcttc atccccggct acccctggca tatctggctc      180
gactcgccgg cctgggcgat cggccgcggc ttcgtgcagc gttatttcga caattcgctc      240
gcttatgata gtccgcaggc cgagcggctc cgcgcagcgg tccgcaaggc ggcctgacc      300
gccgtgatcg gcctttcgga gcggagcggc ggcagcctct acatcgcgca atggctcgtt      360
ggccccgacg gcgagaccat cgcaagcgc cgcaagctcc gtccgacgca tgcgagcgc      420
acggctctatg gcgagggcga cggcagcgat ctggcggctcc atgaccggcc cgatatcgga      480
cggctcgggc cgctgtgctg ctgggaacat ctgcaaccgt tgcgaaata tgcgatgtat      540
gcccagaacg agcaggcca tgtggcgta tggccgagtt ttgcgtcta cgatcccttt      600
gccccggcgc tcggcgcgga ggtgaacaat gcggcctccc gggctctatg ggtcgaaggc      660
tcctgcttcg tgcggcgcc gtgcgcgacc gtctcgagg ccatgatcga tgagctgtgc      720
gaccggcccc acaagcacgc gctgctccat gccggcggtg gctttgccgc gatctacggg      780
cccgacggca gttcgctggc cgaaaagctc gcgccggacc aggaggccct gctttacggc      840
gacatcgatc tcggcgcgat cggcgctcgc aagaacgccg ccgaccggc agggcattat      900
tcggggcccg atgtcacgcg gctgctgctg aacaacaagc cctacaagcg cgtggagcat      960
tttgctttgc ccggcgatac cgtggcgctt gccgatgtgg atgcggcggc gagctga      1017

```

<210> 198

<211> 338

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 198

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Met Gly Ile Glu His Pro Lys Tyr Arg Val Ala Ala Val Gln Ala Ala
 1              5              10              15
Pro Ala Trp Leu Asp Leu Asp Arg Ser Ile Asp Lys Ala Ile Ala Leu
 20              25              30
Ile Glu Glu Ala Ala Ala Asn Gly Ala Arg Leu Ile Ala Phe Pro Glu
 35              40              45
Val Phe Ile Pro Gly Tyr Pro Trp His Ile Trp Leu Asp Ser Pro Ala
 50              55              60
Trp Ala Ile Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
 65              70              75              80
Ala Tyr Asp Ser Pro Gln Ala Glu Arg Leu Arg Ala Ala Val Arg Lys
 85              90              95
Ala Arg Leu Thr Ala Val Ile Gly Leu Ser Glu Arg Ser Gly Gly Ser
100              105              110
Leu Tyr Ile Ala Gln Trp Leu Val Gly Pro Asp Gly Glu Thr Ile Ala
115              120              125
Lys Arg Arg Lys Leu Arg Pro Thr His Ala Glu Arg Thr Val Tyr Gly
130              135              140
Glu Gly Asp Gly Ser Asp Leu Ala Val His Asp Arg Pro Asp Ile Gly
145              150              155              160
Arg Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys
165              170              175
Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ser Trp Pro
180              185              190
Ser Phe Ser Leu Tyr Asp Pro Phe Ala Pro Ala Leu Gly Ala Glu Val
195              200              205
Asn Asn Ala Ala Ser Arg Val Tyr Ala Val Glu Gly Ser Cys Phe Val
210              215              220
Leu Ala Pro Cys Ala Thr Val Ser Gln Ala Met Ile Asp Glu Leu Cys
225              230              235              240
Asp Arg Pro Asp Lys His Ala Leu Leu His Ala Gly Gly Gly Phe Ala
245              250              255
Ala Ile Tyr Gly Pro Asp Gly Ser Ser Leu Ala Glu Lys Leu Ala Pro
260              265              270

```

Asp Gln Glu Gly Leu Leu Tyr Ala Asp Ile Asp Leu Gly Ala Ile Gly
 275 280 285
 Val Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
 290 295 300
 Val Thr Arg Leu Leu Leu Asn Asn Lys Pro Tyr Lys Arg Val Glu His
 305 310 315 320
 Phe Ala Leu Pro Gly Asp Thr Val Ala Pro Ala Asp Val Asp Ala Ala
 325 330 335
 Ala Ser

<210> 199

<211> 993

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 199

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atgtcaaacg cactgaagcc gttcaaaatc gccgccgttc aggcgacgcc ggtttttctg      60
aaccgggaag ccacggcgga gaagcccgcg gctttgatcc gcgaagcggg aagcgccgga      120
gccaaagtcca tcgtttttccc ggaatcgttt attccggcct atccggactg ggtctgggtg      180
gtccctctcg ggagggatcg ccttctcagc ggcctctacg gggagatgct cgaaaacgcc      240
gtggaaatcc ccggcccggc cacggggcat atcgcccggg cggcgaagga atcgggcgct      300
tatgtcgtca tgggcgtgac cgagcgggac acggaggcga gcggagccag tttgttcaac      360
accttgattt atttcggtcc gaccggggaa attttgggca aacaccggaa gctgggtccc      420
accgggggcg aacggatcgt ctggggcccag ggggacggaa gcaccctgga ggtctacgat      480
acgcccctgg gaaaactggg cgggctgata tgctgggaaa actacatgcc cctggcccgg      540
tacgccatgt acgcttgggg aaccacgctt tacgtggccg ccacctggga ccgagggcga      600
ccctggcttt cgacgcttcg gcatatcgcc aaggaaggcg ggtgtatgt catcggtgac      660
tgcatcgcca tcgggaaagg ggatatcccg gatcggttcg aacacaaggg gctctacgcc      720
cccgaacggg actggatcaa ccccgcgac agcgcgatcg tcaaccccca gggggagatg      780
atcgccgggc ccgcttccaa taaggaaagag atcctttatg cggaagtcga cccgcagatg      840
atgcgcgggc ccaaattgat gctcgatgtg gccggccatt acgcgcggcc cgatgtcttc      900
gagctcaccg tccgccggga accgcggcgg atgatccgcg tggcgggagg cgcgggcggg      960
accgaaccca aagagaagaa gaccgccggc tga                                     993
  
```

<210> 200

<211> 330

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 200

Met Ser Asn Ala Leu Lys Pro Phe Lys Ile Ala Ala Val Gln Ala Thr
 1 5 10 15
 Pro Val Phe Leu Asn Arg Glu Ala Thr Ala Glu Lys Ala Ala Ala Leu
 20 25 30
 Ile Arg Glu Ala Gly Ser Ala Gly Ala Lys Leu Ile Val Phe Pro Glu
 35 40 45
 Ser Phe Ile Pro Ala Tyr Pro Asp Trp Val Trp Val Val Pro Ser Gly
 50 55 60
 Arg Asp Arg Leu Leu Ser Gly Leu Tyr Gly Glu Met Leu Glu Asn Ala
 65 70 75 80
 Val Glu Ile Pro Gly Pro Ala Thr Gly His Ile Gly Arg Ala Ala Lys
 85 90 95
 Glu Ser Gly Ala Tyr Val Val Met Gly Val Thr Glu Arg Asp Thr Glu
 100 105 110

Ala Ser Gly Ala Ser Leu Phe Asn Thr Leu Ile Tyr Phe Gly Pro Thr
 115 120 125
 Gly Glu Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly Gly Glu
 130 135 140
 Arg Ile Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Glu Val Tyr Asp
 145 150 155 160
 Thr Pro Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn Tyr Met
 165 170 175
 Pro Leu Ala Arg Tyr Ala Met Tyr Ala Trp Gly Thr Gln Leu Tyr Val
 180 185 190
 Ala Ala Thr Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Leu Arg His
 195 200 205
 Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys Ile Ala Met
 210 215 220
 Arg Lys Gly Asp Ile Pro Asp Arg Phe Glu His Lys Gly Leu Tyr Ala
 225 230 235 240
 Pro Asp Arg Asp Trp Ile Asn Pro Gly Asp Ser Ala Ile Val Asn Pro
 245 250 255
 Gln Gly Glu Met Ile Ala Gly Pro Ala Ser Asn Lys Glu Glu Ile Leu
 260 265 270
 Tyr Ala Glu Val Asp Pro Gln Met Met Arg Gly Pro Lys Trp Met Leu
 275 280 285
 Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Glu Leu Thr Val
 290 295 300
 Arg Arg Glu Pro Arg Pro Met Ile Arg Val Ala Gly Gly Ala Gly Gly
 305 310 315 320
 Thr Glu Pro Lys Glu Lys Lys Thr Ala Gly
 325 330

<210> 201

<211> 930

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 201

atgaccacga	agagcatccg	catcgcggcc	gtacaggcgg	ctcccgcggt	tctcgacctg	60
gctggtacgc	tggaccggct	cgaggcctgg	gcccgcaagg	ccgccgccac	cggtgcccgc	120
gtcatcgcg	tccccgagac	ctggctgccc	ggctacccgg	cgtggatcga	ctcgtcgccg	180
gaggccgcga	tctggggcca	tcccggctcg	cgcgacctgc	accagcgcc	gatggagaat	240
gccgtcgagg	tccccggccc	cgcgaccgcg	cgcatcgcg	agctcgccgg	cgagctcggc	300
gtgacgatcg	tggctggcgc	gcacgagcgg	gcggggaaca	ccctctacaa	cacggcgctg	360
acgttcgggc	ccgagggcag	gctgctcaat	caccaccgga	agctggtgcc	gacctacagc	420
gaacggctgc	tgtggggcta	cggcgacggc	gctggactgg	tggcgccggc	ggtggacggg	480
gtgaaggctg	gggcgctgg	gtgctgggag	cactggatgc	cgctcaccg	ccaggcgatg	540
cacgacgtcg	gcgagcacgt	gcacgtcgcc	ctgtggcccc	gcgtccacga	gatgcaccag	600
gtggcctcgc	ggcactatgc	gttcgagggc	cgctgtttcg	tgatcgcggt	cgggagcatc	660
ctgcgcgtgg	accagatgcc	gaagcagctg	ccgccgctgg	agaagtacgc	gaagagcgcc	720
aaggggctga	tgatcgcggg	cggcagcgcc	atcatcgcg	cgaacggccg	ctacgtcgcg	780
gcgccggtgt	acgacgagga	gacgatcgtc	accgccgact	gcgacctcgg	cgagatcccc	840
cgcgaggcgc	agacgctcga	tgtctcgggc	cactacagcc	ggccggacgt	gttcagcttc	900
ggggtggtca	gacaccggcc	gcgtgcgtaa				930

<210> 202

<211> 309

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 202

```

Met Thr Thr Lys Ser Ile Arg Ile Ala Ala Val Gln Ala Ala Pro Ala
 1          5          10          15
Phe Leu Asp Leu Ala Gly Thr Leu Asp Arg Leu Glu Ala Trp Ala Arg
 20          25          30
Lys Ala Ala Ala Thr Gly Ala Arg Val Ile Ala Phe Pro Glu Thr Trp
 35          40          45
Leu Pro Gly Tyr Pro Ala Trp Ile Asp Ser Ser Pro Glu Ala Ala Ile
 50          55          60
Trp Gly His Pro Gly Ser Arg Asp Leu His Gln Arg Leu Met Glu Asn
 65          70          75          80
Ala Val Glu Val Pro Gly Pro Ala Thr Ala Arg Ile Ala Lys Leu Ala
 85          90          95
Gly Glu Leu Gly Val Thr Ile Val Val Gly Ala His Glu Arg Ala Gly
100          105          110
Asn Thr Leu Tyr Asn Thr Ala Leu Thr Phe Gly Pro Glu Gly Arg Leu
115          120          125
Leu Asn His His Arg Lys Leu Val Pro Thr Tyr Ser Glu Arg Leu Leu
130          135          140
Trp Gly Tyr Gly Asp Gly Ala Gly Leu Val Ala Pro Ala Val Asp Gly
145          150          155          160
Val Lys Val Gly Ala Leu Val Cys Trp Glu His Trp Met Pro Leu Thr
165          170          175
Arg Gln Ala Met His Asp Val Gly Glu His Val His Val Ala Leu Trp
180          185          190
Pro Gly Val His Glu Met His Gln Val Ala Ser Arg His Tyr Ala Phe
195          200          205
Glu Gly Arg Cys Phe Val Ile Ala Val Gly Ser Ile Leu Arg Val Asp
210          215          220
Gln Met Pro Lys Gln Leu Pro Pro Leu Glu Lys Tyr Ala Lys Ser Ala
225          230          235          240
Lys Gly Leu Met Ile Ala Gly Gly Ser Ala Ile Ile Ala Pro Asn Gly
245          250          255
Arg Tyr Val Ala Ala Pro Val Tyr Asp Glu Glu Thr Ile Val Thr Ala
260          265          270
Asp Cys Asp Leu Gly Glu Ile Pro Arg Glu Ala Gln Thr Leu Asp Val
275          280          285
Ser Gly His Tyr Ser Arg Pro Asp Val Phe Ser Phe Gly Val Val Arg
290          295          300
His Arg Pro Arg Ala
305

```

<210> 203

<211> 966

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 203

```

atgtcaagct tacccacatc cgcgttcacc gtcgccgccg cgcaagcgtc gccagtgttc      60
ctcgaccgcg acgcgacgct gcagaaggct tgcgggctga tcgccgacgc cgggcgcgcg      120
ggcgcgcgcg tgatcgtctt cccgaagcc ttcattccgg cctaccccca ttgggtgtgg      180
gcgggtcccag ctggcgaaga ggggatgctg agcgagctct acgccgagct ggtcgcgaat      240
tcgctggcta ttccgagcga cgcgaccgat cggctatgtc gcgcggcgca ggccgcgcac      300
atcaatgtgg tcgtgggggt gagcgaagcgc aatgtcgagg ccagcggcgc cagcctctac      360
aacacgctgc tgtatatcga cgcggcggga acgatacctg gtaaacaccg caagcttgtg      420
ccgaccggcg gggagcgccct ggtctgggcg cagggcgacg gcagcacgct cgatgtgtac      480

```

```

gacaccgcgc tcggcaagct cggcgccctg atctgttggg aaaactacat gccgctggca 540
cgctacgcgc tgtacgcctg ggggtgtgcaa atctatgtcg cggccacctg ggatcgcggc 600
gagccctggc tttctactct gcgacatata gccaaaggaag gccgtgtcta cgtgatcggc 660
tgtggcatgg cgctgcgcag agatgatatt cccgatcgct tcgctttcaa gcagcgcttc 720
tatgcccagg ccggcgcaatg gatcaacgtc ggcgacagcg cgatcgctcaa cccgagcggc 780
gagtttattg ccggacctgt gcgcgaacgc gaggagattc tgtacgcgga ggtcgacccg 840
gagcagatga gcgggccaaa gtggatgctc gacgtggccg ggcactacgg gcggccggat 900
gtcttcgggc tcagcgtcaa ccgggcgccc caccagatga tccagacgga gaaccgggag 960
acctga 966

```

<210> 204

<211> 321

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 204

```

Met Ser Ser Leu Pro Thr Ser Ala Phe Thr Val Ala Ala Ala Gln Ala
1      5      10      15
Ser Pro Val Phe Leu Asp Arg Asp Ala Thr Leu Gln Lys Ala Cys Gly
20     25     30
Leu Ile Ala Asp Ala Gly Arg Ala Gly Ala Arg Leu Ile Val Phe Pro
35     40     45
Glu Ala Phe Ile Pro Ala Tyr Pro Asp Trp Val Trp Ala Val Pro Ala
50     55     60
Gly Glu Glu Gly Met Leu Ser Glu Leu Tyr Ala Glu Leu Val Ala Asn
65     70     75     80
Ser Leu Ala Ile Pro Ser Asp Ala Thr Asp Arg Leu Cys Arg Ala Ala
85     90     95
Gln Ala Ala His Ile Asn Val Val Val Gly Leu Ser Glu Arg Asn Val
100    105    110
Glu Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Ile Asp Ala
115    120    125
Ala Gly Thr Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly Gly
130    135    140
Glu Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Asp Val Tyr
145    150    155    160
Asp Thr Ala Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn Tyr
165    170    175
Met Pro Leu Ala Arg Tyr Ala Leu Tyr Ala Trp Gly Val Gln Ile Tyr
180    185    190
Val Ala Ala Thr Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Leu Arg
195    200    205
His Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Gly Met Ala
210    215    220
Leu Arg Arg Asp Asp Ile Pro Asp Arg Phe Ala Phe Lys Gln Arg Phe
225    230    235    240
Tyr Ala Gln Ala Gly Glu Trp Ile Asn Val Gly Asp Ser Ala Ile Val
245    250    255
Asn Pro Ser Gly Glu Phe Ile Ala Gly Pro Val Arg Glu Arg Glu Glu
260    265    270
Ile Leu Tyr Ala Glu Val Asp Pro Glu Gln Met Ser Gly Pro Lys Trp
275    280    285
Met Leu Asp Val Ala Gly His Tyr Gly Arg Pro Asp Val Phe Arg Leu
290    295    300
Ser Val Asn Arg Ala Pro His Gln Met Ile Gln Thr Glu Asn Arg Glu
305    310    315    320
Thr

```

<210> 205
 <211> 969
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 205
 atgaccaccg taaaagccgc cgcagtagc atcagccccg tgctctatag ccgggaggcc 60
 accgtagaca aggtcgttcg caagatccgc gagctcggcc aaaagggagt gcagttcgcc 120
 accttcccgc aaaccgtagt gccgtactac ccctacttcg ctgcagtcca gacaggcatc 180
 gaactgttgt ccggcaagga acacatgcgc ctgctggagc aggcggttac cgtcccctcg 240
 cccgccacgc atgcgattgc tcaggcggcg cgcgaagcca atatgggtgt gtccatcgcc 300
 gtcaacgagc gcgacggcgc caccatctac aacacgcagc tgctcttcga tgccgacggc 360
 acgctcgtgc agcgccgccc caagataacg ccaacgcact tcgagcgcat ggtctggggc 420
 cagggcgatg gttcgggatt gcgcgcgcgc gacaccaagg ttggccgcat cggccagttg 480
 gcctgcttcg agcacaacaa cccgctcgcc cgttacgcca tgatggccga tggcgagcag 540
 atccactccg ccatgtatccc gggctcggcc ttcggcgagg gcttcgcgca gcgatggag 600
 atcaacatcc gccagcatgc cctggagtct ggtgcttcg tggatgaatgc gaccgcctgg 660
 ctgatgccc accaacaggc gcagatcatg aaggacaccg gttgctcgat cggcccgatc 720
 tccggcggtc gcttcacgac catcgtcacg cctgagggca tgctgattgg cgagccgctc 780
 cgcgaggggc aaggcgaaat catcgccgac ctcgatttct cgatgatcga tcgccgcaag 840
 ctgctgatgg actcggtcgg tcaactacaac cgtccggagc ttctgagcct cctgatcgat 900
 cgcacgcctg ccgcgaactt ccatgaacgt accgcgagcc aggcgaacgc cggcgctcgaa 960
 atcctctga 969

<210> 206
 <211> 322
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 206
 Met Thr Thr Val Lys Ala Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
 1 5 10 15
 Ser Arg Glu Ala Thr Val Asp Lys Val Val Arg Lys Ile Arg Glu Leu
 20 25 30
 Gly Gln Lys Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
 35 40 45
 Tyr Tyr Pro Tyr Phe Ala Ala Val Gln Thr Gly Ile Glu Leu Leu Ser
 50 55 60
 Gly Lys Glu His Met Arg Leu Leu Glu Gln Ala Val Thr Val Pro Ser
 65 70 75 80
 Pro Ala Thr Asp Ala Ile Ala Gln Ala Ala Arg Glu Ala Asn Met Val
 85 90 95
 Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Ile Tyr Asn Thr
 100 105 110
 Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Val Gln Arg Arg Arg Lys
 115 120 125
 Ile Thr Pro Thr His Phe Glu Arg Met Val Trp Gly Gln Gly Asp Gly
 130 135 140
 Ser Gly Leu Arg Ala Ala Asp Thr Lys Val Gly Arg Ile Gly Gln Leu
 145 150 155 160
 Ala Cys Phe Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Met Met Ala
 165 170 175
 Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Ala Phe Gly
 180 185 190

Glu Gly Phe Ala Gln Arg Met Glu Ile Asn Ile Arg Gln His Ala Leu
 195 200 205
 Glu Ser Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp
 210 215 220
 Gln Gln Ala Gln Ile Met Lys Asp Thr Gly Cys Ser Ile Gly Pro Ile
 225 230 235 240
 Ser Gly Gly Cys Phe Thr Thr Ile Val Thr Pro Glu Gly Met Leu Ile
 245 250 255
 Gly Glu Pro Leu Arg Glu Gly Glu Gly Ile Ile Ala Asp Leu Asp
 260 265 270
 Phe Ser Met Ile Asp Arg Arg Lys Leu Leu Met Asp Ser Val Gly His
 275 280 285
 Tyr Asn Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro Ala
 290 295 300
 Ala Asn Phe His Glu Arg Thr Ala Ser Gln Ala Asn Ala Gly Val Glu
 305 310 315 320
 Ile Leu

<210> 207

<211> 966

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 207

atgtcaaacg	agaacaacaa	cgctacattc	aaagttgccg	cagtacaggc	tacacctgtt	60
tttctcgatc	gtgaagcgac	tctcgacaag	gcttgcgatt	tgatcgccgc	cgccggaggt	120
gaaggggcac	gattggttgt	ctttccagaa	gccttcatac	cggcctatcc	ggattgggta	180
tgggcaatcc	caccgggtga	agagggcgta	cttaatgagt	tgtacgcaga	gctgctctcc	240
aactcgggtca	cgattcccag	tgacgcgacg	gacagactgt	gccggggccg	gaggcttgct	300
aatgcttacg	tggatgatgg	gataagcgaa	cgcaatgtcg	aggcgagtgg	agcaagcctg	360
tataacacgc	tgtgtgtacat	cgatgcgcag	ggtgagattc	taggcaaaca	tcgaaagcta	420
gtgccaacgg	gcggcgagcg	gctgggtgtg	gcgcagggcg	atggcagcac	actgcaggtc	480
tacgatactc	cactgggaaa	actcggcggt	ttaatttgct	gggagaatta	tatgccgctg	540
gcccgctata	ccatgtatgc	ctggggcaca	caaatctatg	tcgccgctac	gtgggatcgc	600
gggcaaccct	ggctctccac	tttgcggcat	atcgccaaag	aaggcagggt	gtacgtgatt	660
ggttggtgta	tcgcgatgcy	caaagacgat	atccctgatc	gttacgcaat	gaagcagaag	720
ttttacgcgg	aggcagatga	gtggatcaat	ataggtgaca	gcgcgattgt	caatcctgaa	780
gggcaattta	tcgcagggcc	agtagcgaag	caggaagaga	ttctctacgc	agagattgat	840
ccgcgcgatg	tacaagggcc	gaagtggatg	ctcgacgtgg	cggggcacta	tgccaggccg	900
gatgtgttcc	agttgacggt	gcatacggat	gtgcgacaga	tgattcggat	ggaacacgat	960
tcttaa						966

<210> 208

<211> 321

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 208

Met	Ser	Asn	Glu	Asn	Asn	Asn	Ala	Thr	Phe	Lys	Val	Ala	Ala	Val	Gln
1				5					10					15	
Ala	Thr	Pro	Val	Phe	Leu	Asp	Arg	Glu	Ala	Thr	Leu	Asp	Lys	Ala	Cys
			20					25				30			
Asp	Leu	Ile	Ala	Ala	Ala	Gly	Gly	Glu	Gly	Ala	Arg	Leu	Val	Val	Phe
	35						40					45			

Pro Glu Ala Phe Ile Pro Ala Tyr Pro Asp Trp Val Trp Ala Ile Pro
 50 55 60
 Pro Gly Glu Glu Gly Val Leu Asn Glu Leu Tyr Ala Glu Leu Leu Ser
 65 70 75 80
 Asn Ser Val Thr Ile Pro Ser Asp Ala Thr Asp Arg Leu Cys Arg Ala
 85 90 95
 Ala Arg Leu Ala Asn Ala Tyr Val Val Met Gly Ile Ser Glu Arg Asn
 100 105 110
 Val Glu Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Ile Asp
 115 120 125
 Ala Gln Gly Glu Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly
 130 135 140
 Gly Glu Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Gln Val
 145 150 155 160
 Tyr Asp Thr Pro Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn
 165 170 175
 Tyr Met Pro Leu Ala Arg Tyr Thr Met Tyr Ala Trp Gly Thr Gln Ile
 180 185 190
 Tyr Val Ala Ala Thr Trp Asp Arg Gly Gln Pro Trp Leu Ser Thr Leu
 195 200 205
 Arg His Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys Ile
 210 215 220
 Ala Met Arg Lys Asp Asp Ile Pro Asp Arg Tyr Ala Met Lys Gln Lys
 225 230 235 240
 Phe Tyr Ala Glu Ala Asp Glu Trp Ile Asn Ile Gly Asp Ser Ala Ile
 245 250 255
 Val Asn Pro Glu Gly Gln Phe Ile Ala Gly Pro Val Arg Lys Gln Glu
 260 265 270
 Glu Ile Leu Tyr Ala Glu Ile Asp Pro Arg Met Val Gln Gly Pro Lys
 275 280 285
 Trp Met Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Gln
 290 295 300
 Leu Thr Val His Thr Asp Val Arg Gln Met Ile Arg Met Glu His Asp
 305 310 315 320
 Ser

<210> 209

<211> 993

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 209

atgaaagtcg	tcaaagccgc	cgctgtccag	atcagtcccg	ttctctacag	ccgtgaggca	60
accgtcgaaa	aggtcgtgaa	gaaaattcac	gagcttggcc	aactgggcgt	gcagttcgcc	120
acctttcccg	agaccgtagt	gccttactac	ccgtactttt	ccgccgtcca	gacaggcatt	180
gagcttctgt	ccggaactga	gcatctgcgg	ctgctcgatc	aggccgtgac	ggtaccgtct	240
cccgctaccg	atcgatcgg	agaggcgcc	cgcaaggcgg	gcatggtggt	gtccatcggc	300
gtgaatgaac	gcgacggcgg	cacctgttac	aacacacagt	tgctcttcga	tgccgatggc	360
accttgatcc	agcgccgccc	caagatcacg	cccacccact	tcgaacggat	gatctggggc	420
cagggggacg	gctcgggcct	gcgcgccgtc	gacagcaagg	ttggtcgcat	tggtcagctt	480
gctgcttcg	agcacaacaa	cccgttgccc	cgctacgcgc	tgattgccga	cggcgagcag	540
atccattccg	ccatgtatcc	gggttctgct	ttcggcgaag	gctttgcccc	aaggatggaa	600
atcaatatcc	gccagcatgc	gctggagtct	ggtgcctttg	tcgtcaacgc	aacggcctgg	660
ctggatgctg	accagcaggc	gcaaatcatc	aaggacaccg	gctgtgggat	tggcccgatc	720
tcgggcggct	gcttcaccac	gatcgtggca	cccgcgggca	tgctgatggc	cgaacctctg	780
cgttcgggcg	aggggtgaggt	catcgtggat	ctcgacttca	cgctgatcga	ccgacgcaag	840
atgttgatgg	actcggcggg	ccactataac	cgtccagaac	tgctcagttc	catgattgac	900

cgtaccgcga cggcgcatgt tcacgaacgc gctgcgcac cgggtgcggg cgcggagcag 960
 ggtccggagg atctgcgcac tccggccgcg tga 993

<210> 210
 <211> 330
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 210
 Met Lys Val Val Lys Ala Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
 1 5 10 15
 Ser Arg Glu Ala Thr Val Glu Lys Val Val Lys Lys Ile His Glu Leu
 20 25 30
 Gly Gln Leu Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
 35 40 45
 Tyr Tyr Pro Tyr Phe Ser Ala Val Gln Thr Gly Ile Glu Leu Leu Ser
 50 55 60
 Gly Thr Glu His Leu Arg Leu Leu Asp Gln Ala Val Thr Val Pro Ser
 65 70 75 80
 Pro Ala Thr Asp Ala Ile Gly Glu Ala Ala Arg Lys Ala Gly Met Val
 85 90 95
 Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn Thr
 100 105 110
 Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln Arg Arg Arg Lys
 115 120 125
 Ile Thr Pro Thr His Phe Glu Arg Met Ile Trp Gly Gln Gly Asp Gly
 130 135 140
 Ser Gly Leu Arg Ala Val Asp Ser Lys Val Gly Arg Ile Gly Gln Leu
 145 150 155 160
 Ala Cys Phe Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Leu Ile Ala
 165 170 175
 Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Ala Phe Gly
 180 185 190
 Glu Gly Phe Ala Gln Arg Met Glu Ile Asn Ile Arg Gln His Ala Leu
 195 200 205
 Glu Ser Gly Ala Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp
 210 215 220
 Gln Gln Ala Gln Ile Ile Lys Asp Thr Gly Cys Gly Ile Gly Pro Ile
 225 230 235 240
 Ser Gly Gly Cys Phe Thr Thr Ile Val Ala Pro Asp Gly Met Leu Met
 245 250 255
 Ala Glu Pro Leu Arg Ser Gly Glu Gly Glu Val Ile Val Asp Leu Asp
 260 265 270
 Phe Thr Leu Ile Asp Arg Arg Lys Met Leu Met Asp Ser Ala Gly His
 275 280 285
 Tyr Asn Arg Pro Glu Leu Leu Ser Leu Met Ile Asp Arg Thr Ala Thr
 290 295 300
 Ala His Val His Glu Arg Ala Ala His Pro Val Ser Gly Ala Glu Gln
 305 310 315 320
 Gly Pro Glu Asp Leu Arg Thr Pro Ala Ala
 325 330

<210> 211
 <211> 1062
 <212> DNA
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 211

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atgggcgctcg cacatccgaa atacaaagtg gccgccgtgc aggcagcgcc cgcttttctc      60
gacctggacg cctcggtcga aaaggccgtc cgtttcatcg acgaagccgg cgccgccggc      120
gcccgcctca tcgcctttcc ggagacctgg atacccggtt acccctggtg gatctggcta      180
ggcgcgccgg cctgggctat catgcgcggc ttcgtctcgc gctatttcga caactcgctc      240
agctacgaca gcccgcaggc cgagaagctc cgcgccgccc ccaagcgcaa caagatggtg      300
gtggtgctcg gcctctccga gcgcgacggc ggagcctttt acatcgcgca atggatcatc      360
ggcccggaag cgaaaccat cgccaagcgc cgcaagctca agccgaccca cgcgagcgcg      420
accgtgttcg gcgaaggcga cggctcgcat cttgcggtgc acgagcttga tgttgccggg      480
ctcggcgcgc tgtgctgctg ggaacacctg cagccgctgt ccaaatacgc catgtatgcg      540
cagaacgaac aggtgcatgt cgcggcctgg ccgagctttt cgctttacga tccgttcgcg      600
cacgcgctcg gcgcggaagt gaacaatgcg gcgagcaaaa tctatgcggg cgagggctcg      660
tgtttcgtca tcgcgccgtg cgcgaccgtt tcgcaggcga tgatcgacga actctgcat      720
acgcccggaga agcatcagtt cctgcatgcc ggcgcgcggt ttgccgtgat ttacggcccc      780
gacggcgccc cgctcgcggc gccgctgccg cccgacaagg aaggcttgct ctacggcgac      840
atcgatctcg ggatgatttc ggttgccaaa gcggcagccg atccggccgg gcattatgca      900
cgccccgacg tcacccggtt tctgttcaac aatcggcctg ggtatcggtt cgagaccatg      960
gcgttgccga tcgatgcgga gaccaaggcg gaagcaccgg ctaagccgga acccaaggca     1020
ccgaacgtgg cgccgttcgc gccgtgcaa gcggccgagt ga                               1062

```

<210> 212

<211> 353

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 212

```

Met Gly Val Ala His Pro Lys Tyr Lys Val Ala Ala Val Gln Ala Ala
 1          5          10          15
Pro Ala Phe Leu Asp Leu Asp Ala Ser Val Glu Lys Ala Val Arg Phe
 20          25          30
Ile Asp Glu Ala Gly Ala Ala Gly Ala Arg Leu Ile Ala Phe Pro Glu
 35          40          45
Thr Trp Ile Pro Gly Tyr Pro Trp Trp Ile Trp Leu Gly Ala Pro Ala
 50          55          60
Trp Ala Ile Met Arg Gly Phe Val Ser Arg Tyr Phe Asp Asn Ser Leu
 65          70          75          80
Ser Tyr Asp Ser Pro Gln Ala Glu Lys Leu Arg Ala Ala Ala Lys Arg
 85          90          95
Asn Lys Met Val Val Val Leu Gly Leu Ser Glu Arg Asp Gly Gly Ser
100          105          110
Leu Tyr Ile Ala Gln Trp Ile Ile Gly Pro Asp Gly Glu Thr Ile Ala
115          120          125
Lys Arg Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly
130          135          140
Glu Gly Asp Gly Ser His Leu Ala Val His Glu Leu Asp Val Gly Arg
145          150          155          160
Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr
165          170          175
Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ala Trp Pro Ser
180          185          190
Phe Ser Leu Tyr Asp Pro Phe Ala His Ala Leu Gly Ala Glu Val Asn
195          200          205
Asn Ala Ala Ser Lys Ile Tyr Ala Val Glu Gly Ser Cys Phe Val Ile
210          215          220
Ala Pro Cys Ala Thr Val Ser Gln Ala Met Ile Asp Glu Leu Cys Asp
225          230          235          240

```

Thr Pro Glu Lys His Gln Phe Leu His Ala Gly Gly Gly Phe Ala Val
 245 250 255
 Ile Tyr Gly Pro Asp Gly Ala Pro Leu Ala Ala Pro Leu Pro Pro Asp
 260 265 270
 Lys Glu Gly Leu Leu Tyr Ala Asp Ile Asp Leu Gly Met Ile Ser Val
 275 280 285
 Ala Lys Ala Ala Ala Asp Pro Ala Gly His Tyr Ala Arg Pro Asp Val
 290 295 300
 Thr Arg Leu Leu Phe Asn Asn Arg Pro Gly Tyr Arg Val Glu Thr Met
 305 310 315 320
 Ala Leu Pro Ile Asp Ala Glu Thr Lys Ala Glu Ala Pro Ala Lys Pro
 325 330 335
 Glu Pro Lys Ala Pro Asn Val Ala Pro Phe Ala Pro Val Gln Ala Ala
 340 345 350
 Glu

<210> 213
 <211> 993
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 213
 atgagagttg ttaaagccgc tgctgtccaa ctgagtcctg tcctctatag tcgcgaggga 60
 acggtcgaaa aggtcggtcg gaagatccat gaacttgccg aagaggaggc cgagttcgcc 120
 accttcctg agaccgtggt gccttactac ccgtactttt ccttcgttca gacgcccttg 180
 gagcaaatct tcggaacaga gtatctgagg ctgctcgacc aggcagtcac cgtgccatcc 240
 cctgccaccg acgcgatcgg cgaggcagcc aggttcgctg gagttgttgt ctcgatcggc 300
 gtcaacgagc gagacggggg aactctatac aacactcagc ttctcttcga tgcgacggc 360
 aggataattc agcgcgcgcc caagatcacg cccaccatt acgagcgcat gatctggggc 420
 cagggcgacg gctcaggtct gcgggcccgt gatagcaagg ccggccgtat tggtcagctg 480
 gcatgctggg agcacaacaa tccactggcg cgctacgcgc tgatggccga cggcgagcag 540
 atccattccg ccatgtatcc gggctccatg ttcggcgact cgtttgcccc gaagaccgaa 600
 atcaatatcc ggcagcatgc cctagagtct ggggtgcttc tcgtgaacgc aacggccctg 660
 ctggacggcg atcagcaggg gcatatcatg aaggacaccg gctgcagcat cggcccgatc 720
 tccggcggtt gcttactcgc gatcgctgca cccgatggta gcctgctggg cgaaccatc 780
 cgttccggtg agggcggtgt catcgccgac ctcgacttca cgttgatcga caggcgtaag 840
 caggtgatgg actcgcgagg ccattacagc cggccggagt tgctcagcct cttaatagac 900
 cgcacccta ccgcgcactt tcacgaacgc gcttcgcccc ccacgacaga agctgagcaa 960
 ggctccgagg atgtgttcga ggctcgcatt taa 993

<210> 214
 <211> 330
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 214
 Met Arg Val Val Lys Ala Ala Ala Val Gln Leu Ser Pro Val Leu Tyr
 1 5 10 15
 Ser Arg Glu Gly Thr Val Glu Lys Val Arg Lys Ile His Glu Leu
 20 25 30
 Ala Glu Glu Gly Val Glu Phe Ala Thr Phe Pro Glu Thr Val Val Pro
 35 40 45
 Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Thr Pro Leu Glu Gln Ile Phe
 50 55 60

Gly Thr Glu Tyr Leu Arg Leu Leu Asp Gln Ala Val Thr Val Pro Ser
 65 70 75 80
 Pro Ala Thr Asp Ala Ile Gly Glu Ala Ala Arg Phe Ala Gly Val Val
 85 90 95
 Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn Thr
 100 105 110
 Gln Leu Leu Phe Asp Ala Asp Gly Arg Ile Ile Gln Arg Arg Arg Lys
 115 120 125
 Ile Thr Pro Thr His Tyr Glu Arg Met Ile Trp Gly Gln Gly Asp Gly
 130 135 140
 Ser Gly Leu Arg Ala Val Asp Ser Lys Ala Gly Arg Ile Gly Gln Leu
 145 150 155 160
 Ala Cys Trp Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Leu Met Ala
 165 170 175
 Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Met Phe Gly
 180 185 190
 Asp Ser Phe Ala Gln Lys Thr Glu Ile Asn Ile Arg Gln His Ala Leu
 195 200 205
 Glu Ser Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Gly Asp
 210 215 220
 Gln Gln Ala His Ile Met Lys Asp Thr Gly Cys Ser Ile Gly Pro Ile
 225 230 235 240
 Ser Gly Gly Cys Phe Thr Ala Ile Val Ala Pro Asp Gly Ser Leu Leu
 245 250 255
 Gly Glu Pro Ile Arg Ser Gly Glu Gly Val Val Ile Ala Asp Leu Asp
 260 265 270
 Phe Thr Leu Ile Asp Arg Arg Lys Gln Val Met Asp Ser Arg Gly His
 275 280 285
 Tyr Ser Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro Thr
 290 295 300
 Ala His Phe His Glu Arg Ala Ser Pro Pro Thr Thr Glu Ala Glu Gln
 305 310 315 320
 Gly Ser Glu Asp Val Phe Glu Ala Arg Ile
 325 330

<210> 215
 <211> 1008
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 215
 atgagtatta cccaccccaa atttaaagct gctgtgttc aagctgcccc agtatttcta 60
 gacctagatg ggtctgttaa taaggcgatt aatctcattg atgaagctgc cgctgccgga 120
 gccaaagctca ttgccttccc tgaaaccttc attccaggct atccatgggtg gatttggctg 180
 ggatcgccgg cgtgggctct gggccggggg ttctgttcagc gttacttcga caattccctg 240
 cagtagcaca gcccgaggc ggatcgctta cgcgaggcgg cagcagcaa cagcattacg 300
 gtcgtgctgg gcttgtccga gcgtgatggc gggtctctct atatcgaca gtggctgatc 360
 ggcccgatg gcgaaccat cgcgagcgg cgcaagcttc gtcctactca tggggagcgc 420
 acggtattcg gtgaaggga tggcagcgat ctggtggttc atcaaaccga actgggcccgt 480
 cttggcgcgc ttaactgctg ggagaacatc ctgtctctga acaaatatgt gatgtactcc 540
 cagcatgaac aggtccatgt agcatcctgg ccagtttct cgacgtatga accgttcgcg 600
 catgcgctcg gctatgaggt aaacaacgca attagccagg tctatgcggg ggaaggcggg 660
 tgcttcgtgt tggccccgtg ctctaccatc tctgaagaaa tgattgccga actgtgcat 720
 acaccgata aattcgagct gacgcagct ggtggcgcc acgcaatcat ctatggtccg 780
 gacggtcgtg ctctgtgcga aaagctgccc gagaaccagg agggcctgct gtacgcggaa 840
 atcgatctgg ggggtatttc tatggcaaaa agtgccatgg atcctgtcgg ccattactct 900
 cgccccgatg tctaccgtgt gctgttcaat aagatcccgg caaagcgtat cgagcacttc 960
 aatttgcgct tggatgagca agcaggggaa gagccaccag ctgattaa 1008

<210> 216
 <211> 335
 <212> PRT
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 216

```

Met Ser Ile Thr His Pro Lys Phe Lys Ala Ala Val Val Gln Ala Ala
 1          5          10          15
Pro Val Phe Leu Asp Leu Asp Gly Ser Val Asn Lys Ala Ile Asn Leu
 20          25          30
Ile Asp Glu Ala Ala Ala Ala Gly Ala Lys Leu Ile Ala Phe Pro Glu
 35          40          45
Thr Phe Ile Pro Gly Tyr Pro Trp Trp Ile Trp Leu Gly Ser Pro Ala
 50          55          60
Trp Ala Leu Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
 65          70          75          80
Gln Tyr Asp Ser Pro Gln Ala Asp Arg Leu Arg Glu Ala Ala Arg Arg
 85          90          95
Asn Ser Ile Thr Val Val Leu Gly Leu Ser Glu Arg Asp Gly Gly Ser
 100         105         110
Leu Tyr Ile Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
 115         120         125
Gln Arg Arg Lys Leu Arg Pro Thr His Gly Glu Arg Thr Val Phe Gly
 130         135         140
Glu Gly Asp Gly Ser Asp Leu Val Val His Gln Thr Glu Leu Gly Arg
 145         150         155         160
Leu Gly Ala Leu Asn Cys Trp Glu Asn Ile Leu Ser Leu Asn Lys Tyr
 165         170         175
Val Met Tyr Ser Gln His Glu Gln Val His Val Ala Ser Trp Pro Ser
 180         185         190
Phe Ser Thr Tyr Glu Pro Phe Ala His Ala Leu Gly Tyr Glu Val Asn
 195         200         205
Asn Ala Ile Ser Gln Val Tyr Ala Val Glu Gly Gly Cys Phe Val Leu
 210         215         220
Ala Pro Cys Ser Thr Ile Ser Glu Glu Met Ile Ala Glu Leu Cys Asp
 225         230         235         240
Thr Pro Asp Lys Phe Glu Leu Thr His Ala Gly Gly Gly His Ala Ile
 245         250         255
Ile Tyr Gly Pro Asp Gly Arg Ala Leu Cys Glu Lys Leu Pro Glu Asn
 260         265         270
Gln Glu Gly Leu Leu Tyr Ala Glu Ile Asp Leu Gly Val Ile Ser Met
 275         280         285
Ala Lys Ser Ala Met Asp Pro Val Gly His Tyr Ser Arg Pro Asp Val
 290         295         300
Tyr Arg Val Leu Phe Asn Lys Ile Pro Ala Lys Arg Ile Glu His Phe
 305         310         315         320
Asn Leu Pro Leu Asp Glu Gln Ala Gly Glu Glu Pro Pro Ala Asp
 325         330         335

```

<210> 217
 <211> 1011
 <212> DNA
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 217

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gtgggtatca gccatccgaa attcaaggct gcggtcgtac aggccggggc tgccttcctc 60
gacctcgacg gcggcgctga acgagccgtg tcgctcatcg gccaaagcag gcccgaaagg 120
gcacagctga ttgcctttcc tgaacgtgg attcccgggt acccggtggc cacctggctt 180
ggcagcccg cgtgggcaat ggaaaaaggc ttgtccaac gatatttcga caacgcgttg 240
cgcatggtt ctccgcaagc cgagcgaatc tccggggctg cggcggagca caagattatg 300
gtgtcgcttg ggtttgcgga acgcgatgga ggcacgcttt atatcgcgca gtggctcatc 360
ggaccgcagc gccaaactat ctacacgacg cggaagctta agccgactca cgtcgagcgc 420
actgtatttg gcgagggaga cggaagcgat ctctccgtgc atgatacggc gcttgagcgt 480
atcggtcac tttgttgctg ggagcatttg caaccgttgt cgaaatacgc aatgtacgcc 540
cagaatgaac agattcacat tggcgcatgg cccagctttt cgctatacca gccatttgcg 600
aatgcgctga gtcccgaagt caatatcgca gtaagccgcg tgtacgccgt ggaaggccag 660
tggtttcttc tcgcccgtg cgcgacggtt tcggacgcca tgatcgaaac actgtgcgat 720
acgcccgaag agcagggact gattcgggcg ggtggcgggc acgcccgcgt cttcgcccca 780
gatggaagtc tgctgacgcc tacggtagcg gatacttacg agggcctgct gtatgcagaa 840
ctcgacctcg gcgtcatttc gatcgccaag agtgcagcgg accccgccgg ccactattcg 900
cggccagatg tcacacgcct tctattgaat cagacgcctt cgaagcgcg tccagaatatg 960
gtgttaccac tggagacggt cacggagccc gaaggccgg ttcagcccta g 1011

```

<210> 218

<211> 336

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 218

```

Val Gly Ile Ser His Pro Lys Phe Lys Ala Ala Val Val Gln Ala Gly
1      5      10      15
Pro Ala Phe Leu Asp Leu Asp Gly Gly Val Glu Arg Ala Val Ser Leu
20     25     30
Ile Gly Gln Ala Ala Ala Glu Gly Ala Gln Leu Ile Ala Phe Pro Glu
35     40     45
Thr Trp Ile Pro Gly Tyr Pro Trp His Thr Trp Leu Gly Ser Pro Ala
50     55     60
Trp Ala Met Glu Lys Gly Phe Val Gln Arg Tyr Phe Asp Asn Ala Leu
65     70     75     80
Arg His Gly Ser Pro Gln Ala Glu Arg Ile Ser Gly Ala Ala Ala Glu
85     90     95
His Lys Ile Met Val Ser Leu Gly Phe Ala Glu Arg Asp Gly Gly Thr
100    105    110
Leu Tyr Ile Ala Gln Trp Leu Ile Gly Pro Asp Gly Gln Thr Ile Ser
115    120    125
Arg Arg Arg Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly
130    135    140
Glu Gly Asp Gly Ser Asp Leu Ser Val His Asp Thr Ala Leu Gly Arg
145    150    155    160
Ile Gly Ser Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr
165    170    175
Ala Met Tyr Ala Gln Asn Glu Gln Ile His Ile Gly Ala Trp Pro Ser
180    185    190
Phe Ser Leu Tyr Gln Pro Phe Ala Asn Ala Leu Ser Pro Glu Val Asn
195    200    205
Ile Ala Val Ser Arg Val Tyr Ala Val Glu Gly Gln Cys Phe Phe Leu
210    215    220
Ala Pro Cys Ala Thr Val Ser Asp Ala Met Ile Glu Thr Leu Cys Asp
225    230    235    240
Thr Pro Glu Lys Gln Gly Leu Ile Arg Ala Gly Gly Gly His Ala Ala
245    250    255
Ile Phe Gly Pro Asp Gly Ser Leu Leu Thr Pro Thr Val Ala Asp Thr

```


260 265 270
 Tyr Glu Gly Leu Leu Tyr Ala Glu Leu Asp Leu Gly Val Ile Ser Ile
 275 280 285
 Ala Lys Ser Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val
 290 295 300
 Thr Arg Leu Leu Leu Asn Gln Thr Pro Ser Lys Arg Val Gln Asn Met
 305 310 315 320
 Val Leu Pro Leu Glu Thr Val Thr Glu Pro Glu Gly Pro Val Gln Pro
 325 330 335

<210> 219
 <211> 996
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 219
 atgaaaatcg tcaaagctgc cgccgttcaa attagtcccg tgctttatag ccgcgatgga 60
 acggtggaaa aagttgtgcg gaagatccat gagctcggcc aacagggagt gcagttcga 120
 accttccccg agaccgtgat tccgtactat ccctattttt cctttctgca acccgctac 180
 cagatcgcg cggggcagga gcacctcaag ttgctcgacc aggcggtgac ggtgccgtcc 240
 gctgccacgc acgcgatcgg ccaggcatgc aaacaggcag gagggtgtgt ttcgatcggc 300
 atcaatgagc gggacaatgg aacgatctac aacaccagc ttctcttcga ctccgacgga 360
 accctgctgc agcggcgccg caagatctca ccacttacc acgaacggat gatctggggc 420
 cagggcgacg gtcccgccct gcgcgcgtg gatagcaagg ccggccggat tgggcagctc 480
 gcctgttggg agcactacaa ccctttggcg cgctacgcga tgatggccga cggcgagcag 540
 atccattccg ccatgtaccc tggctccatc ttcggcgatc tgtttgccga acagaccag 600
 atcaacgtcc ggcagcacgc gttggagtc ggcgtgttcg tagtctgctc caccgcctgg 660
 ttggatcccg atcaacaagc gcaaatcgtc aaggacacag gcggcgccat tggtcgcatc 720
 tcgggcggct gtttcacggc gattgtggcc ccgcatagca ctctgctcgg agagccgatc 780
 cgctccggcg aaggcgtggt cattgcggat ctgcacttca cccggatcga caagcgtaaa 840
 cagttgatgg attcccgagg tcattacagc cggccggaat tgctgagtc gctgattgat 900
 cgcaattcca ccgcacatgt gcaaaaccgc gtgcggccg atccattcgg cgccggctgt 960
 gttgcagaac caggagtaga aacatgccca cgatag 996

<210> 220
 <211> 331
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 220
 Met Lys Ile Val Lys Ala Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
 1 5 10 15
 Ser Arg Asp Gly Thr Val Glu Lys Val Val Arg Lys Ile His Glu Leu
 20 25 30
 Gly Gln Gln Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Ile Pro
 35 40 45
 Tyr Tyr Pro Tyr Phe Ser Phe Leu Gln Pro Ala Tyr Gln Ile Ala Ala
 50 55 60
 Gly Gln Glu His Leu Lys Leu Leu Asp Gln Ala Val Thr Val Pro Ser
 65 70 75 80
 Ala Ala Thr His Ala Ile Gly Gln Ala Cys Lys Gln Ala Gly Val Val
 85 90 95
 Val Ser Ile Gly Ile Asn Glu Arg Asp Asn Gly Thr Ile Tyr Asn Thr
 100 105 110
 Gln Leu Leu Phe Asp Ser Asp Gly Thr Leu Leu Gln Arg Arg Lys

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      115      120      125
Ile Ser Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly Asp Gly
      130      135      140
Ser Gly Leu Arg Ala Val Asp Ser Lys Ala Gly Arg Ile Gly Gln Leu
145      150      155      160
Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Met Met Ala
      165      170      175
Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Ile Phe Gly
      180      185      190
Asp Leu Phe Ala Glu Gln Thr Gln Ile Asn Val Arg Gln His Ala Leu
      195      200      205
Glu Ser Gly Cys Phe Val Val Cys Ser Thr Ala Trp Leu Asp Pro Asp
210      215      220
Gln Gln Ala Gln Ile Val Lys Asp Thr Gly Gly Ala Ile Gly Ala Ile
225      230      235      240
Ser Gly Gly Cys Phe Thr Ala Ile Val Ala Pro Asp Ser Thr Leu Leu
      245      250      255
Gly Glu Pro Ile Arg Ser Gly Glu Gly Val Val Ile Ala Asp Leu Asp
      260      265      270
Phe Thr Arg Ile Asp Lys Arg Lys Gln Leu Met Asp Ser Arg Gly His
      275      280      285
Tyr Ser Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Ser Thr
290      295      300
Ala His Val Gln Asn Arg Val Pro Ala Asp Pro Phe Gly Ala Gly Cys
305      310      315      320
Val Ala Glu Pro Gly Val Glu Thr Cys Pro Arg
      325      330

```

<210> 221
 <211> 1146
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 221
atgttgacct acaaaggcgt gttcaaagca gcgacagttc aggcggagcc ggtgtggatg      60
gacgctgacg ccaccattac caaagccatc cggatcatcg aagaggcggc tgataacggg      120
gcgaagtttg tcgcattccc ggaggtgttc atccctggat acccttggtg gatctggctg      180
ggcactgcga tgtggggagc caaattcgtc gtgcccttcc acgaaaattg ccttgagctt      240
ggcgacaagc ggatgcagcg cattcaagct gcggcaaac aaaatggcat tgcactcgtc      300
atgggttacg gtgaacgtga cggaggtagc cgctacatga gccaggtatt catcgacgat      360
agcggaaaaa ttgtggcgaa ccgccgcaag ctcaaaccga cgcacgaaga gcgaacgatt      420
ttcggcgagg gaaacggatc cgatttcac acccatgact tcccatttgc gagagtcgga      480
ggcttcaact gctgggaaca ccttcagccc ctgagcaaat acatgatgta cagcctgcag      540
gaacagggtgc atgtcgcgtc gtggccggcc atgtgcacct atcagcctga cgtgccccag      600
ttaggtgcag gcgctaacga ggcggtcacc cgctcttacg cgatcgaagg cgcatgttat      660
gtgctgggag cgacactcgt tatcggaag gcagcccatg atgcattctg cgacactgaa      720
gagcatcaca agctgcttgg catgggcgga ggggtggccc gaattttcgg cccggacggt      780
gagtatctcg cagaatcgct cgctcatgac gcggagggca tcctgtacgc tgacattgat      840
ctgagcaaga tcctgctcgc caaagcaaac acggacacag ttggccacta cgcgcgacct      900
gacgtcttgt cattgctcgt caacacacac aatcccgggc ctgtacgcta tcttgacgaa      960
gagggccggc aggtttcaac gtcaattcgc aggcacgaaa aactggaagg ccagagcctc     1020
gacctcgagg ttacgccagc gacaccagcg accctggaca tcgcgagcct ggtacaacag     1080
gctaagccat cgaccgttaa gagcgagagt aacgcgagca caaaacaacc ggatctcgcg     1140
gtctga

```

<210> 222
 <211> 381
 <212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 222

```

Met Leu Thr Tyr Lys Gly Val Phe Lys Ala Ala Thr Val Gln Ala Glu
 1          5          10          15
Pro Val Trp Met Asp Ala Asp Ala Thr Ile Thr Lys Ala Ile Arg Ile
 20          25          30
Ile Glu Glu Ala Ala Asp Asn Gly Ala Lys Phe Val Ala Phe Pro Glu
 35          40          45
Val Phe Ile Pro Gly Tyr Pro Trp Trp Ile Trp Leu Gly Thr Ala Met
 50          55          60
Trp Gly Ala Lys Phe Val Val Pro Phe His Glu Asn Cys Leu Glu Leu
 65          70          75          80
Gly Asp Lys Arg Met Gln Arg Ile Gln Ala Ala Lys Gln Asn Gly
 85          90          95
Ile Ala Leu Val Met Gly Tyr Gly Glu Arg Asp Gly Gly Ser Arg Tyr
100          105          110
Met Ser Gln Val Phe Ile Asp Asp Ser Gly Lys Ile Val Ala Asn Arg
115          120          125
Arg Lys Leu Lys Pro Thr His Glu Glu Arg Thr Ile Phe Gly Glu Gly
130          135          140
Asn Gly Ser Asp Phe Ile Thr His Asp Phe Pro Phe Ala Arg Val Gly
145          150          155          160
Gly Phe Asn Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr Met Met
165          170          175          180
Tyr Ser Leu Gln Glu Gln Val His Val Ala Ser Trp Pro Ala Met Cys
180          185          190
Thr Tyr Gln Pro Asp Val Pro Gln Leu Gly Ala Gly Ala Asn Glu Ala
195          200          205
Val Thr Arg Ser Tyr Ala Ile Glu Gly Ala Cys Tyr Val Leu Gly Ala
210          215          220
Thr Leu Val Ile Gly Lys Ala Ala His Asp Ala Phe Cys Asp Thr Glu
225          230          235          240
Glu His His Lys Leu Leu Gly Met Gly Gly Gly Trp Ala Arg Ile Phe
245          250          255
Gly Pro Asp Gly Glu Tyr Leu Ala Glu Ser Leu Ala His Asp Ala Glu
260          265          270
Gly Ile Leu Tyr Ala Asp Ile Asp Leu Ser Lys Ile Leu Leu Ala Lys
275          280          285
Ala Asn Thr Asp Thr Val Gly His Tyr Ala Arg Pro Asp Val Leu Ser
290          295          300
Leu Leu Val Asn Thr His Asn Pro Gly Pro Val Arg Tyr Leu Asp Glu
305          310          315          320
Glu Gly Arg Gln Val Ser Thr Ser Ile Arg Arg His Glu Lys Leu Glu
325          330          335
Gly Gln Ser Leu Asp Leu Glu Val Thr Pro Ala Thr Pro Ala Thr Leu
340          345          350
Asp Ile Ala Ser Leu Val Gln Gln Ala Lys Pro Ser Thr Val Lys Ser
355          360          365
Glu Ser Asn Ala Ser Thr Lys Gln Pro Asp Leu Ala Val
370          375          380

```

<210> 223

<211> 996

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 223

atgagagttg	ttaaagccag	cgcagttcaa	ctgaagcctg	tactttatag	ccgcgagggg	60
acgggtcgaaa	aggtcgtagc	gaagattcat	gagctagggc	agcaggggtg	gcagttcgcc	120
gcgttcctctg	agaccgtggt	gccttattac	ccgtactttt	cgatcgtgca	gtccggctat	180
caaatccttc	gcggcgggtga	gttcgtcaag	ctcctcgatc	agtccgtgac	ggtgccatct	240
tatagcactg	aagccatcgg	cgaagcctgc	aggcaggagg	agatggttgt	ctccataggg	300
gtcaacgagc	gtgatggcgg	aacgatctac	aacgcgcagt	tactctttga	ttccgacggc	360
acgttgatcc	aaagacgacg	caagatcacc	cccacccatt	acgaacgcat	gatctggggc	420
cagggcgatg	gctcaggtct	gcgcgctgtt	gacagcaatg	tcgcacgcat	tggccaactg	480
gcattgctttg	agcaactaaa	ccctcttgcg	cggtagcgga	tgatggccga	tggcgagcag	540
atccattccg	ccatgttccc	cggttccatg	ttcggcgatg	gttttgcgga	gaggacggaa	600
attgccgtaa	ggcaacatgc	gatggagtcc	gggtgctttg	tcgtttgcgc	tacggcctgg	660
ctcgatcccg	gccagcaggc	tcagatcgcc	aacgacaccg	gtatcaccga	catcggcccg	720
atctccgggg	gttgctttcac	tgcatcatc	gcaccgatg	ggagcctgct	gggccaacct	780
atccgctcgg	gtgaaggcga	agtcacgtc	gacctcgatt	tcacgttaat	tgacaagcgg	840
aaacatatgt	tcgactcgag	aggacattac	agccggccag	aattgctgag	cctgctgac	900
gatcgactc	ccaccgcgca	ccttcacgac	cgcgctgtgc	agcacaatgc	cggatcgga	960
ggagcgtcgg	aacatcttcg	cgaagacgcc	gcctga			996

<210> 224

<211> 331

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 224

Met	Arg	Val	Val	Lys	Ala	Ser	Ala	Val	Gln	Leu	Lys	Pro	Val	Leu	Tyr
1				5					10					15	
Ser	Arg	Glu	Gly	Thr	Val	Glu	Lys	Val	Val	Ala	Lys	Ile	His	Glu	Leu
			20					25					30		
Gly	Gln	Gln	Gly	Val	Gln	Phe	Ala	Ala	Phe	Pro	Glu	Thr	Val	Val	Pro
		35					40					45			
Tyr	Tyr	Pro	Tyr	Phe	Ser	Ile	Val	Gln	Ser	Gly	Tyr	Gln	Ile	Leu	Arg
	50				55					60					
Gly	Gly	Glu	Phe	Val	Lys	Leu	Leu	Asp	Gln	Ser	Val	Thr	Val	Pro	Ser
65					70				75					80	
Tyr	Ser	Thr	Glu	Ala	Ile	Gly	Glu	Ala	Cys	Arg	Gln	Glu	Glu	Met	Val
			85						90					95	
Val	Ser	Ile	Gly	Val	Asn	Glu	Arg	Asp	Gly	Gly	Thr	Ile	Tyr	Asn	Ala
			100					105						110	
Gln	Leu	Leu	Phe	Asp	Ser	Asp	Gly	Thr	Leu	Ile	Gln	Arg	Arg	Arg	Lys
		115					120					125			
Ile	Thr	Pro	Thr	His	Tyr	Glu	Arg	Met	Ile	Trp	Gly	Gln	Gly	Asp	Gly
	130					135					140				
Ser	Gly	Leu	Arg	Ala	Val	Asp	Ser	Asn	Val	Ala	Arg	Ile	Gly	Gln	Leu
145					150					155				160	
Ala	Cys	Phe	Glu	His	Tyr	Asn	Pro	Leu	Ala	Arg	Tyr	Ala	Met	Met	Ala
			165						170					175	
Asp	Gly	Glu	Gln	Ile	His	Ser	Ala	Met	Phe	Pro	Gly	Ser	Met	Phe	Gly
		180					185						190		
Asp	Gly	Phe	Ala	Glu	Arg	Thr	Glu	Ile	Ala	Val	Arg	Gln	His	Ala	Met
		195					200					205			
Glu	Ser	Gly	Cys	Phe	Val	Val	Cys	Ala	Thr	Ala	Trp	Leu	Asp	Pro	Gly
	210					215					220				
Gln	Gln	Ala	Gln	Ile	Ala	Asn	Asp	Thr	Gly	Ile	Thr	Asp	Ile	Gly	Pro
225					230					235				240	
Ile	Ser	Gly	Gly	Cys	Phe	Thr	Ala	Ile	Ile	Ala	Pro	Asp	Gly	Ser	Leu

```

                245                250                255
Leu Gly Gln Pro Ile Arg Ser Gly Glu Gly Glu Val Ile Val Asp Leu
                260                265                270
Asp Phe Thr Leu Ile Asp Lys Arg Lys His Ile Val Asp Ser Arg Gly
                275                280                285
His Tyr Ser Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro
                290                295                300
Thr Ala His Leu His Asp Arg Ala Val Gln His Asn Ala Gly Ser Glu
305                310                315                320
Gly Ala Ser Glu His Leu Arg Glu Asp Ala Ala
                325                330

```

<210> 225
 <211> 951
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 225
atgaccaccg tcaaagccgc cgctgtccag atgagtcgcc tgctttacag tcgcgacgat      60
accatcgaga aaatttgctg acagatcatc gagcttgccc gacagggagt gcagttcgcc      120
acgtttccag agacagttat tccgtattat ccatatttcg ccttcgtgca gcggccttac      180
gaaatgtcgg cccaatatca tcagttgctt gatcaagcgg tgaccgtgcc ttccggttca      240
acgcacgccca ttggggccgc ctgtaaacia gccggaattg ttgtctcaat cggcgtcaac      300
gagcgggagg gcggcacgct ctatggcaca cagttgctgt ttgatgcaga cggcctcttg      360
atccagcgtc gccgcaagat cactccgacc taccacgagc ggatgatttg gggacagggg      420
gacggttccg ggctgcgagc cgtagatagc gcggtcggtc gaatcggaca gttggcgtgt      480
tgggaaacacc acaatccgct ggctcgttat gctttagcgg ccgatggcga acaaattcac      540
gcggcgatgt accctggctc gatcttgggt gaactatttg ccgagcagat tcaggtcaac      600
atccggcagc acgccatgga atctggttgc ttcgtcgtga acgccacggc ctgggctaagc      660
gaggaacacg aagcccgaaat catgaaggac accggatcat tcgatagccc aatcaccggt      720
ggttgcttta ccgccattgt cgcgcccaac gggcagataa tcggtgaacc gctgcgcatc      780
ggcgaaggcg tcgtgattgc cgatttggac ttcgctttga ttgatgagag gaagcggctg      840
atggactcac gcggcctcta tagccgccct gagttgctaa gcttggtaat cgacagaatg      900
cctacatccc atgtgcatga acgggttgag cgtagcatgg cgatggcatg a          951

```

<210> 226
 <211> 316
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 226
Met Thr Thr Val Lys Ala Ala Ala Val Gln Met Ser Pro Val Leu Tyr
 1                5                10                15
Ser Arg Asp Asp Thr Ile Glu Lys Ile Cys Arg Gln Ile Ile Glu Leu
 20                25                30
Gly Arg Gln Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Ile Pro
 35                40                45
Tyr Tyr Pro Tyr Phe Ala Phe Val Gln Arg Pro Tyr Glu Met Ser Ala
 50                55                60
Gln Tyr His Gln Leu Leu Asp Gln Ala Val Thr Val Pro Ser Gly Ser
 65                70                75                80
Thr His Ala Ile Gly Ala Ala Cys Lys Gln Ala Gly Ile Val Val Ser
 85                90                95
Ile Gly Val Asn Glu Arg Glu Gly Gly Thr Leu Tyr Gly Thr Gln Leu
100                105                110

```

Leu Phe Asp Ala Asp Gly Leu Leu Ile Gln Arg Arg Arg Lys Ile Thr
 115 120 125
 Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly Asp Gly Ser Gly
 130 135 140
 Leu Arg Ala Val Asp Ser Ala Val Gly Arg Ile Gly Gln Leu Ala Cys
 145 150 155 160
 Trp Glu His His Asn Pro Leu Ala Arg Tyr Ala Leu Ala Ala Asp Gly
 165 170 175
 Glu Gln Ile His Ala Ala Met Tyr Pro Gly Ser Ile Leu Gly Glu Leu
 180 185 190
 Phe Ala Glu Gln Ile Gln Val Asn Ile Arg Gln His Ala Met Glu Ser
 195 200 205
 Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Ser Glu Glu Gln Gln
 210 215 220
 Ala Arg Ile Met Lys Asp Thr Gly Ser Phe Asp Ser Pro Ile Thr Gly
 225 230 235 240
 Gly Cys Phe Thr Ala Ile Val Ala Pro Asn Gly Gln Ile Ile Gly Glu
 245 250 255
 Pro Leu Arg Ile Gly Glu Gly Val Val Ile Ala Asp Leu Asp Phe Ala
 260 265 270
 Leu Ile Asp Glu Arg Lys Arg Leu Met Asp Ser Arg Gly Leu Tyr Ser
 275 280 285
 Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Met Pro Thr Ser His
 290 295 300
 Val His Glu Arg Val Glu Arg Ser Met Ala Met Ala
 305 310 315

<210> 227
 <211> 1035
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 227
 atgtccgcatc gacgcatcgt tcgcgcggca gccattcaga tcgccccgga tctcgaagcgc 60
 tgcagtgttaa cgctcgagaa ggtttgctcg gcgatcgacg aagccgcggg caaaggcgct 120
 caactgagcg tctttcccga gaccttcgtc ccgtactacc cctatttctc gtttgtccgc 180
 cctccgggtcg catcgggggc cgatcacatg cggctatacg aggaagcggg ggtgggtgccg 240
 ggtcccgtga cgcaggctgt ttccgaacgt gcgcgcgatgc atgggatggg ggtgggtgctc 300
 ggcgtaaacg agcgcgacca cgggagcctc tacaacaccc aactgatttt cgattgcgat 360
 ggtcggctcg ctctgaaacg ccgcaagatc acgccgacgt ttcacgagcg catgatctgg 420
 ggccagggcg acgccagtgg actgaaagtc gcgcgcacgg gtatcgggcg ggtcggcgcg 480
 ctccggtgct gggagcatta caaccgcgtc gcgcgctacg cgctgatgac ccagcacgaa 540
 gagatccatt gcagtcaatt tccaggctcg ctgcgtcggtc cgatcttctc cgagcagatg 600
 gacgtgacga tccgccatca cgccctcgaa tcgggggtgct tcgtcgtgaa cgcaaccggg 660
 tggctcacgg acgcgcgatg cgcctcgatc accgatgacc cgaagcttca acgggcgctg 720
 cgcggtggct gcaacacggc gatcgtttca ccggaaggcc agcatctggc ggagccggtg 780
 cgcgaaaggcg aggggatggg ggtcgcggac ctgcacatgt cgctcatcac caagcgcaag 840
 cgaatgatgg attcggtcgg ccactatgcg cggccggaac tgttgagcct cgcgatcaac 900
 gatcgtcccg cagccccttt cggccggatg tgcgctgccg aagcaatgcg gggagccgac 960
 gacgtcgtca cagtaggagc atttcatgag cgccagcgag aacgtgtcgg cgaagagccg 1020
 gcaattgatg actga 1035

<210> 228
 <211> 344
 <212> PRT
 <213> Unknown
 <220>

<223> Obtained from an environmental sample

<400> 228

```

Met Ser Asp Arg Arg Ile Val Arg Ala Ala Ala Ile Gln Ile Ala Pro
 1           5           10           15
Asp Leu Glu Arg Cys Ser Val Thr Leu Glu Lys Val Cys Ser Ala Ile
      20           25           30
Asp Glu Ala Ala Gly Lys Gly Ala Gln Leu Ser Val Phe Pro Glu Thr
      35           40           45
Phe Val Pro Tyr Tyr Pro Tyr Phe Ser Phe Val Arg Pro Pro Val Ala
      50           55           60
Ser Gly Ala Asp His Met Arg Leu Tyr Glu Glu Ala Val Val Val Pro
65           70           75           80
Gly Pro Val Thr Gln Ala Val Ser Glu Arg Ala Arg Met His Gly Met
      85           90           95
Val Val Val Leu Gly Val Asn Glu Arg Asp His Gly Ser Leu Tyr Asn
      100          105          110
Thr Gln Leu Ile Phe Asp Cys Asp Gly Arg Leu Ala Leu Lys Arg Arg
      115          120          125
Lys Ile Thr Pro Thr Phe His Glu Arg Met Ile Trp Gly Gln Gly Asp
      130          135          140
Ala Ser Gly Leu Lys Val Ala Arg Thr Gly Ile Gly Arg Val Gly Ala
145          150          155          160
Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met
      165          170          175
Thr Gln His Glu Glu Ile His Cys Ser Gln Phe Pro Gly Ser Leu Val
      180          185          190
Gly Pro Ile Phe Ser Glu Gln Met Asp Val Thr Ile Arg His His Ala
      195          200          205
Leu Glu Ser Gly Cys Phe Val Val Asn Ala Thr Gly Trp Leu Thr Asp
      210          215          220
Ala Gln Ile Ala Ser Ile Thr Asp Asp Pro Lys Leu Gln Arg Ala Leu
225          230          235          240
Arg Gly Gly Cys Asn Thr Ala Ile Val Ser Pro Glu Gly Gln His Leu
      245          250          255
Ala Glu Pro Leu Arg Glu Gly Glu Gly Met Val Val Ala Asp Leu Asp
      260          265          270
Met Ser Leu Ile Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His
      275          280          285
Tyr Ala Arg Pro Glu Leu Leu Ser Leu Ala Ile Asn Asp Arg Pro Ala
      290          295          300
Ala Pro Phe Gly Arg Met Cys Ala Ala Glu Ala Met Arg Gly Ala Asp
305          310          315          320
Asp Val Val Thr Val Gly Ala Phe His Glu Arg Gln Arg Glu Arg Val
      325          330          335
Gly Glu Glu Pro Ala Ile Asp Asp
      340

```

<210> 229

<211> 975

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 229

```

atgcctgaaa acaaagtcaa agttgccctc gttcagcatc cgctgtttt tctgaatttg      60
ccgaaaacgt tggaaaaagt agaaggtttg gcgcgagagt gcgccgcaa tgaagcgaaa      120
atcgttgtct ttcctgaaac ctggctgacc ggctatccgg tctggcttga tgaagcgccg      180
agagccgcgc tgtgggatta tccgcccgcc aagcgtttgt atcaatacct cacggaaaaat      240

```

```

tcattgcaga ttccgagcgc tgagtttgaa tctttgcgcg aaatcgctaa gaaaaattcc 300
ctttatttag tcgttgaggt tcacgaacga agcggcgga cgtctacaa tacgataatt 360
tatctcacgc ccgacggcag ttataaaact caccgcaa atgttccaac ttacacggaa 420
agacttgctt ggggcgcagg cgacggaagc ggtctaaatg ttgtggaaac gccttacggg 480
attctcggag gtttgatttg ctgggaacat tggatgcctc tggctagggc ggcaatgcat 540
tcaaaaaatg aagcgattca cgtttgccaa tttccacgg ttcacgagcg acatcaaadc 600
gccagccgctc attacgcctt cgaagggcag tgtttgtct tgacttccgg ttgcgcgatg 660
acgaaaaacgg atgttttgga aggttttgaa tcgctcgaaa caaacgacca cgaagtttct 720
gggcttttgg attcgataga aaaggaagaa ctgatgcgtg gcggaagcgc gattattgct 780
cccgatttga gctattcggc cgagccggtt tttgacgaaa aaacgattgt ttacggcgaa 840
ttaaatctcg atttaaccaa gcagggacat ctgttttgg ataccgacgg acattattcg 900
cgtcccgatg ttttcgagtt gcgcgtcaac gataaagcga accgaaacgt ccgttttgca 960
tccgaaacag tatag 975

```

<210> 230

<211> 324

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 230

```

Met Pro Glu Asn Lys Val Lys Val Ala Leu Val Gln His Pro Pro Val
1          5          10          15
Phe Leu Asn Leu Pro Lys Thr Leu Glu Lys Val Glu Gly Leu Ala Arg
20          25          30
Glu Cys Ala Ala Asn Glu Ala Lys Ile Val Val Phe Pro Glu Thr Trp
35          40          45
Leu Thr Gly Tyr Pro Val Trp Leu Asp Glu Ala Pro Arg Ala Ala Leu
50          55          60
Trp Asp Tyr Pro Pro Ala Lys Arg Leu Tyr Gln Tyr Leu Thr Glu Asn
65          70          75          80
Ser Leu Gln Ile Pro Ser Ala Glu Phe Glu Ser Leu Arg Glu Ile Ala
85          90          95
Lys Lys Asn Ser Leu Tyr Leu Val Val Gly Val His Glu Arg Ser Gly
100          105          110
Gly Thr Leu Tyr Asn Thr Ile Ile Tyr Leu Thr Pro Asp Gly Ser Tyr
115          120          125
Lys Thr His Arg Lys Leu Val Pro Thr Tyr Thr Glu Arg Leu Val Trp
130          135          140
Gly Ala Gly Asp Gly Ser Gly Leu Asn Val Val Glu Thr Pro Tyr Gly
145          150          155          160
Ile Leu Gly Gly Leu Ile Cys Trp Glu His Trp Met Pro Leu Ala Arg
165          170          175
Ala Ala Met His Ser Lys Asn Glu Ala Ile His Val Cys Gln Phe Pro
180          185          190
Thr Val His Glu Arg His Gln Ile Ala Ser Arg His Tyr Ala Phe Glu
195          200          205
Gly Gln Cys Phe Val Leu Thr Ser Gly Cys Ala Met Thr Lys Thr Asp
210          215          220
Val Leu Glu Gly Phe Glu Ser Leu Glu Thr Asn Asp His Glu Val Phe
225          230          235          240
Gly Leu Leu Asp Ser Ile Glu Lys Glu Glu Leu Met Arg Gly Gly Ser
245          250          255
Ala Ile Ile Ala Pro Asp Leu Ser Tyr Ser Val Glu Pro Val Phe Asp
260          265          270
Glu Lys Thr Ile Val Tyr Gly Glu Leu Asn Leu Asp Leu Thr Lys Gln
275          280          285
Gly His Leu Phe Leu Asp Thr Asp Gly His Tyr Ser Arg Pro Asp Val
290          295          300

```


Phe Glu Leu Arg Val Asn Asp Lys Ala Asn Arg Asn Val Arg Phe Ala
 305 310 315 320
 Ser Glu Thr Val

<210> 231
 <211> 1062
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 231
 atgagtcaga tccatccaaa acttaaggtc gcggccgtgc aggctgcccc cgcctttctc 60
 gatctcgatg catcgatcga aaagacaata cgctatgtcg acgaagcggc tgcggccggg 120
 gcgaagttga ttgcgtttcc ggaaacctgg attcccggct acccatggtg gatctggctc 180
 ggcgctccgg cctgggcat catgcgtggc ttcgtctcgc gctatttcga caactcgctg 240
 caatatggca gtccggaagc tgaacggctg cgggacggc ccaggcgcaa caagatatac 300
 atcgccctcg gcctgtccga gcgcgacggg ggcagtcttt atatcgcgca atggatcatc 360
 gggcctggcg gcgaaacggt tgcacaacgc cgcaagctca agcccacgca cgcgcgagcg 420
 actgtattcg gcgaaggcga tggttcacat ctggccgtgc atgatctcga tattggaaga 480
 ttgggcgcgc tttgttgctg ggaacatctg caaccgttgt cgaaatatgc aatgtacgcc 540
 cagaacgagc aaattcacgt cgcgcctgg ccgagcttct cgctatacga tccctttgca 600
 cgcgcactcg gcgcgaggt caataacgct gcgagcaaga tctatgcggt cgagggatcg 660
 tgcttcgtca ttgcgcgtg cgcaacggtt tcgcagggtga tgatcgatga gctctgcgat 720
 acccccga aaagcatcaatt ccttcacgtc ggccggcggt tcgccgtcat ttacgggtcc 780
 gacggctcgc cactggccaa acctcttccg ccagaccagg agggacttct ctatgccgac 840
 atcgatctcg gcatgatctc ggtcgccaag gccgcagccg atcccgcggg acattatgca 900
 cgtcccgatg taactcgcct gctgttcaac aatcgcccg caaaccgct cgagaagctg 960
 gcgttgccgg tcgatcagga ggccgaagt gatagtcgcg tgaaggctcc cgacgcattc 1020
 cccaaagtga cggcgctcaa gccgtcgag gctgcggagt ag 1062

<210> 232
 <211> 353
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 232
 Met Ser Gln Ile His Pro Lys Leu Lys Val Ala Ala Val Gln Ala Ala
 1 5 10 15
 Pro Ala Phe Leu Asp Leu Asp Ala Ser Ile Glu Lys Thr Ile Arg Tyr
 20 25 30
 Val Asp Glu Ala Ala Ala Ala Gly Ala Lys Leu Ile Ala Phe Pro Glu
 35 40 45
 Thr Trp Ile Pro Gly Tyr Pro Trp Trp Ile Trp Leu Gly Ala Pro Ala
 50 55 60
 Trp Ala Ile Met Arg Gly Phe Val Ser Arg Tyr Phe Asp Asn Ser Leu
 65 70 75 80
 Gln Tyr Gly Ser Pro Glu Ala Glu Arg Leu Arg Asp Ala Ala Arg Arg
 85 90 95
 Asn Lys Ile Tyr Ile Ala Leu Gly Leu Ser Glu Arg Asp Gly Gly Ser
 100 105 110
 Leu Tyr Ile Ala Gln Trp Ile Ile Gly Pro Gly Gly Glu Thr Val Ala
 115 120 125
 Gln Arg Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly
 130 135 140
 Glu Gly Asp Gly Ser His Leu Ala Val His Asp Leu Asp Ile Gly Arg

```

145          150          155          160
Leu Gly Ala Leu Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr
          165          170          175
Ala Met Tyr Ala Gln Asn Glu Gln Ile His Val Ala Ala Trp Pro Ser
          180          185          190
Phe Ser Leu Tyr Asp Pro Phe Ala His Ala Leu Gly Ala Glu Val Asn
          195          200          205
Asn Ala Ala Ser Lys Ile Tyr Ala Val Glu Gly Ser Cys Phe Val Ile
          210          215          220
Ala Pro Cys Ala Thr Val Ser Gln Val Met Ile Asp Glu Leu Cys Asp
225          230          235          240
Thr Pro Glu Lys His Gln Phe Leu His Val Gly Gly Gly Phe Ala Val
          245          250          255
Ile Tyr Gly Pro Asp Gly Ser Pro Leu Ala Lys Pro Leu Pro Pro Asp
          260          265          270
Gln Glu Gly Leu Leu Tyr Ala Asp Ile Asp Leu Gly Met Ile Ser Val
          275          280          285
Ala Lys Ala Ala Ala Asp Pro Ala Gly His Tyr Ala Arg Pro Asp Val
          290          295          300
Thr Arg Leu Leu Phe Asn Asn Arg Pro Ala Asn Arg Val Glu Lys Leu
305          310          315          320
Ala Leu Pro Val Asp Gln Glu Ala Glu Val Asp Ser Pro Leu Lys Ala
          325          330          335
Pro Asp Ala Ser Pro Lys Val Thr Ala Leu Lys Pro Ser Gln Ala Ala
          340          345          350
Glu

```

<210> 233

<211> 1002

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 233

```

gtgagcacca tcgtcaaaagc cgcggccgtg cagatcagcc ccgtgctgta cagccgcgag      60
ggcaccgtcg agcgggtcgt gaagaagatc cgggagctgg gcgaaaaggg cgtccagttc      120
gccaccttcc ccgagaccgt catcccttac taccctgact ttcccttcgt tcagacgccc      180
ttgcagatcc tcgccggccc cgagcatctg aagctgctcg accagtcggt gaccgtgccg      240
tcccccgcca cggacgcgat cggccaggcc gccgggcagg caggaatggt ggtgtccatc      300
ggcgtcaacg agcgtgacgg cggcaccctg tacaacacgc agctgctctt cgacgcggac      360
ggcgcgctga tccagcgtcg ccgcaagatc aagcccaccc actacgagcg catgatctgg      420
ggcgagggcg acggctccgg cctgcgcgcc gtcgacagcc aggtcggtcg tatcggccag      480
ctggcctgct gggagcacia caaccccctg gcgcgctacg ccatgatggc cgacggcgag      540
cagatccatt cggccatgta tccgggctcg atgttcggcg acccgttcgc ccagaagacg      600
gaaatcaaca tccggcagca tgcgctggaa tccggatgct tcgtcgtctg ctcgacggcc      660
tggtttggag ccgatcagca ggcgcaaata atgcaggaca cgggctgcgc catcgggccc      720
atctcggggc gctgcctcac ggcgatcgtg gcgcccgcgc gcacgttcct gggcgaaccg      780
ctcacgtcgg gcgagggcga ggtcatcgcc gacctcgatt tcaagctgat cgacaagcgc      840
aagcagacga tggactcgcg cggccactac aaccgccccg aactgctcag cctgctgatc      900
gatcgaacgc cgacgtcgaa cgtccatgag cgcgccgcgc acccgaaggc cgaggcgtca      960
caaacggctg gcgacacgga gcggaccgcg gaggtcctgt aa      1002

```

<210> 234

<211> 333

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 234

```

Val Ser Thr Ile Val Lys Ala Ala Ala Val Gln Ile Ser Pro Val Leu
 1          5          10          15
Tyr Ser Arg Glu Gly Thr Val Glu Arg Val Val Lys Lys Ile Arg Glu
 20          25          30
Leu Gly Glu Lys Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Ile
 35          40          45
Pro Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Thr Pro Leu Gln Ile Leu
 50          55          60
Ala Gly Pro Glu His Leu Lys Leu Leu Asp Gln Ser Val Thr Val Pro
 65          70          75          80
Ser Pro Ala Thr Asp Ala Ile Gly Gln Ala Ala Arg Gln Ala Gly Met
 85          90          95
Val Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn
100          105          110
Thr Gln Leu Leu Phe Asp Ala Asp Gly Ala Leu Ile Gln Arg Arg Arg
115          120          125
Lys Ile Lys Pro Thr His Tyr Glu Arg Met Ile Trp Gly Glu Gly Asp
130          135          140
Gly Ser Gly Leu Arg Ala Val Asp Ser Gln Val Gly Arg Ile Gly Gln
145          150          155          160
Leu Ala Cys Trp Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Met Met
165          170          175
Ala Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Met Phe
180          185          190
Gly Asp Pro Phe Ala Gln Lys Thr Glu Ile Asn Ile Arg Gln His Ala
195          200          205
Leu Glu Ser Gly Cys Phe Val Val Cys Ser Thr Ala Trp Leu Asp Ala
210          215          220
Asp Gln Gln Ala Gln Ile Met Gln Asp Thr Gly Cys Ala Ile Gly Pro
225          230          235          240
Ile Ser Gly Gly Cys Leu Thr Ala Ile Val Ala Pro Asp Gly Thr Phe
245          250          255
Leu Gly Glu Pro Leu Thr Ser Gly Glu Gly Glu Val Ile Ala Asp Leu
260          265          270
Asp Phe Lys Leu Ile Asp Lys Arg Lys Gln Thr Met Asp Ser Arg Gly
275          280          285
His Tyr Asn Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro
290          295          300
Thr Ser Asn Val His Glu Arg Ala Ala His Pro Lys Val Glu Ala Ser
305          310          315          320
Gln Thr Ala Gly Asp Thr Glu Arg Thr Arg Glu Val Leu
325          330

```

<210> 235

<211> 993

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 235

```

atgaaaattg ttaaagcggc agcagttcag ctgagcccg tcctctatag ccgcgagggg      60
acggtcgaaa gagtagtgcg gaagattcat caacttggtc aacagggagt gcagtttgcc      120
accttcccg aaacagtggg gccttactac ccgtattttt cgatcgtgca gtccgggtat      180
caaatccttc gcggcggtga gttcgtgaag ctgctcgatc agtcagtgac ggtgccatct      240
cttgccaccg aagcgatcgc cgaggcctgc aggcaggcgg gcgtcgttgt ctccatcggc      300
gtcaatgagc gtgacggcgg aactatatac aatgcgcagc ttctgtttga ttcggacggc      360

```

```

acattgattc agaggcgacg caagatcacg cccacccact acgagcgcat gatctggggc 420
cagggcgatg gctcgggtct gcgggctgtg gacagcaagg tggcacgtat tggtaactg 480
gcgtgctttg agcattacaa cccctcgca cgatacgca tgatcgccga tggcgagcag 540
atccactctg caatgtttcc cggttccatg ttcggcgatg gtttcgcgga gaggaccgag 600
atcgcggtca ggcagcatgc gcaggagtcc ggatgctttg tagtttgtgc tacggcgtgg 660
ctggatgccg accagcaggc tcaaattgcc gcggacacag gcatcaccga cctgggaccg 720
atctccggcg gttgcttcac tgcgatcatt gcacctgatg ggagcctgct gggtaacca 780
atccgctcgg gcgaagggtga cgctattgtc gatctcgatt tcactctgat cgacaggcgg 840
aagcatgttg tggactcgag aggtcactac agccggcccg aattgctaag cctgctgac 900
gaccgtactc ccacagcgca cgttcacgaa cgggccgcgc actctcactt ggccgccgag 960
caatgcttgg aggatcttaa cgcgcttgct taa 993

```

<210> 236

<211> 330

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 236

```

Met Lys Ile Val Lys Ala Ala Ala Val Gln Leu Ser Pro Val Leu Tyr
 1           5           10          15
Ser Arg Glu Gly Thr Val Glu Arg Val Arg Lys Ile His Gln Leu
      20           25           30
Gly Gln Gln Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
      35           40           45
Tyr Tyr Pro Tyr Phe Ser Ile Val Gln Ser Gly Tyr Gln Ile Leu Arg
      50           55           60
Gly Gly Glu Phe Val Lys Leu Leu Asp Gln Ser Val Thr Val Pro Ser
65           70           75           80
Leu Ala Thr Glu Ala Ile Ala Glu Ala Cys Arg Gln Ala Gly Val Val
      85           90           95
Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Ile Tyr Asn Ala
      100          105          110
Gln Leu Leu Phe Asp Ser Asp Gly Thr Leu Ile Gln Arg Arg Arg Lys
      115          120          125
Ile Thr Pro Thr His Tyr Glu Arg Met Ile Trp Gly Gln Gly Asp Gly
      130          135          140
Ser Gly Leu Arg Ala Val Asp Ser Lys Val Ala Arg Ile Gly Gln Leu
145          150          155          160
Ala Cys Phe Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Met Ile Ala
      165          170          175
Asp Gly Glu Gln Ile His Ser Ala Met Phe Pro Gly Ser Met Phe Gly
      180          185          190
Asp Gly Phe Ala Glu Arg Thr Glu Ile Ala Val Arg Gln His Ala Gln
      195          200          205
Glu Ser Gly Cys Phe Val Val Cys Ala Thr Ala Trp Leu Asp Ala Asp
      210          215          220
Gln Gln Ala Gln Ile Ala Ala Asp Thr Gly Ile Thr Asp Leu Gly Pro
225          230          235          240
Ile Ser Gly Gly Cys Phe Thr Ala Ile Ile Ala Pro Asp Gly Ser Leu
      245          250          255
Leu Gly Gln Pro Ile Arg Ser Gly Glu Gly Asp Val Ile Val Asp Leu
      260          265          270
Asp Phe Thr Leu Ile Asp Arg Arg Lys His Val Val Asp Ser Arg Gly
      275          280          285
His Tyr Ser Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro
      290          295          300
Thr Ala His Val His Glu Arg Ala Ala His Ser His Leu Ala Ala Glu
305          310          315          320

```

Gln Cys Leu Glu Asp Leu Asn Ala Leu Ala
325 330

<210> 237
<211> 993
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 237
atgaaagtcg tcaaagccgc cgcagtgacg atcagtcctg ttctctacag ccgagaggca 60
accgtcgcca aggtcgtgca gaagatccac gaactcggcc agaaaggcgt gcagttcgcc 120
acctttccag agaccgtagt gccttactac ccgtactttt ccgccgtcca gacaggcatc 180
gagcttctgt ccggcacgga gcatctccgg ctgctcgatc aggccgtgac ggtgccgtct 240
gccgctaccg acgcgatcgg agaggcagcc cggaaaggcag gcatgggtgt gtcgatcggc 300
gtcaatgaac gcgatggcgg cactttgtac aacacacagt tgctcttcga tgcgatggc 360
accttgatcc agcgcgcgcg caagatcacg ccgacccact tcgaacgcat gatctggggc 420
caggggggacg gttcgggcct gcgcgctgtc gacagcaagg tcggtcgcat tggccagtgt 480
gcctgcttgc agcacaacaa cccgctggcc cgctacgcgt tgattgccga cggcgagcag 540
atccattccg ccatgtatcc ggggtctgct tttggcgaag gatttgccca aaggatggaa 600
atcaatatcc gccagcatgc gctggagtcg ggtgcgttcg tcgtcaacgc aacggcctgg 660
ctggatgctg accagcaggc gcagatcatg aaggacaccg gctgcgggat tggcccgatc 720
tcgggcggtt gcttcaccac gatcgtgtca cccgacggca tgctgatggc cgaaccctg 780
cgctcgggcg agggtgaggt catcgtcgat ctcgacttca cgctgatcga ccgtcgcaag 840
atgttgatgg actcggcggg ccactataac cgcccgaac tgctcagtc catgatcgac 900
cgacccccga ccgcgcacgt tcatgaacgc gctgcgcgtc cgggtgcggg cggtgagcag 960
aaccgggagg aacttcgcat cccggccgcg tga 993

<210> 238
<211> 330
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 238
Met Lys Val Val Lys Ala Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
1 5 10 15
Ser Arg Glu Ala Thr Val Ala Lys Val Val Gln Lys Ile His Glu Leu
20 25 30
Gly Gln Lys Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
35 40 45
Tyr Tyr Pro Tyr Phe Ser Ala Val Gln Thr Gly Ile Glu Leu Leu Ser
50 55 60
Gly Thr Glu His Leu Arg Leu Leu Asp Gln Ala Val Thr Val Pro Ser
65 70 75 80
Ala Ala Thr Asp Ala Ile Gly Glu Ala Ala Arg Lys Ala Gly Met Val
85 90 95
Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn Thr
100 105 110
Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln Arg Arg Arg Lys
115 120 125
Ile Thr Pro Thr His Phe Glu Arg Met Ile Trp Gly Gln Gly Asp Gly
130 135 140
Ser Gly Leu Arg Ala Val Asp Ser Lys Val Gly Arg Ile Gly Gln Leu
145 150 155 160
Ala Cys Phe Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Leu Ile Ala
165 170 175

Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Ala Phe Gly
 180 185 190
 Glu Gly Phe Ala Gln Arg Met Glu Ile Asn Ile Arg Gln His Ala Leu
 195 200 205
 Glu Ser Gly Ala Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp
 210 215 220
 Gln Gln Ala Gln Ile Met Lys Asp Thr Gly Cys Gly Ile Gly Pro Ile
 225 230 235 240
 Ser Gly Gly Cys Phe Thr Thr Ile Val Ser Pro Asp Gly Met Leu Met
 245 250 255
 Ala Glu Pro Leu Arg Ser Gly Glu Gly Glu Val Ile Val Asp Leu Asp
 260 265 270
 Phe Thr Leu Ile Asp Arg Arg Lys Met Leu Met Asp Ser Ala Gly His
 275 280 285
 Tyr Asn Arg Pro Glu Leu Leu Ser Leu Met Ile Asp Arg Thr Pro Thr
 290 295 300
 Ala His Val His Glu Arg Ala Ala Arg Pro Val Ser Gly Val Glu Gln
 305 310 315 320
 Asn Pro Glu Glu Leu Arg Ile Pro Ala Ala
 325 330

<210> 239

<211> 969

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 239

atgtccaatg	agaataagta	tgacacattt	aaagttgctg	cagtcaggc	cacacctgtg	60
tttcttgatc	gtgaagcaac	catcgacaaa	gcttgcgagt	tgattgctac	tgcaaggctgt	120
gaaggtgctc	gcctgattgt	ctttccagaa	gcgttcaccc	catcctatcc	cgagtgggta	180
tggggatttc	cctctggtga	gcaagggtta	ctcaacgaac	tttattcaga	gttgctcacc	240
aatgcgggta	ccataccag	cgacgcgact	gacagattgt	gcgaggcggc	aaagcttgcg	300
aatgcctatg	tagtgatggg	aatgagcgaa	cggaaatgtcg	aagcgagtgg	tgcaagcctg	360
tataacacga	tgttgatat	agatgcacag	ggggagattt	tagggaaaca	tcggaagctg	420
gtgccaacgg	gtggtgaacg	cctgggtatg	gcgcaagggt	atggcagcac	gctgcaggctc	480
tacgatactc	cattgggaaa	acttgggtgg	ttaatttgct	gggaaaatta	tatgccgctg	540
gcacgctata	cgatgtatgc	ctggggaaca	caaattctatg	ttgcagcaac	gtgggattgc	600
ggccaaccct	ggctctcaac	gatacggcat	attgctaaag	aaggcagggt	atacgtgggt	660
ggttgctgta	tcgcgatgcg	taaagatgat	attccagatc	gttactctat	gaagcagaaa	720
tattatgctg	aaatggatga	atggataaat	gttggggata	gcgcgattgt	caatcccga	780
ggacatttta	ttgcagggcc	tgtgcgcaag	caagaagaaa	ttctctatgc	ggagattgat	840
ccacgtatga	tgcaaggccc	gaagtggatg	cttgacgtgg	cgggacatta	tgcaagacca	900
gatgtgttcc	agttgacggt	gcatacggat	gtgaggcaga	tgatacgggt	ggaagatgat	960
tctcaatga						969

<210> 240

<211> 322

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 240

Met	Ser	Asn	Glu	Asn	Lys	Tyr	Asp	Thr	Phe	Lys	Val	Ala	Ala	Val	Gln
1				5				10						15	
Ala	Thr	Pro	Val	Phe	Leu	Asp	Arg	Glu	Ala	Thr	Ile	Asp	Lys	Ala	Cys
			20					25						30	

Glu Leu Ile Ala Thr Ala Gly Arg Glu Gly Ala Arg Leu Ile Val Phe
 35 40 45
 Pro Glu Ala Phe Ile Pro Ser Tyr Pro Glu Trp Val Trp Gly Ile Pro
 50 55 60
 Ser Gly Glu Gln Gly Leu Asn Glu Leu Tyr Ser Glu Leu Leu Thr
 65 70 75 80
 Asn Ala Val Thr Ile Pro Ser Asp Ala Thr Asp Arg Leu Cys Glu Ala
 85 90 95
 Ala Lys Leu Ala Asn Ala Tyr Val Val Met Gly Met Ser Glu Arg Asn
 100 105 110
 Val Glu Ala Ser Gly Ala Ser Leu Tyr Asn Thr Met Leu Tyr Ile Asp
 115 120 125
 Ala Gln Gly Glu Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly
 130 135 140
 Gly Glu Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Gln Val
 145 150 155 160
 Tyr Asp Thr Pro Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn
 165 170 175
 Tyr Met Pro Leu Ala Arg Tyr Thr Met Tyr Ala Trp Gly Thr Gln Ile
 180 185 190
 Tyr Val Ala Ala Thr Trp Asp Cys Gly Gln Pro Trp Leu Ser Thr Ile
 195 200 205
 Arg His Ile Ala Lys Glu Gly Arg Val Tyr Val Val Gly Cys Cys Ile
 210 215 220
 Ala Met Arg Lys Asp Asp Ile Pro Asp Arg Tyr Ser Met Lys Gln Lys
 225 230 235 240
 Tyr Tyr Ala Glu Met Asp Glu Trp Ile Asn Val Gly Asp Ser Ala Ile
 245 250 255
 Val Asn Pro Glu Gly His Phe Ile Ala Gly Pro Val Arg Lys Gln Glu
 260 265 270
 Glu Ile Leu Tyr Ala Glu Ile Asp Pro Arg Met Met Gln Gly Pro Lys
 275 280 285
 Trp Met Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Gln
 290 295 300
 Leu Thr Val His Thr Asp Val Arg Gln Met Ile Arg Val Glu Asp Asp
 305 310 315 320
 Ser Gln

<210> 241

<211> 972

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 241

atgatattcca	acgagcataa	caataactcca	ttcaagggttg	ctgctgtgca	ggctacacct	60
gtgtttcttg	atcgcgaaagc	aacgatcgat	aaagcgtgtg	aactgatcgc	tactgccggt	120
catgaaggcg	ctcgtttgat	tgtttttcca	gaagcgttca	tcccatccta	tcccagagtgg	180
gtatggggaa	ttccctctgg	cgagcaaggt	ttgctcaacg	atctgtatgc	agagttactc	240
accaattcag	ttacgatacc	cagcaacgca	actgacaggc	tttgtagagc	cgcgaaagctt	300
gctaattgcct	acgtgggtgat	ggggatgagc	gaacggaata	tcgaagcgag	cgcgcaagc	360
ctgtacaata	cgatgttata	tatagatgca	cagggtgaga	ttttgggcaa	acatcgaaag	420
ctggtgccaa	cgggcgggaga	acgcctggta	tgggcacaag	gagatggaag	cacgctgcag	480
gtttacgata	cacctctagg	aaagcttggg	ggtttaattt	gctgggaaaa	ttatatgccg	540
ctggcacgct	acgctatgta	tgcctgggga	actcaaatct	acgtcgcggc	aacgtgggat	600
cgcgccaac	cctggctctc	aacgatacgg	catatcgcta	aagagggcag	ggtatacgta	660
atcggttgct	gtatcgcgat	gcgtaaagac	gatattccag	atagggtactc	catgaagcag	720
aagtattatg	cggagatgga	tgaatggatc	aacgtagggtg	acagcgcgat	tgtcaatcct	780

gagggggact tcattgcggg gcctgtgagc aagcaggagg aaattctcta tgcggagatt 840
 gatccgcgga tgggtgcaagg tccgaagtgg atgctggatg tggcggggca ttacgcgagg 900
 cctgatgtgt tcgagttgac ggtgcatacg gatgtgaggg agatgatgcg ggtggagcat 960
 gattatcaat ga 972

<210> 242
 <211> 323
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 242
 Met Ile Ser Asn Glu His Asn Asn Thr Pro Phe Lys Val Ala Ala Val
 1 5 10 15
 Gln Ala Thr Pro Val Phe Leu Asp Arg Glu Ala Thr Ile Asp Lys Ala
 20 25 30
 Cys Glu Leu Ile Ala Thr Ala Gly His Glu Gly Ala Arg Leu Ile Val
 35 40 45
 Phe Pro Glu Ala Phe Ile Pro Ser Tyr Pro Glu Trp Val Trp Gly Ile
 50 55 60
 Pro Ser Gly Glu Gln Gly Leu Leu Asn Asp Leu Tyr Ala Glu Leu Leu
 65 70 75 80
 Thr Asn Ser Val Thr Ile Pro Ser Asn Ala Thr Asp Arg Leu Cys Arg
 85 90 95
 Ala Ala Lys Leu Ala Asn Ala Tyr Val Val Met Gly Met Ser Glu Arg
 100 105 110
 Asn Ile Glu Ala Ser Gly Ala Ser Leu Tyr Asn Thr Met Leu Tyr Ile
 115 120 125
 Asp Ala Gln Gly Glu Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr
 130 135 140
 Gly Gly Glu Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Gln
 145 150 155 160
 Val Tyr Asp Thr Pro Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu
 165 170 175
 Asn Tyr Met Pro Leu Ala Arg Tyr Ala Met Tyr Ala Trp Gly Thr Gln
 180 185 190
 Ile Tyr Val Ala Ala Thr Trp Asp Arg Gly Gln Pro Trp Leu Ser Thr
 195 200 205
 Ile Arg His Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys
 210 215 220
 Ile Ala Met Arg Lys Asp Asp Ile Pro Asp Arg Tyr Ser Met Lys Gln
 225 230 235 240
 Lys Tyr Tyr Ala Glu Met Asp Glu Trp Ile Asn Val Gly Asp Ser Ala
 245 250 255
 Ile Val Asn Pro Glu Gly Asp Phe Ile Ala Gly Pro Val Ser Lys Gln
 260 265 270
 Glu Glu Ile Leu Tyr Ala Glu Ile Asp Pro Arg Met Val Gln Gly Pro
 275 280 285
 Lys Trp Met Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe
 290 295 300
 Glu Leu Thr Val His Thr Asp Val Arg Glu Met Met Arg Val Glu His
 305 310 315 320
 Asp Tyr Gln

<210> 243
 <211> 999
 <212> DNA
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 243

atgaagcaaa	ctcagtagc	gatcattcag	gcggaacctg	tatatctcaa	tttgcaagcg	60
agtgttgcca	gggctatcga	tcttgccgga	cgcgccgcga	agcaaggagc	gcgtctgata	120
gtgtttggag	agacctggtt	gccgggttat	cccgcgtggc	tggttacttg	tcccgccatg	180
gcgttctggg	atcaccggcc	gacaaaagaa	gtgtttgccc	ggacccgcga	gaacagtgtt	240
gtaattcccg	gaaaggaaat	cgaacagctc	tgtaaaactg	cggcggagct	gggagttgta	300
atttcgatcg	gtgtaaacga	aaaaattctg	gaaggccccc	gaaacggcac	gctctacaat	360
tctcttttgc	tgattgatga	atcaggaaaa	ctggccggcc	atcaccgcaa	actggttccg	420
acttatacgg	aacggatggt	gtggggaatg	ggtgatggag	gtggaatgga	agccatatcg	480
actgcagccc	gcagggttgg	cggattgatt	tgctgggagc	actggatgcc	attgagccgg	540
cagggtctgc	acatgtcggg	tgaggaaatt	catgtggcag	tgtggcccac	ggttcattgag	600
gtgcaccagc	ttgcatcacg	ccattatgca	tttgaagggc	gtgttttgtg	gctcgcagcc	660
ggattgttga	tgaaggtccg	ggatattcct	ccggagctgg	aattgccttc	tcagatgtcg	720
cgtgaatccg	aagactggct	tctgcgcggc	gggagcgcgg	tcattgggtcc	ggatggaaaag	780
tacattgtgg	agccgttgtt	tgatcgagag	gcgatttctca	cagccgatct	tgaattagcc	840
gcatgcgacg	gtgaaaaaat	gacgctggac	gtaacggggac	attattcccc	ccccgatcct	900
tttcacctgg	aattcaggaa	acagcaatcc	ggccatatgt	cgggagcagg	aacgatcagc	960
cggcaaaaaa	cagcgccgga	ccgcgcggac	gatcactaa			999

<210> 244

<211> 332

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 244

Met	Lys	Gln	Thr	Arg	Val	Ala	Ile	Ile	Gln	Ala	Glu	Pro	Val	Tyr	Leu	1	5	10	15
Asn	Leu	Gln	Ala	Ser	Val	Ala	Arg	Ala	Ile	Asp	Leu	Ala	Gly	Arg	Ala	20	25	30	
Ala	Lys	Gln	Gly	Ala	Arg	Leu	Ile	Val	Phe	Gly	Glu	Thr	Trp	Leu	Pro	35	40	45	
Gly	Tyr	Pro	Ala	Trp	Leu	Asp	Tyr	Cys	Pro	Gly	Met	Ala	Phe	Trp	Asp	50	55	60	
His	Arg	Pro	Thr	Lys	Glu	Val	Phe	Ala	Arg	Thr	Arg	Glu	Asn	Ser	Val	65	70	75	80
Val	Ile	Pro	Gly	Lys	Glu	Ile	Glu	Gln	Leu	Cys	Lys	Thr	Ala	Ala	Glu	85	90	95	
Leu	Gly	Val	Val	Ile	Ser	Ile	Gly	Val	Asn	Glu	Lys	Ile	Leu	Glu	Gly	100	105	110	
Pro	Gly	Asn	Gly	Thr	Leu	Tyr	Asn	Ser	Leu	Leu	Leu	Ile	Asp	Glu	Ser	115	120	125	
Gly	Lys	Leu	Ala	Gly	His	His	Arg	Lys	Leu	Val	Pro	Thr	Tyr	Thr	Glu	130	135	140	
Arg	Met	Val	Trp	Gly	Met	Gly	Asp	Gly	Gly	Gly	Met	Glu	Ala	Ile	Ser	145	150	155	160
Thr	Ala	Ala	Gly	Arg	Val	Gly	Gly	Leu	Ile	Cys	Trp	Glu	His	Trp	Met	165	170	175	
Pro	Leu	Ser	Arg	Gln	Val	Leu	His	Met	Ser	Gly	Glu	Glu	Ile	His	Val	180	185	190	
Ala	Val	Trp	Pro	Thr	Val	His	Glu	Val	His	Gln	Leu	Ala	Ser	Arg	His	195	200	205	
Tyr	Ala	Phe	Glu	Gly	Arg	Cys	Phe	Val	Leu	Ala	Ala	Gly	Leu	Leu	Met	210	215	220	
Lys	Val	Arg	Asp	Ile	Pro	Pro	Glu	Leu	Glu	Leu	Pro	Ser	Gln	Met	Ser				

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225          230          235          240
Arg Glu Ser Glu Asp Trp Leu Leu Arg Gly Gly Ser Ala Val Ile Gly
          245          250          255
Pro Asp Gly Lys Tyr Ile Val Glu Pro Leu Phe Asp Arg Glu Ala Ile
          260          265          270
Leu Thr Ala Asp Leu Glu Leu Ala Ala Cys Asp Arg Glu Lys Met Thr
          275          280          285
Leu Asp Val Thr Gly His Tyr Ser Arg Pro Asp Leu Phe His Leu Glu
          290          295          300
Phe Arg Lys Gln Gln Ser Gly His Ile Ala Gly Ala Gly Thr Ile Ser
305          310          315          320
Arg Gln Lys Ser Ala Pro Asp Arg Ala Asp Asp His
          325          330

```

<210> 245
 <211> 999
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 245
atgggtgaga atgccaactt caccgtcgca gctgtccagg caacgccggt cttcttagac      60
cgggatgcga cggtcgagaa ggcttgcgag ctcatcgctg aagccgggcg aaacggagcg      120
cgcttgcccg tttttcccgga ggcgtttgtg cgggcttacc cggactgggt ctgggctgtt      180
ccgccgggcg attcaaggct gctgcacgag ctctacgggt agctgatcca gaactctgtc      240
acgattccca gcgagtcgac ggagaaactc tgccggggcg cccgcggggc caaagtctgc      300
gtggcgatcg gcatcaacga gaggaatgcg gaggcaagcg ggggtagcct ctacaacagc      360
ctcctgtaca tcagcccgga cggccaggtc ctccgggaagc accgcaagct cgttcccacc      420
ggagcggagc ggcttgtctg ggcgcagggc gacggcagca ctatcgacgt gtttgagttg      480
cctttctgtc gtttggtgtg cctcatctgt tgggagaact acatgccgct ggcccgttat      540
gcatgttacg cctggggcac gcaggtctac gtccgcgcaa cgtgggacca cggcgaaact      600
tggctctcaa ccttgaggca tatcgccagg gagggcgctg catatgtcat tggcgtttgc      660
atgccgatgc gcatgagcga catcccggac cgatacgagt tcaagcgcaa gtactatggc      720
gggcgcgact ggatcaatac tggtgacagc gccatcgtgg gtccggacgg aaacttcatt      780
gccggccccc tgagcgagcg cgaagagatc ctgtacgccg atatagacct gaatcggctt      840
gcgaactcga agtggtgctt ggacgtcgcc gggcactatg cacggccgga cgtcttccag      900
ttgaccgtta accgcgagcc gaaccgatg atctctgagg atgggcacaa gacggttccc      960
acgctaccga aacgtgcggg gaagagtagg acgagatga

```

<210> 246
 <211> 332
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 246
Met Gly Glu Asn Ala Asn Phe Thr Val Ala Ala Val Gln Ala Thr Pro
1          5          10          15
Val Phe Leu Asp Arg Asp Ala Thr Val Glu Lys Ala Cys Glu Leu Ile
20          25          30
Ala Glu Ala Gly Arg Asn Gly Ala Arg Leu Ala Val Phe Pro Glu Ala
35          40          45
Phe Val Pro Ala Tyr Pro Asp Trp Val Trp Ala Val Pro Pro Gly Asp
50          55          60
Ser Arg Leu Leu His Glu Leu Tyr Gly Glu Leu Ile Gln Asn Ser Val
65          70          75          80
Thr Ile Pro Ser Glu Ser Thr Glu Lys Leu Cys Arg Ala Ala Arg Gly

```

$\langle 210 \rangle$	248
$\langle 211 \rangle$	329

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 248

```

Met Pro Thr Pro Lys Glu Lys Phe Arg Ile Ala Ala Val Gln Ala Cys
 1          5          10          15
Pro Val Phe Leu Asp Arg Gly Glu Thr Val Lys Lys Ala Cys Arg Leu
      20          25          30
Ala Ala Glu Ala Gly Gly Gln Gly Ala Arg Leu Ile Val Phe Pro Glu
      35          40          45
Ser Phe Ile Pro Ala Tyr Pro Asp Trp Val Trp Ala Val Pro Pro Gly
      50          55          60
Arg Glu Lys Leu Leu Asn Glu Met Tyr Ala Glu Phe Leu Ala Gly Ala
65          70          75          80
Val Glu Val Pro Gly Pro Val Thr Glu Glu Leu Gly Arg Ala Ala Glu
      85          90          95
Arg Ala Gly Ala Tyr Leu Val Met Gly Val Thr Glu Arg Asp Thr Glu
      100          105          110
Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Phe Gly Pro Gln
      115          120          125
Gly Ser Leu Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly Gly Glu
      130          135          140
Arg Thr Val Trp Ala Arg Gly Asp Gly Ser Thr Leu Gln Val Tyr Asp
145          150          155          160
Thr Pro Leu Gly Lys Ile Gly Gly Leu Ile Cys Trp Glu Asn Tyr Met
      165          170          175
Pro Leu Ala Arg Tyr Ala Met Tyr Ala Trp Gly Thr Gln Ile Tyr Leu
      180          185          190
Ala Pro Thr Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Leu Arg His
      195          200          205
Ile Ala Lys Glu Gly Arg Val Tyr Val Val Gly Cys Cys Met Ala Met
      210          215          220
Gln Lys Gly Asp Ile Pro Asp Arg Phe Glu Tyr Lys Gln Lys Tyr Tyr
225          230          235          240
Pro Ala Ala Arg Glu Trp Ile Asn Thr Gly Asp Ser Ala Ile Leu Asn
      245          250          255
Pro Glu Gly Glu Phe Ile Ala Gly Pro Ala Gly Lys Lys Glu Glu Ile
      260          265          270
Leu Tyr Ala Glu Ile Asp Pro Arg Gln Met Gly Gly Pro Lys Trp Met
      275          280          285
Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Glu Leu Ile
      290          295          300
Val His Arg Glu Ala Arg Pro Met Ile Arg Val Thr Glu Ala Pro Ser
305          310          315          320
Pro Gly Glu Lys Glu Thr Gly Glu Gly
      325

```

<210> 249

<211> 1017

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 249

```

atgggcattc aacatccgaa atatcgctgc gcggtggtgc aggcggcacc ggcctggctc
gacctcgagg cgctcggtcag caagagcatc gcgctgatag aggaggccgc cgccaagggc

```

60
120

```

gccaagctga tcgcgttccc cgaggccttc atccccggct atccctggta catctggctg 180
gactcgccgg cctgggcgat cggccgcggc ttctgtcagc gctatttcga caattcgctc 240
agctatgaca gcccgagcgc ggagcgccct aggctcgag tgaagaaggc cggcatgacc 300
gcagtgtctg gcctgtccga gcgcgacggc ggcaagcctt atctcgcgca atggttgatc 360
ggacccgacg gcgagaccat cgcaaagcgg cgcaagctgc ggccgaccca tgccgagcgc 420
accgtctacg gcgagggcga cggcagcgac cttgcggtgc atgaccgccc cggcatcggc 480
cggctcggtg cgctgtgctg ctgggagcat ctgcagccgc tgtcgaaata cgcatgtac 540
gccagaacg agcaggtgca tgtcgcgcc tggccgagct tctcgctgta cgatccgttc 600
gcgcggcgcg tcgctggga ggtcaacaat gcggcctcgc gcgtctatgc cgtcgagggc 660
tctgtcttcg tgctggcgcc ctgcgccacc gtctcgagc cgatgatcga cgagctctgc 720
gaccgcgacg acaagcatgc gctgctgcat gttggcgcg gccatgccgc gatcttcggc 780
cccgcaggca gcgcgatcgc ggacaagctt ccgtccgacc aggagggcct cctgttcgcc 840
gacatcgatc tcggcgcgat cgggatcgcg aagaatgccg ctgatccggc cgggcactat 900
tcgcgcccgg acgtgacgcg gctgctgctc aacaagaagc cctcgaagcg cgtcgagcac 960
ttcgcgctgc cgctcgacac gctcgcgggc gaggagatcg acgcgccgcg aagctaa 1017

```

<210> 250

<211> 338

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 250

```

Met Gly Ile Gln His Pro Lys Tyr Arg Val Ala Val Val Gln Ala Ala
1          5          10          15
Pro Ala Trp Leu Asp Leu Glu Ala Ser Val Ser Lys Ser Ile Ala Leu
20        25        30
Ile Glu Glu Ala Ala Ala Lys Gly Ala Lys Leu Ile Ala Phe Pro Glu
35        40        45
Ala Phe Ile Pro Gly Tyr Pro Trp Tyr Ile Trp Leu Asp Ser Pro Ala
50        55        60
Trp Ala Ile Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
65        70        75        80
Ser Tyr Asp Ser Pro Gln Ala Glu Arg Leu Arg Leu Ala Val Lys Lys
85        90        95
Ala Gly Met Thr Ala Val Leu Gly Leu Ser Glu Arg Asp Gly Gly Ser
100       105       110
Leu Tyr Leu Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
115       120       125
Lys Arg Arg Lys Leu Arg Pro Thr His Ala Glu Arg Thr Val Tyr Gly
130       135       140
Glu Gly Asp Gly Ser Asp Leu Ala Val His Asp Arg Pro Gly Ile Gly
145       150       155       160
Arg Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys
165       170       175
Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ala Trp Pro
180       185       190
Ser Phe Ser Leu Tyr Asp Pro Phe Ala Pro Ala Leu Gly Trp Glu Val
195       200       205
Asn Asn Ala Ala Ser Arg Val Tyr Ala Val Glu Gly Ser Cys Phe Val
210       215       220
Leu Ala Pro Cys Ala Thr Val Ser Gln Ala Met Ile Asp Glu Leu Cys
225       230       235       240
Asp Arg Asp Asp Lys His Ala Leu Leu His Val Gly Gly Gly His Ala
245       250       255
Ala Ile Phe Gly Pro Asp Gly Ser Ala Ile Ala Asp Lys Leu Pro Ser
260       265       270
Asp Gln Glu Gly Leu Leu Phe Ala Asp Ile Asp Leu Gly Ala Ile Gly
275       280       285

```

Ile Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
 290 295 300
 Val Thr Arg Leu Leu Leu Asn Lys Lys Pro Ser Lys Arg Val Glu His
 305 310 315 320
 Phe Ala Leu Pro Leu Asp Thr Leu Ala Gly Glu Glu Ile Asp Ala Ala
 325 330 335
 Ala Ser

<210> 251
 <211> 978
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 251
 gtgaccatcg tgagagctgc cgccgtgcag atcagtcgcc tgctctacag ccgggaagcc 60
 accgtagaaa aagtcgttcg caagatccgc gaactgggaa gaaacggcgt gcagttcgcc 120
 accttcccgg aaaccctggt gccctactac ccgtacttcg cggccgtgca gacgggcatc 180
 gaactgctgt ccggcaagga gcacctgcga ctgctggaac aatccgtaac gggtccctcg 240
 cccgccaccg atgccattgc ccaggcggca cgcgaagccg gcatggtggt gtccatcggt 300
 gtcaacgagc gcgacggagg caccatctac aacacgcagc tgctgtttga cgccgacggc 360
 acgctggtac agcgccggcg caagatcacg ccgacgcatt tcgagcgcgt ggtctggggc 420
 cagggcgacg gctcgggcct gcgagccgtg gacaccaagg ccggccgcat cggtcagctc 480
 gcctgcttcg agcacaacaa cccgctggcg cgctacgccg tgatcgccga cggtagcag 540
 atccattcgg ccatgtaccc gggctctgcc ttcggcgagg gcttcgcgca gcgcattggaa 600
 atcaacatac gccagcacgc cctggagtct ggctgcttcg tggtagaatgc gaccgcgtgg 660
 ctggatgccg accagcaggc gcagatcatg aaggatacgg gctgcggcat cgcccgatc 720
 tccggcggct gcttcacgac catcgtcacg ccggacggca tgctgatcgg tgaaccctc 780
 cggaaggcg aaggcgaagt catcgccgac ctcgatttca ccctgatcga ccggcgcaag 840
 ctgctggtgg actcgggtgg ccaactacaac cgtccggagc tgctgagcct gctgatcgat 900
 cgacccctg cggcgaactt ccatgagcgc aatgcgcttc cgtccgtcaa caccgccagc 960
 agcctcgaaa tcgtctga 978

<210> 252
 <211> 325
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 252
 Val Thr Ile Val Arg Ala Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
 1 5 10 15
 Ser Arg Glu Ala Thr Val Glu Lys Val Val Arg Lys Ile Arg Glu Leu
 20 25 30
 Gly Arg Asn Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Leu Val Pro
 35 40 45
 Tyr Tyr Pro Tyr Phe Ala Ala Val Gln Thr Gly Ile Glu Leu Leu Ser
 50 55 60
 Gly Lys Glu His Leu Arg Leu Leu Glu Gln Ser Val Thr Val Pro Ser
 65 70 75 80
 Pro Ala Thr Asp Ala Ile Ala Gln Ala Ala Arg Glu Ala Gly Met Val
 85 90 95
 Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Ile Tyr Asn Thr
 100 105 110
 Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Val Gln Arg Arg Arg Lys
 115 120 125

```

Ile Thr Pro Thr His Phe Glu Arg Met Val Trp Gly Gln Gly Asp Gly
  130                135                140
Ser Gly Leu Arg Ala Val Asp Thr Lys Ala Gly Arg Ile Gly Gln Leu
 145                150                155                160
Ala Cys Phe Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Met Ile Ala
                165                170                175
Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Ala Phe Gly
                180                185                190
Glu Gly Phe Ala Gln Arg Met Glu Ile Asn Ile Arg Gln His Ala Leu
 195                200                205
Glu Ser Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp
 210                215                220
Gln Gln Ala Gln Ile Met Lys Asp Thr Gly Cys Gly Ile Gly Pro Ile
 225                230                235                240
Ser Gly Gly Cys Phe Thr Thr Ile Val Thr Pro Asp Gly Met Leu Ile
                245                250                255
Gly Glu Pro Leu Arg Glu Gly Glu Gly Glu Val Ile Ala Asp Leu Asp
                260                265                270
Phe Thr Leu Ile Asp Arg Arg Lys Leu Leu Val Asp Ser Val Gly His
 275                280                285
Tyr Asn Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro Ala
 290                295                300
Ala Asn Phe His Glu Arg Asn Ala Leu Pro Ser Val Asn Thr Ala Ser
 305                310                315                320
Ser Leu Glu Ile Val
                325

```

<210> 253
 <211> 924
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 253
atgtcaaacy agaaccacaa ccaaacattc aaagttgccg cggtgcaggc cacacctgta      60
ttcctcgatc gtgaagcgac catcgacaaa gcttgcgagt tgattgctgc agccggcaat      120
gaaggggcga ggctggttgt cttcccgag gcattcatcc cgtcctatcc agattgggta      180
tgggcaatcc caccgggcga agaaggcgtg ctcaatgagt tgtacgcgga actgctctcc      240
aattcgggtca cgattcccag tgacgtgacg gatagactgt gccgggccgc gaggcttgcc      300
aatgcctacg tagtgatggg gatgagcgaa tgcaatgccg aggccagtgg cgcaagcctg      360
tataacacgc tattgtacat cgatgcgaag ggtgaaatcc tgggtaaaca tcgaaagttg      420
gtgccaaactg gcggcgagcg actggtgtgg gcacaggcg atggcagcac gctgcaggtc      480
tacgatactc cactgggtaa actcggcggt ttaatttget gggagaatta tatgccgctg      540
gcccgtaca ccatgtacgc ctggggcaca caaatctata tcgcagcgac atgggatcgc      600
gggcaaccct ggctctccac cttgcggcat atcgccaaag aaggcagggt gtacgtgatc      660
ggctgttgta tcgcgatgcg caaagatgat atccagagc gttaccat gaagcagaag      720
ttttacgcgg aggcgatga gtggatcaat ataggcgaca gcgcgatcgt caatcctgaa      780
gggcagttta tcgcggggcc ggtacgcaaa caggaagaga ttctctacgc ggagattaat      840
ccgcgcatgg tgcaaggccc gaagtggatg ctcgacgtgg cagggcacta cgccaggccg      900
gacgtattcc agttgacagt gtaa

```

<210> 254
 <211> 307
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 254

```

Met Ser Asn Glu Asn His Asn Gln Thr Phe Lys Val Ala Ala Val Gln
 1           5           10           15
Ala Thr Pro Val Phe Leu Asp Arg Glu Ala Thr Ile Asp Lys Ala Cys
      20           25           30
Glu Leu Ile Ala Ala Ala Gly Asn Glu Gly Ala Arg Leu Val Val Phe
      35           40           45
Pro Glu Ala Phe Ile Pro Ser Tyr Pro Asp Trp Val Trp Ala Ile Pro
      50           55           60
Pro Gly Glu Glu Gly Val Leu Asn Glu Leu Tyr Ala Glu Leu Leu Ser
65           70           75           80
Asn Ser Val Thr Ile Pro Ser Asp Val Thr Asp Arg Leu Cys Arg Ala
      85           90           95
Ala Arg Leu Ala Asn Ala Tyr Val Val Met Gly Met Ser Glu Cys Asn
      100          105          110
Ala Glu Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Ile Asp
      115          120          125
Ala Lys Gly Glu Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly
      130          135          140
Gly Glu Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Gln Val
145          150          155          160
Tyr Asp Thr Pro Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn
      165          170          175
Tyr Met Pro Leu Ala Arg Tyr Thr Met Tyr Ala Trp Gly Thr Gln Ile
      180          185          190
Tyr Ile Ala Ala Thr Trp Asp Arg Gly Gln Pro Trp Leu Ser Thr Leu
      195          200          205
Arg His Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys Ile
      210          215          220
Ala Met Arg Lys Asp Asp Ile Pro Glu Arg Tyr Pro Met Lys Gln Lys
225          230          235          240
Phe Tyr Ala Glu Ala Asp Glu Trp Ile Asn Ile Gly Asp Ser Ala Ile
      245          250          255
Val Asn Pro Glu Gly Gln Phe Ile Ala Gly Pro Val Arg Lys Gln Glu
      260          265          270
Glu Ile Leu Tyr Ala Glu Ile Asn Pro Arg Met Val Gln Gly Pro Lys
      275          280          285
Trp Met Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Gln
      290          295          300
Leu Thr Val
305

```

<210> 255

<211> 1005

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 255

```

atgacaatgt ctaagaccaa atttaggggt gcagctgtgc aggcggcgcc ggttttcctt      60
gatcggaag cgacgttgga taaagcttgt ggattgattg aggagggcgg ccgcaacggc      120
gccagcctcg tcgtcttccc tgagtcattc attccggcct accccgattg ggtttgggct      180
gtgccggcgg gcgaagaagc ttactcaat gaactgtacg cacaactgtt ggccaacgcc      240
gttgaaattc ccggcccggc cactcaacgt ttgagccagg cggtctaaaa ggctaagggt      300
cacctggcta tgggcctgac cgaacgcaac agcagggcca gcggcggcag cctttacaac      360
accttgctct atottgacct gcagggccac attctgggca agcatcgtaa gctgggtgcc      420
accggcggtg agcggctggt ttgggcccag ggcgacggca gcactttgca agtttacgat      480
acgcctctgg gtaaacctcag cggcctgatt tgctgggaaa attatatgcc gctggcgcg      540
tacgcgctgt atgcctgggg tacgcaaatt tatattgcgg ccacctggga tcggggtgag      600

```


<210>	256
<211>	334
<212>	PRT
<213>	Unknown

<220>
<223> Obtained from an environmental sample

<210> 257

<211> 942
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 257
atgaacaaga tcgcgatcat tcagcgccca cccgtgctac tcgaccgcat cgccacgctg    60
gcggttgccg tggagtcgat cgacgaagct gccgcagccg gtgcctcact gatcggtcct    120
ccagaaacct tcatccccgg ctaccctgcc tggatctggc gtctcgcgcc ggggagggat    180
ggtgcgctca ttgccagtt gcatgccga ctgctcgcca acgcggtcga tcttgcggct    240
ggagatctgg atgccctgtg tgaagttgcg cacggccacc gggtgaccgt ggtgtgcggc    300
ctcaacgaat gcgagcgcgag tcgcgggcggg ggcactctct acaacacggt cgtcgtgatc    360
gaccccgacg gcaagctgtg caatcgccac cgcaagctga tgccgacca cccggaacgc    420
atggtgcacg gtctgggtga tgcacggggc ctgcgcgccg tcgacacccc ggtgggtcga    480
gtggggcgac tcactgtgtg ggaaaaactat atgccgctgg cacgctacgc actttacgcc    540
gagggggtgg aagtctacgt ggcgcccacc tatgacagcg gcgatggctg gatcagtacg    600
atgctgcata ttgcgcttga gggacgctgc tgggtgctgg gtagcggaac cgtactgcgt    660
ggcagcgacg tcccagaaga ctttccgtca cactggacc tgtttccga cgcggaggaa    720
tggatcaatc cgggcgactc ggtggtcgtc gatcctcagg gcaagatcgt cgcaggcccc    780
atgcgacgtg agacaggcat tctctacgca gaaatcgacg ccgaacgggt cgcgccttcg    840
cgccgcacgc tcgatgtcgc cggacactac gcccgcccgg atattttcga gctccatgtc    900
cgacgtacgc cggcgatgcc ggtccacgcc gttgatgcat ga                      942
  
```

<210> 258
 <211> 313
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 258
Met Asn Lys Ile Ala Ile Ile Gln Arg Pro Pro Val Leu Leu Asp Arg
  1           5           10           15
Ile Ala Thr Leu Ala Val Ala Val Glu Ser Ile Asp Glu Ala Ala Ala
  20           25           30
Ala Gly Ala Ser Leu Ile Val Leu Pro Glu Thr Phe Ile Pro Gly Tyr
  35           40           45
Pro Ser Trp Ile Trp Arg Leu Ala Pro Gly Arg Asp Gly Ala Leu Ile
  50           55           60
Ala Gln Leu His Ala Arg Leu Leu Ala Asn Ala Val Asp Leu Ala Ala
  65           70           75           80
Gly Asp Leu Asp Ala Leu Cys Glu Val Ala His Gly His Arg Val Thr
  85           90           95
Val Val Cys Gly Leu Asn Glu Cys Glu Arg Ser Arg Gly Gly Gly Thr
  100          105          110
Leu Tyr Asn Thr Val Val Val Ile Asp Pro Asp Gly Lys Leu Cys Asn
  115          120          125
Arg His Arg Lys Leu Met Pro Thr Asn Pro Glu Arg Met Val His Gly
  130          135          140
Leu Gly Asp Ala Ser Gly Leu Arg Ala Val Asp Thr Pro Val Gly Arg
  145          150          155          160
Val Gly Ala Leu Ile Cys Trp Glu Asn Tyr Met Pro Leu Ala Arg Tyr
  165          170          175
Ala Leu Tyr Ala Glu Gly Val Glu Val Tyr Val Ala Pro Thr Tyr Asp
  180          185          190
Ser Gly Asp Gly Trp Ile Ser Thr Met Arg His Ile Ala Leu Glu Gly
  195          200          205
Arg Cys Trp Val Leu Gly Ser Gly Thr Val Leu Arg Gly Ser Asp Val
  
```

```

      210              215              220
Pro Glu Asp Phe Pro Ser His Leu Asp Leu Phe Pro Asp Ala Glu Glu
225              230              235              240
Trp Ile Asn Pro Gly Asp Ser Val Val Val Asp Pro Gln Gly Lys Ile
      245              250              255
Val Ala Gly Pro Met Arg Arg Glu Thr Gly Ile Leu Tyr Ala Glu Ile
      260              265              270
Asp Ala Glu Arg Val Ala Pro Ser Arg Arg Thr Leu Asp Val Ala Gly
      275              280              285
His Tyr Ala Arg Pro Asp Ile Phe Glu Leu His Val Arg Arg Thr Pro
      290              295              300
Ala Met Pro Val His Ala Val Asp Ala
305              310

```

<210> 259

<211> 981

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 259

```

atggccatca tcaaagccgc cgccgtccag atcagtcggtg tgctgtatag ccgcgagggg 60
accgtggaca aggtctgcca gcagatcatc gccctcgggtc agcaaggcgt gcaatttgcg 120
gtctttccgg aaacgggtgt gccgtactac ccttatttct ccttcgtcca gccgccgttc 180
gcatgggcca aggaacacct gaaactgttg gaacaatcgg tgattgtgcc gtcggctgcc 240
accttggcga tcggcggaagc gtgcaaacaa gcgggaatgg tgggtgtctat cggcgtaaat 300
gagcgcgatg gcggcacgat ctacaacgcc cagttgctgt ttgacgctga tggcagcttg 360
attcagcacc gtcgcaaaat aaccccgacg taccacgagc ggatgatctg gggtaaggc 420
gacggctccg ggttgcgcg ccatcgacagc gcggtcgggc gtattggctc gctggcctgc 480
tggaacatt acaaccctt ggcccgctac gccctgatgg ccgacggcga gcagattcac 540
gcggctatgt ttcccggtc tctggtgggt gacatttttg ccgatcagat agaggctcact 600
attcgtcatc acgccttgga gtccggctgc ttcgtggtca actccaccgc gtggcttgat 660
gctgatcagc aaggccaaat catcgaggac accggttgca gcattggccc aatctcgggt 720
ggctgcttca cggccatcgt ttcccgga ggcgaattac tcggcgaaac gctgcgttca 780
ggtgagggcg cagtcacgc cgacctggac atggcattga tcgacaagcg caaacgatg 840
atggattccg tcggccatta cagccgccca gaactgctca gtttattgat cgaccgcacg 900
cccaccgtc atgtgcatga gcgcggcgcc catcaccttg ccgtagcctc tatcggggag 960
cttgaccatg caaaccaatg a 981

```

<210> 260

<211> 326

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 260

```

Met Ala Ile Ile Lys Ala Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
1              5              10              15
Ser Arg Glu Gly Thr Val Asp Lys Val Cys Gln Gln Ile Ile Ala Leu
      20              25              30
Gly Gln Gln Gly Val Gln Phe Ala Val Phe Pro Glu Thr Val Val Pro
      35              40              45
Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Pro Pro Phe Ala Met Gly Lys
      50              55              60
Glu His Leu Lys Leu Leu Glu Gln Ser Val Ile Val Pro Ser Ala Ala
      65              70              75              80
Thr Leu Ala Ile Gly Glu Ala Cys Lys Gln Ala Gly Met Val Val Ser

```

<210> 262
<211> 337

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 262

```

Met Gly Leu Val His Gln Lys Tyr Lys Val Ala Val Val Gln Ala Ala
 1          5          10          15
Pro Val Phe Leu Asp Leu Asp Ala Thr Val Asp Lys Thr Ile Ala Leu
 20          25          30
Ile Glu Glu Ala Ser Ala Gln Gly Ala Lys Leu Val Ala Phe Pro Glu
 35          40          45
Thr Phe Ile Pro Gly Tyr Pro Trp Gln Ile Trp Leu Gly Ala Pro Ala
 50          55          60
Trp Ala Ile Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
 65          70          75          80
Gly Phe Asp Ser Pro Gln Ala Glu Lys Ile Arg Gln Ala Val Lys Arg
 85          90          95
Ala Lys Leu Thr Ala Val Leu Gly Leu Ser Glu Arg Asp Gly Gly Ser
100          105          110
Leu Tyr Ile Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
115          120          125
Lys Arg Arg Lys Leu Arg Pro Thr His Ala Glu Arg Thr Val Phe Gly
130          135          140
Glu Gly Asp Gly Ser Asp Leu Ala Val His Asp Arg Ala Asp Val Gly
145          150          155          160
Arg Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys
165          170          175
Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Gly Ala Trp Pro
180          185          190
Ser Phe Ser Leu Tyr Asp Pro Phe Ala His Ala Leu Gly His Glu Val
195          200          205
Asn Asn Ala Ala Ser Lys Val Tyr Ala Val Glu Gly Ser Cys Phe Phe
210          215          220
Leu Gly Pro Cys Ala Val Val Ser Gln Ala Met Ile Asp Glu Leu Cys
225          230          235          240
Asp Ser Pro Glu Lys His Ala Phe Leu His Val Gly Gly Gly His Ala
245          250          255
Val Ile Tyr Gly Pro Asp Gly Ser Ser Leu Ala Glu Lys Leu Pro Pro
260          265          270
Asp Gln Glu Gly Ile Leu Tyr Ala Asp Ile Asp Leu Gly Met Ile Gly
275          280          285
Val Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
290          295          300
Val Thr Arg Leu Leu Leu Asn Thr Thr Arg Ala Asn Arg Val Glu His
305          310          315          320
Phe Ser Leu Pro Val Asp Ala Glu Val Met Ser Glu Ile Arg Leu Gln
325          330          335
Ala

```

<210> 263

<211> 1014

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 263

```

atgaaaagtcg tcaaagcggc agcgggttcag ttgagccctg tcctctacag ccgcgaggca      60
accgtcgcga aggtcgtgcg gaagatccac gagcttgggc agcagggcgt gcagttcgcc      120
accttcccgg aaaccgttgt gccgtactac ccgtatttct ccgcggtcca gacgccgatg      180
cagcttctgg ctggaaccga gcatctgaaa ttgctcgacc aggccgtgac ggtgccgtct      240
cccgcgaccg acgcgatcgg cgaggcagcc cgggaaggcg gcgatggtgg gtccatcggc      300
gtcaacgagc gtgatggtgg aaccctgtac aacacccaat tgctcttcga cgccgatggc      360
accctgatcc agcgcgcggc caagatcacg cccacccatt tcgagcgcat gatctggggc      420
cagggtgacg ggtcgggcct gcgtgccgtc gacagcaagg tcggccgcat tggccagctg      480
gcatgcttcg agcacaacaa tcctctggcg cgctacgcga tgatggccga cggcgagcag      540
atccattcgg ccatgtatcc gggttctgcc ttcggcgagg gctttgccca gaggatggaa      600
atcaatatcc gccagcacgc actggagtcc gggtgcttcg tcgtgaacgc gacggcctgg      660
ctggatgccg accagcaggc gcaaatcatg aaagacacgg gctgcgggat cgggtccgatc      720
tcgggcgggt gcttcaccac gatcgtggca cccgacggca cgctgctggg ggaacctctg      780
cgctcgggcg agggcgaggt catcgccgat ctcgatttca cggagatcga ccggcgcaag      840
atgctgatgg actcggcagg ccactacaac cgtccggaac tgctcagtct gctgatcgac      900
cgcacgccga ccgcaaactg gcacgaacgg atggcgcatc cccaagcgag cacgaagcag      960
ccgcgctccg gcgatctgcc cgctgcgctg gctggcgcgc aggagatcct gtga      1014

```

<210> 264

<211> 337

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 264

```

Met Lys Val Val Lys Ala Ala Ala Val Gln Leu Ser Pro Val Leu Tyr
 1          5          10          15
Ser Arg Glu Ala Thr Val Ala Lys Val Val Arg Lys Ile His Glu Leu
 20          25          30
Gly Gln Gln Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
 35          40          45
Tyr Tyr Pro Tyr Phe Ser Ala Val Gln Thr Pro Met Gln Leu Leu Ala
 50          55          60
Gly Thr Glu His Leu Lys Leu Leu Asp Gln Ala Val Thr Val Pro Ser
 65          70          75          80
Pro Ala Thr Asp Ala Ile Gly Glu Ala Ala Arg Lys Ala Gly Met Val
 85          90          95
Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn Thr
 100         105         110
Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln Arg Arg Arg Lys
 115         120         125
Ile Thr Pro Thr His Phe Glu Arg Met Ile Trp Gly Gln Gly Asp Gly
 130         135         140
Ser Gly Leu Arg Ala Val Asp Ser Lys Val Gly Arg Ile Gly Gln Leu
 145         150         155         160
Ala Cys Phe Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Met Met Ala
 165         170         175
Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Ala Phe Gly
 180         185         190
Glu Gly Phe Ala Gln Arg Met Glu Ile Asn Ile Arg Gln His Ala Leu
 195         200         205
Glu Ser Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp
 210         215         220
Gln Gln Ala Gln Ile Met Lys Asp Thr Gly Cys Gly Ile Gly Pro Ile
 225         230         235         240
Ser Gly Gly Cys Phe Thr Thr Ile Val Ala Pro Asp Gly Thr Leu Leu
 245         250         255
Gly Glu Pro Leu Arg Ser Gly Glu Gly Glu Val Ile Ala Asp Leu Asp
 260         265         270

```

Phe Thr Glu Ile Asp Arg Arg Lys Met Leu Met Asp Ser Ala Gly His
 275 280 285
 Tyr Asn Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro Thr
 290 295 300
 Ala Asn Val His Glu Arg Met Ala His Pro Gln Ala Ser Thr Lys Gln
 305 310 315 320
 Pro Arg Ser Gly Asp Leu Pro Ala Ala Leu Ala Gly Ala Gln Glu Ile
 325 330 335
 Leu

<210> 265

<211> 999

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 265

atgcttaatc	taggcatagt	ccagatgaac	gcagagccgc	tcaacgtgga	aggcaacctg	60
ctcaaggcgg	agcgcctatgt	cgcgaaagtgc	gccgcgggacg	gcgcccact	cgtggtgctg	120
ccggagatgt	tcaacgtcgg	cttccacctc	ggcgagtccc	tgatgatggt	cgccgagccc	180
ctggacggca	agaccgtgca	gtggctgcaa	cggcaggcgt	ccaccataa	catatatatc	240
accgggagct	tatacgagcg	ttacgacgag	catttctaca	acaccatggt	catggtggga	300
tacgacggca	gcgtgcagta	ctaccgcaag	cgcaatccta	cctggtccga	gtcggcggtg	360
tggcgccgca	gcgaggtgcc	aggccccggt	atattcgata	ccccgttcgg	gcgcatcggg	420
ggcgctcatct	gcttcgattc	cttcgcgcgc	gagaccacg	agggttcaa	gcagagcggg	480
gtcgaaggcgg	tggtaatcat	cgccctgtgg	ggcgccaacc	gtgcgcgggc	attcttctg	540
cgccccggacc	tcctgctaag	ccgggaagg	ctgggtccgtt	ggtcccggct	ggcctcgag	600
gacgtcccc	gaaatcacgc	gaaagagctc	gggtgcccg	tcgccttcgt	caaccagagt	660
ggcaccatcc	gcatgaccag	ccccatccct	ttccccgact	ggccggtgca	gagctccttc	720
tacgaactca	tcggcaagtc	ccacgtccgg	gacgcatccg	gagaggatgat	cgcgagggtg	780
gacgaggggg	agatcgactc	ctgcctggtg	gtcccggtag	aggtcgagca	ggcgagagc	840
aggccggaga	tcaggaagtc	aaatatatcg	cccggctacc	tcggcaagga	ttactatttc	900
gtggagccgc	cgcttatctg	caagctcttc	caggtctggt	tcctcagcgg	cctggtgccc	960
accgaatacg	aggcgcggcg	tctgcgccac	ctgttctga			999

<210> 266

<211> 332

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 266

Met	Leu	Asn	Leu	Gly	Ile	Val	Gln	Met	Asn	Ala	Glu	Pro	Leu	Asn	Val
1			5					10					15		
Glu	Gly	Asn	Leu	Leu	Lys	Ala	Glu	Arg	Tyr	Val	Ala	Lys	Cys	Ala	Ala
		20						25				30			
Asp	Gly	Ala	Gln	Leu	Val	Val	Leu	Pro	Glu	Met	Phe	Asn	Val	Gly	Phe
	35						40				45				
His	Leu	Gly	Glu	Ser	Leu	Met	Met	Val	Ala	Glu	Pro	Leu	Asp	Gly	Lys
	50					55					60				
Thr	Val	Gln	Trp	Leu	Gln	Arg	Gln	Ala	Ser	Thr	His	Asn	Ile	Tyr	Ile
	65				70					75				80	
Thr	Gly	Ser	Leu	Tyr	Glu	Arg	Tyr	Asp	Glu	His	Phe	Tyr	Asn	Thr	Met
			85					90					95		
Val	Met	Val	Gly	Tyr	Asp	Gly	Ser	Val	Gln	Tyr	Tyr	Arg	Lys	Arg	Asn
			100					105					110		

```

Pro Thr Trp Ser Glu Ser Ala Val Trp Arg Arg Ser Glu Val Pro Gly
      115      120      125
Pro Gly Ile Phe Asp Thr Pro Phe Gly Arg Ile Gly Gly Val Ile Cys
      130      135      140
Phe Asp Ser Phe Ala Arg Glu Thr His Glu Gly Phe Lys Gln Ser Gly
      145      150      155      160
Val Glu Ala Val Val Ile Ile Ala Leu Trp Gly Ala Asn Arg Ala Arg
      165      170      175
Ala Phe Phe Trp Arg Pro Asp Leu Leu Leu Ser Arg Glu Gly Leu Val
      180      185      190
Arg Trp Ser Arg Leu Ala Ser Glu Asp Val Pro Arg Asn His Ala Lys
      195      200      205
Glu Leu Gly Val Pro Val Ala Phe Val Asn Gln Ser Gly Thr Ile Arg
      210      215      220
Met Thr Ser Pro Ile Pro Phe Pro Asp Trp Pro Val Gln Ser Ser Phe
      225      230      235      240
Tyr Asp Phe Ile Gly Lys Ser His Val Arg Asp Ala Ser Gly Glu Val
      245      250      255
Ile Ala Arg Val Asp Glu Gly Glu Ile Asp Ser Cys Leu Val Val Pro
      260      265      270
Val Glu Val Glu Gln Ala Gln Ser Arg Pro Glu Ile Arg Lys Ser Asn
      275      280      285
Ile Ser Pro Gly Tyr Leu Gly Lys Asp Tyr Tyr Phe Val Glu Pro Pro
      290      295      300
Leu Ile Cys Lys Leu Phe Gln Val Trp Phe Leu Ser Gly Leu Val Pro
      305      310      315      320
Thr Glu Tyr Glu Ala Arg Arg Leu Arg His Leu Phe
      325      330

```

<210> 267
 <211> 1038
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 267
atgggcatta cgcacccgaa gttcaaggcc gcggcggtac aggcggcgcc gggctttctc      60
gacagcgagg ccaccgtcga caagacgata cgccgatgc aggaagcggc ggaccacggc      120
gcctcgctga tcgtctttcc ggaagcctgg ctgcccggtt atccgtgggtg gatctggctc      180
gggtccgccc cctggggcat gcagttcgtg cagcgctact tcgacaattc gccgagcgtc      240
ggcgatgatc ttttccgccg gatcgagcgc gcgcccgcca aggcgaagat cgaagtggtc      300
ctcgggtctc gcgagcgcgc tgccggctcg ctgtacctcg cgcaggcggt catctcctca      360
acggcgagaa cgcgcgagc gcgccgcaag ttgcgaccaa cgcacgtcga gcgaaccggt      420
ttcggcgagg gcgatggcag cgacttcaag gtgttcgaca ctccgctggg ccgcgtcggt      480
gggtctctgt gctgggaaca cctgcaaccg ctgtcgcgct acgcgatggt ctcgatgaac      540
gagcaggtgc acgccgccg ctggccgacg ttcagcctct acacggattt tgccatgcc      600
ctcggccacg aactgaatct cgcagccagc gctacttacg cggctgaagg gcagtgtac      660
gtgattgccg cctgtggcgt ggtcacgcag gagatgctgg atctgatgaa ggcgcggtgc      720
cccccggaat atctgcgggt cggcggcgga tacgccatga tctttgcgcc cgacggacgg      780
cgcatcgcg cggcgctgcc gccggaacaa gaagggtgta ttacgccga catcgatctt      840
tcgatgatct ctctcgccaa ggcggtgcc gatcccaccg gtcactactc gcggccggat      900
gtcgtgcggc ttatgctgaa taccgaaccg atgcagcggg tcgaaaagct gcagccgccg      960
ctggactcag ccgcgcgccg tgagaatgaa ccggcacgcg agaccgcagc ggcgaccgag      1020
agccgccagc cccagtaa

```

<210> 268
 <211> 344
 <212> PRT
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 268

```

Met Gly Ile Thr His Pro Lys Phe Lys Ala Ala Ala Val Gln Ala Ala
 1           5           10           15
Pro Gly Phe Leu Asp Ser Glu Ala Thr Val Asp Lys Thr Ile Arg Leu
           20           25           30
Met Gln Glu Ala Ala Asp His Gly Ala Ser Leu Ile Val Phe Pro Glu
 35           40           45
Ala Trp Leu Pro Gly Tyr Pro Trp Trp Ile Trp Leu Gly Pro Pro Ala
 50           55           60
Trp Gly Met Gln Phe Val Gln Arg Tyr Phe Asp Asn Ser Pro Ser Val
 65           70           75           80
Gly Asp Asp Leu Phe Arg Arg Ile Glu Arg Ala Ala Ala Lys Ala Lys
           85           90           95
Ile Glu Val Val Leu Gly Leu Ser Glu Arg Ala Ala Gly Ser Leu Tyr
           100          105          110
Leu Ala Gln Ala Phe Ile Ser Ser Thr Gly Glu Thr Arg Ala Val Arg
           115          120          125
Arg Lys Leu Arg Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly
 130          135          140
Asp Gly Ser Asp Phe Lys Val Phe Asp Thr Pro Leu Gly Arg Val Gly
 145          150          155          160
Gly Leu Leu Cys Trp Glu His Leu Gln Pro Leu Ser Arg Tyr Ala Met
           165          170          175
Phe Ser Met Asn Glu Gln Val His Ala Ala Trp Pro Thr Phe Ser
           180          185          190
Leu Tyr Thr Asp Phe Ala His Ala Leu Gly His Glu Leu Asn Leu Ala
           195          200          205
Ala Ser Ala Thr Tyr Ala Ala Glu Gly Gln Cys Tyr Val Ile Ala Ala
 210          215          220
Cys Gly Val Val Thr Gln Glu Met Leu Asp Leu Met Lys Ala Pro Cys
 225          230          235          240
Pro Pro Glu Tyr Leu Arg Val Gly Gly Tyr Ala Met Ile Phe Ala
           245          250          255
Pro Asp Gly Arg Arg Ile Ala Ala Ala Leu Pro Pro Glu Gln Glu Gly
           260          265          270
Leu Ile Tyr Ala Asp Ile Asp Leu Ser Met Ile Ser Leu Ala Lys Ala
           275          280          285
Ala Ala Asp Pro Thr Gly His Tyr Ser Arg Pro Asp Val Val Arg Leu
           290          295          300
Met Leu Asn Thr Glu Pro Met Gln Arg Val Glu Lys Leu Gln Pro Pro
 305          310          315          320
Leu Asp Ser Ala Ala Arg Arg Glu Asn Glu Pro Ala Arg Glu Thr Ala
           325          330          335
Ala Ala Thr Glu Ser Arg Gln Pro
           340

```

<210> 269

<211> 1014

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 269

```

atgtctgaaa cagccttcaa gatcgcggtc gtacaggcgg ctccggtttt tctcgacgca    60
aaggcgacgg tggacaaggc gatcggtctg atggccgaag ccggcgccaa gggcgccaag    120

```

```

ctgctcgcat tcccggaagt attcatcccc ggctaccctt ggtggctgtg gctgggcaca 180
ccggcatggg gcatgcagtt tgttgccaag tatcacgcga actcgcttcg tgcagacggg 240
cctgaattgg cagccctcgc ggcggcggcg gcgaagtcgg atatcaatgc cgtcatcggc 300
ttctcgagaga tcgacggcgg ttccctctac atcagccagg cgctcatcag cgacaagggc 360
gagataatgt tcaaacggcg caagctgaag ccgacgcacg tcgaacgcac gttgttcggc 420
gaaggggacg ggtccgactt ccaggtcgtg gacacgagcg tcggcaggct cggcgccttg 480
tggtgcgccc aacacataca gccgctgtcg aagtacgcga tgtactccat gcacgaacag 540
gtgcacgtcg cctcctggcc gtcatttact ttgtaccgcg gcacggcata tgccttgggc 600
cacgaggtca atctggccgc gagccagatt tatgcgctcg agggaggctg tttcgtcctt 660
catgcgagcg ccatcaccgg ccaggacatg tttgacgtgc tgtgcgacac tccggagagg 720
acgcaactgc tgaactccga cggcgccaag gtcggcgcg gctactcgat gatcttcggt 780
cccgatggcc agccccttgt tgggcatctg cctcaagaca ccgaggggat actctacgca 840
gatattgacc tggcgaacat ttccgttgcc aaagcggcct acgacccgct cggacactat 900
gcgcgcggag acgtggtgcg cttgatggtc aatcgcaacc cgcggcatac gagtgttgcg 960
ttcggcgggg gcgcggcgga ggcagcaacc tggacggaag caaaagcggga gtga 1014

```

<210> 270

<211> 337

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 270

```

Met Ser Glu Thr Ala Phe Lys Ile Ala Val Val Gln Ala Ala Pro Val
1      5      10      15
Phe Leu Asp Ala Lys Ala Thr Val Asp Lys Ala Ile Gly Leu Met Ala
20     25     30
Glu Ala Gly Ala Lys Gly Ala Lys Leu Leu Ala Phe Pro Glu Val Phe
35     40     45
Ile Pro Gly Tyr Pro Trp Trp Leu Trp Leu Gly Thr Pro Ala Trp Gly
50     55     60
Met Gln Phe Val Ala Lys Tyr His Ala Asn Ser Leu Arg Ala Asp Gly
65     70     75     80
Pro Glu Leu Ala Ala Leu Ala Ala Ala Ala Lys Ser Asp Ile Asn
85     90     95
Ala Val Ile Gly Phe Ser Glu Ile Asp Gly Gly Ser Leu Tyr Ile Ser
100    105    110
Gln Ala Leu Ile Ser Asp Lys Gly Glu Ile Met Phe Lys Arg Arg Lys
115    120    125
Leu Lys Pro Thr His Val Glu Arg Thr Leu Phe Gly Glu Gly Asp Gly
130    135    140
Ser Asp Phe Gln Val Val Asp Thr Ser Val Gly Arg Leu Gly Ala Leu
145    150    155    160
Cys Cys Ala Glu His Ile Gln Pro Leu Ser Lys Tyr Ala Met Tyr Ser
165    170    175
Met His Glu Gln Val His Val Ala Ser Trp Pro Ser Phe Thr Leu Tyr
180    185    190
Arg Gly Thr Ala Tyr Ala Leu Gly His Glu Val Asn Leu Ala Ala Ser
195    200    205
Gln Ile Tyr Ala Leu Glu Gly Gly Cys Phe Val Leu His Ala Ser Ala
210    215    220
Ile Thr Gly Gln Asp Met Phe Asp Val Leu Cys Asp Thr Pro Glu Arg
225    230    235    240
Thr Gln Leu Leu Asn Ser Asp Gly Gly Lys Val Gly Gly Gly Tyr Ser
245    250    255
Met Ile Phe Gly Pro Asp Gly Gln Pro Leu Val Gly His Leu Pro Gln
260    265    270
Asp Thr Glu Gly Ile Leu Tyr Ala Asp Ile Asp Leu Ala Asn Ile Ser
275    280    285

```

Val Ala Lys Ala Ala Tyr Asp Pro Ser Gly His Tyr Ala Arg Gly Asp
 290 295 300
 Val Val Arg Leu Met Val Asn Arg Asn Pro Arg His Thr Ser Val Ala
 305 310 315 320
 Phe Gly Gly Gly Ala Gly Glu Ala Ala Thr Trp Thr Glu Ala Lys Ala
 325 330 335
 Glu

<210> 271
 <211> 966
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 271
 atgtccagcg agaataacaa cgctacattc aaagttgccg cagttcaggc cacacctgtg 60
 tatcttgatc gtgaagcaac catcgacaag gcttgcgagt tgatcgctac tgctggcagc 120
 gaaggagctc gcctgattat ctttccagaa gcgttcatcc caacctatcc tgagtgggta 180
 tgggggtattc cttctggtga gcaagggtta ctcaacgagc tctattcaga gttgctcacc 240
 aattcggtca cgattcccag cgacgcgact gacagactgt gcgaggccgc gaagcttgct 300
 aatgcctacg tggatgatgg aatgagtgaa cggaatgtcg aagcgagtgg tgcaagcctg 360
 tataatacgc tcttgatcat agatgcgcag ggggagattt tagggaaaca tcgaaagtgt 420
 gtaccaacgg gcggtgagcg cctggtatgg gcgcaagggt atggcagcac gctgcaggtc 480
 tacgatactc cattgggaaa actcggtggt ttaatttgct gggaaaatta tatgccactg 540
 gcacgctacg ctatgtatgc ctggggtaca caaatctatg tcgcagcaac gtgggatcgc 600
 ggccaaccct ggctctcaac gttacggcat attgccaaag aaggcagggt atacgtaatt 660
 ggttgctgta ttgcgatgcg taaagatgat attccagatc gttactccat gaagcagaag 720
 tattacgctg aaatggagga atggattaat attggtgaca gcgcgattgt caatcccga 780
 'ggacacttta ttgcagggcc tgtgcgcaag caagaagaaa ttctttacgc ggagatcgat 840
 ccacgcatgg tgcaaggccc gaagtggatg ctcgatgtgg ctgggcacta tgcgagacca 900
 gatgtgttcc agttgacggg gcatacggat gtgaggcaga tgattcgggt ggaacatgat 960
 tcataa 966

<210> 272
 <211> 321
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 272
 Met Ser Ser Glu Asn Asn Ala Thr Phe Lys Val Ala Ala Val Gln
 1 5 10 15
 Ala Thr Pro Val Tyr Leu Asp Arg Glu Ala Thr Ile Asp Lys Ala Cys
 20 25 30
 Glu Leu Ile Ala Thr Ala Gly Ser Glu Gly Ala Arg Leu Ile Ile Phe
 35 40 45
 Pro Glu Ala Phe Ile Pro Thr Tyr Pro Glu Trp Val Trp Gly Ile Pro
 50 55 60
 Ser Gly Glu Gln Gly Leu Leu Asn Glu Leu Tyr Ser Glu Leu Leu Thr
 65 70 75 80
 Asn Ser Val Thr Ile Pro Ser Asp Ala Thr Asp Arg Leu Cys Glu Ala
 85 90 95
 Ala Lys Leu Ala Asn Ala Tyr Val Val Met Gly Met Ser Glu Arg Asn
 100 105 110
 Val Glu Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Ile Asp
 115 120 125

Ala Gln Gly Glu Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly
 130 135 140
 Gly Glu Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Gln Val
 145 150 155 160
 Tyr Asp Thr Pro Leu Gly Lys Leu Gly Gly Leu Ile Cys Trp Glu Asn
 165 170 175
 Tyr Met Pro Leu Ala Arg Tyr Ala Met Tyr Ala Trp Gly Thr Gln Ile
 180 185 190
 Tyr Val Ala Thr Trp Asp Arg Gly Gln Pro Trp Leu Ser Thr Leu
 195 200 205
 Arg His Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys Ile
 210 215 220
 Ala Met Arg Lys Asp Asp Ile Pro Asp Arg Tyr Ser Met Lys Gln Lys
 225 230 235 240
 Tyr Tyr Ala Glu Met Glu Glu Trp Ile Asn Ile Gly Asp Ser Ala Ile
 245 250 255
 Val Asn Pro Glu Gly His Phe Ile Ala Gly Pro Val Arg Lys Gln Glu
 260 265 270
 Glu Ile Leu Tyr Ala Glu Ile Asp Pro Arg Met Val Gln Gly Pro Lys
 275 280 285
 Trp Met Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Gln
 290 295 300
 Leu Thr Val His Thr Asp Val Arg Gln Met Ile Arg Val Glu His Asp
 305 310 315 320
 Ser

<210> 273

<211> 1023

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 273

atgaataact	caccaccaac	catccgcgct	gctgccattc	agctcagtc	agttctgttt	60
agtcgggatg	ggactaccga	gaaggtgttg	caggcgatcg	ctagtgcctg	caaggaagg	120
gcacaactgg	ttgtttttcc	agaaactttc	atcccctact	accctattt	ctcattcatt	180
caacccccctg	tgttgatggg	caaagagcac	atgcggctct	atgaggaagc	cgtgacggtc	240
ccgggtcccg	tgacagatgc	ggtcagtcga	gcagcccgtt	cttacggcat	ggtggtagtg	300
ctgggggtga	atgagcgaga	tggtagctca	atttacaata	cacagttgat	tttcgatgct	360
gacggcacat	tgttgctgaa	gcgacgcaaa	atcaccctca	cctatcatga	gcgcatggtc	420
tgggggcagg	gagacggtgc	tggattgaag	gtattggata	cagcagtcgg	taagggtggg	480
gcgctggcat	gttggaaca	ttacaatccc	ctggcacgat	ttgcgctgat	ggcacagcat	540
gagcagattc	actgcgctca	gttccccggt	tctctggtg	gacaaatttt	cactgatcag	600
attgaggtaa	cgattcggca	tcatgcgttg	gaatcgggtt	gtttgtggt	gaatgctact	660
ggctggctct	ctccagaaca	ggtggcacaa	atcaccacgg	atgaaaagt	gcaacgggtg	720
ctgagtggtg	ggtgtaatac	cgccattatt	ggacctgaag	gcaatcatct	ctgtcctccc	780
attaccgatg	gtgagggcat	agcgatcgcc	gatctcgact	tctcactaat	caccaaaccg	840
aaacgcatga	tggattgcgt	cggtcactac	tccgcctctg	acttggtgaa	gctgcaactc	900
aatgcaacgg	catggtcggg	gctggctggg	gagcaggggg	caggtgccag	ggagcagggg	960
ctaggtgtgc	cggatgccat	gctgtctacg	cctaagccag	aatactcaac	actggatcag	1020
tag						1023

<210> 274

<211> 340

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 274

```

Met Asn Asn Ser Pro Pro Thr Ile Arg Ala Ala Ala Ile Gln Leu Ser
 1          5          10          15
Pro Val Leu Phe Ser Arg Asp Gly Thr Thr Glu Lys Val Leu Gln Ala
 20          25          30
Ile Ala Ser Ala Ala Lys Glu Gly Ala Gln Leu Val Val Phe Pro Glu
 35          40          45
Thr Phe Ile Pro Tyr Tyr Pro Tyr Phe Ser Phe Ile Gln Pro Pro Val
 50          55          60
Leu Met Gly Lys Glu His Met Arg Leu Tyr Glu Glu Ala Val Thr Val
 65          70          75          80
Pro Gly Pro Val Thr Asp Ala Val Ser Arg Ala Ala Arg Ser Tyr Gly
 85          90          95
Met Val Val Val Leu Gly Val Asn Glu Arg Asp Gly Gly Ser Ile Tyr
 100          105          110
Asn Thr Gln Leu Ile Phe Asp Ala Asp Gly Thr Leu Leu Lys Arg
 115          120          125
Arg Lys Ile Thr Pro Thr Tyr His Glu Arg Met Val Trp Gly Gln Gly
 130          135          140
Asp Gly Ala Gly Leu Lys Val Leu Asp Thr Ala Val Gly Lys Val Gly
 145          150          155          160
Ala Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Phe Ala Leu
 165          170          175
Met Ala Gln His Glu Gln Ile His Cys Ala Gln Phe Pro Gly Ser Leu
 180          185          190
Val Gly Gln Ile Phe Thr Asp Gln Ile Glu Val Thr Ile Arg His His
 195          200          205
Ala Leu Glu Ser Gly Cys Phe Val Val Asn Ala Thr Gly Trp Leu Ser
 210          215          220
Pro Glu Gln Val Ala Gln Ile Thr Thr Asp Glu Lys Leu Gln Arg Val
 225          230          235          240
Leu Ser Gly Gly Cys Asn Thr Ala Ile Ile Gly Pro Glu Gly Asn His
 245          250          255
Leu Cys Pro Pro Ile Thr Asp Gly Glu Gly Ile Ala Ile Ala Asp Leu
 260          265          270
Asp Phe Ser Leu Ile Thr Lys Arg Lys Arg Met Met Asp Cys Val Gly
 275          280          285
His Tyr Ser Arg Pro Asp Leu Leu Lys Leu Gln Leu Asn Ala Thr Ala
 290          295          300
Trp Ser Val Leu Ala Gly Glu Gln Gly Ala Gly Ala Arg Glu Gln Gly
 305          310          315          320
Leu Gly Val Pro Asp Ala Met Leu Ser Thr Pro Lys Pro Glu Tyr Ser
 325          330          335
Thr Leu Asp Gln
 340

```

<210> 275

<211> 849

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 275

```

atggagacgg ctcacaaagc aaaggctcgat ttccttgtgc tgggtgagac gtggctctca    60
ggctaccggg cttggctgga ccaactgcccc gatgttgcc ggtgggatta tgaaccgatg    120
aaaaaagtgt attgagatt tcgacaaagt gctatttctg ttcctggcaa agaatttgat    180
ttccttactg gcctctgtaa aaaatattca caaacgcttg ccatcggtgt taatgagaaa    240

```

```

gtagatcatg gggtaggtaa tggtagcatt tataattcat ttctactgat tgattctgat 300
ggaacactgt tgaatcatca tcgcaagtta gttcccactt ttactgagaa attattatac 360
ggccatggag atggccatgg gctgaagtcg atggatactt cggtagggaag aatcggaggg 420
agcatttggt gggaacattg gatgccacta tgcagacaag cacttcatga tgcaggtagag 480
caaatccatg ttgccctttg gccgactggt catgacatcc atcaagtggc aagtagaagc 540
tatgcatttg aagggcgctg ctttgtattg gctgccgggc agatttttgc tgctaaagat 600
tttccaaagg aacttgtctt accagactat ctaaagcaaa atccggatca gtcattttg 660
aatgggggga gctgcgtgat cggccctgat gggaaatatt tgattgagcc cgtgtttgat 720
cgggaagaac tgattgtgtg tgaacttgac cttgacgaag cttataaaga aagaatgacg 780
atggacgttt caggtcacta ccaaagacga gacgttttca gttttgacgt gaaccaacat 840
cgacattga 849

```

<210> 276

<211> 310

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 276

```

Met Thr Lys Leu Lys Ile Ala Ile Gly Gln Phe Ser Ser Asn His Leu
1      5      10      15
Asp Leu Lys Cys Ser Leu Glu Lys Leu Glu Lys Ile Met Glu Thr Ala
20     25     30
His Lys Ala Lys Val Asp Phe Leu Val Leu Gly Glu Thr Trp Leu Ser
35     40     45
Gly Tyr Pro Ala Trp Leu Asp His Cys Pro Asp Val Gly Arg Trp Asp
50     55     60
Tyr Glu Pro Met Lys Lys Val Tyr Leu Arg Phe Arg Gln Ser Ala Ile
65     70     75     80
Ser Val Pro Gly Lys Glu Phe Asp Phe Leu Thr Gly Leu Cys Lys Lys
85     90     95
Tyr Ser Gln Thr Leu Ala Ile Gly Val Asn Glu Lys Val Asp His Gly
100    105    110
Val Gly Asn Gly Thr Ile Tyr Asn Ser Phe Leu Leu Ile Asp Ser Asp
115    120    125
Gly Thr Leu Leu Asn His His Arg Lys Leu Val Pro Thr Phe Thr Glu
130    135    140
Lys Leu Leu Tyr Gly His Gly Asp Gly His Gly Leu Lys Ser Met Asp
145    150    155    160
Thr Ser Val Gly Arg Ile Gly Gly Ser Ile Cys Trp Glu His Trp Met
165    170    175
Pro Leu Cys Arg Gln Ala Leu His Asp Ala Gly Glu Gln Ile His Val
180    185    190
Ala Leu Trp Pro Thr Val His Asp Ile His Gln Val Ala Ser Arg Ser
195    200    205
Tyr Ala Phe Glu Gly Arg Cys Phe Val Leu Ala Ala Gly Gln Ile Phe
210    215    220
Ala Ala Lys Asp Phe Pro Lys Glu Leu Val Leu Pro Asp Tyr Leu Lys
225    230    235    240
Gln Asn Pro Asp Gln Leu Ile Leu Asn Gly Gly Ser Cys Val Ile Gly
245    250    255
Pro Asp Gly Lys Tyr Leu Ile Glu Pro Val Phe Asp Arg Glu Glu Leu
260    265    270
Ile Val Cys Glu Leu Asp Leu Asp Glu Ala Tyr Lys Glu Arg Met Thr
275    280    285
Met Asp Val Ser Gly His Tyr Gln Arg Arg Asp Val Phe Ser Phe Asp
290    295    300
Val Asn Gln His Arg His
305    310

```

<210> 277
 <211> 1056
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 277
 atgccaaacc ccagcgatca tttcaaaatc gccgctgttc aggcctcgcc cgtgtttctg 60
 gaccgggagg ccactgtgga aaaggcctgc cggttgatcg ccgaagccgc aaagcagggc 120
 gcccgctca tcgtctttcc ggaatctttc atcccgacct acccgactg ggtatgggccc 180
 gttcccccg gaagggaaag aatcctgaac cagctgtatt ctgaattcct ggccaatgcc 240
 gtcgatgttc ccggcgcggc gaccgaacaa cttgccagg ctgcacgaat ggccggcgcc 300
 tatgtgatta tgggcgtcac cgaagagac acctcggcca gcggggccag cctctacaac 360
 accctgctct acttcagccc cgaaggcatc ctaatgggca aacaccggaa gctggttccc 420
 acggggggcg aacggctggt ctgggcctac ggagacggca gcacgctgga ggtctacgac 480
 actccgctgg gaaagatcgg cgggctgac tgctgggaga actacatgcc cctggcccgg 540
 tacacgatgt acgcctgggg caccagatt tacatcgccg ccacctggga ccgcggggaa 600
 ccgtggctct ccaccctcgc gcatatcgcc aaggaaggaa gggctctacgt catcgggtgc 660
 tgcacgccc tcgcccagg ggatatccc gaccggttcg agtacaaggg aaaattttat 720
 tccgggtccc gggagtggat caatgagggc gacagcgcca tcgtgaaccc ggacggggaa 780
 ttcacgccc ggcgggtcgc gatgaaggag gagatcctgt atgccgagat agacccccgg 840
 cagatgcggg gcccgaagtg gatgctcgat gtggccggtc attacgcccg gccggatatc 900
 ttcgagctca tcgtccaccg gaatccccac ccgatgatca aaatcgccga agacaggggc 960
 gcggggatcg cctcaagttt gattcgcccc cgccctaacc ttccccatc aagggggagg 1020
 aaatcgcaa gaagcaaacc caagcccaaa aatatga 1056

<210> 278
 <211> 351
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 278
 Met Pro Thr Pro Ser Asp His Phe Lys Ile Ala Ala Val Gln Ala Ser
 1 5 10 15
 Pro Val Phe Leu Asp Arg Glu Ala Thr Val Glu Lys Ala Cys Arg Leu
 20 25 30
 Ile Ala Glu Ala Ala Lys Gln Gly Ala Arg Leu Ile Val Phe Pro Glu
 35 40 45
 Ser Phe Ile Pro Thr Tyr Pro Asp Trp Val Trp Ala Val Pro Pro Gly
 50 55 60
 Arg Glu Arg Ile Leu Asn Gln Leu Tyr Ser Glu Phe Leu Ala Asn Ala
 65 70 75 80
 Val Asp Val Pro Gly Ala Ala Thr Glu Gln Leu Ala Gln Ala Ala Arg
 85 90 95
 Met Ala Gly Ala Tyr Val Ile Met Gly Val Thr Glu Arg Asp Thr Ser
 100 105 110
 Ala Ser Gly Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Phe Ser Pro Glu
 115 120 125
 Gly Ile Leu Met Gly Lys His Arg Lys Leu Val Pro Thr Gly Gly Glu
 130 135 140
 Arg Leu Val Trp Ala Tyr Gly Asp Gly Ser Thr Leu Glu Val Tyr Asp
 145 150 155 160
 Thr Pro Leu Gly Lys Ile Gly Gly Leu Ile Cys Trp Glu Asn Tyr Met
 165 170 175
 Pro Leu Ala Arg Tyr Thr Met Tyr Ala Trp Gly Thr Gln Ile Tyr Ile

```

      180      185      190
Ala Ala Thr Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Leu Arg His
      195      200      205
Ile Ala Lys Glu Gly Arg Val Tyr Val Ile Gly Cys Cys Ile Ala Leu
      210      215      220
Arg Gln Gly Asp Ile Pro Asp Arg Phe Glu Tyr Lys Gly Lys Phe Tyr
225      230      235
Ser Gly Ser Arg Glu Trp Ile Asn Glu Gly Asp Ser Ala Ile Val Asn
      245      250      255
Pro Asp Gly Glu Phe Ile Ala Gly Pro Val Arg Met Lys Glu Glu Ile
      260      265      270
Leu Tyr Ala Glu Ile Asp Pro Arg Gln Met Arg Gly Pro Lys Trp Met
      275      280      285
Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Ile Phe Glu Leu Ile
      290      295      300
Val His Arg Asn Pro His Pro Met Ile Lys Ile Ala Glu Asp Arg Gly
305      310      315
Ala Gly Ile Ala Ser Ser Leu Ile Arg Pro Arg Pro Asn Leu Pro Pro
      325      330      335
Ser Arg Gly Arg Lys Ser Ala Arg Ser Lys Arg Lys Pro Lys Lys
      340      345      350

```

<210> 279

<211> 1014

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 279

```

atggggcatta cccatcccaa atacaaagtc gctgcagtc aggccgcgcc ggtctggctg      60
gacctggatg ccacgggtga caagtgcac cgccctgatcc aggaggccgc tgacaagggc      120
tgcaagctga tcgcgtttcc ggagacgttc attcccggct atccctggca catctggatg      180
ggtgcgccgg cctggggccat cggccggggc tttgtgcagc ggtatttcga caactccctg      240
tcctatgaca gcccgagcgc cgaaaagctg cgccaggccg tcaaggccgc aggcattacc      300
gcgtcgctgg gactgtcgga gcgtctgggc ggcagtcctc acatcgcgca gtgggtcatt      360
ggccccgcag gcgaaacgat ctgcagcgg cgtaagctgc ggcccacgca ttccgaacgc      420
accgtcttcg gcgacggcga tgggagcgac ctcaaggtgc acgacacgcc gctggggccgt      480
gtgggtgagc tggcgtgctg ggagaacatc ctgtcgctga acaagtacgc catgttctcg      540
cagcacgagc aggtgcacat tgcagcctgg cctagcttct ccacctacga gccctttgca      600
catgccctgg gctgggaagt gaacaacgca gtcagcaagg tgtacgcagt ggaaggcggg      660
tgtttcgtgg tggcaccctg cgccatcatt tccaaggaga tggtcgatga actgtgcgac      720
accccggaaca agcacaccct gacctatgtg ggaggcggcc acgcggtgat ctacgggccg      780
gatggcgccc ccctggcgga caagctgcct gaagacgccg agggcctgct gatcgcgagg      840
atcgacctcg ggatgattgg cgtggccaag aacgccatgg acccggtagg gcactactcg      900
cgccccgacg tgcaccgcct gcttctcaac cgcaagaagg cagcgaggt ggagcacttt      960
gcgctgcccg tggacgccat cgattccgag cccaagcca ccacggcgca ctga      1014

```

<210> 280

<211> 337

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 280

```

Met Gly Ile Thr His Pro Lys Tyr Lys Val Ala Ala Val Gln Ala Ala
  1           5           10           15
Pro Val Trp Leu Asp Leu Asp Ala Thr Val Asp Lys Cys Ile Arg Leu

```


20 25 30
 Ile Gln Glu Ala Ala Asp Lys Gly Cys Lys Leu Ile Ala Phe Pro Glu
 35 40 45
 Thr Phe Ile Pro Gly Tyr Pro Trp His Ile Trp Met Gly Ala Pro Ala
 50 55 60
 Trp Ala Ile Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
 65 70 75 80
 Ser Tyr Asp Ser Pro Gln Ala Glu Lys Leu Arg Gln Ala Val Lys Ala
 85 90 95
 Ala Gly Ile Thr Ala Ser Leu Gly Leu Ser Glu Arg Ser Gly Gly Ser
 100 105 110
 Leu Tyr Ile Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ser
 115 120 125
 Gln Arg Arg Lys Leu Arg Pro Thr His Ser Glu Arg Thr Val Phe Gly
 130 135 140
 Asp Gly Asp Gly Ser Asp Leu Lys Val His Asp Thr Pro Leu Gly Arg
 145 150 155 160
 Val Gly Glu Leu Ala Cys Trp Glu Asn Ile Leu Ser Leu Asn Lys Tyr
 165 170 175
 Ala Met Phe Ser Gln His Glu Gln Val His Ile Ala Ala Trp Pro Ser
 180 185 190
 Phe Ser Thr Tyr Glu Pro Phe Ala His Ala Leu Gly Trp Glu Val Asn
 195 200 205
 Asn Ala Val Ser Lys Val Tyr Ala Val Glu Gly Gly Cys Phe Val Val
 210 215 220
 Ala Pro Cys Ala Ile Ile Ser Lys Glu Met Val Asp Glu Leu Cys Asp
 225 230 235 240
 Thr Pro Asp Lys His Thr Leu Thr His Val Gly Gly Gly His Ala Val
 245 250 255
 Ile Tyr Gly Pro Asp Gly Ala Pro Leu Ala Asp Lys Leu Pro Glu Asp
 260 265 270
 Ala Glu Gly Leu Leu Ile Ala Glu Ile Asp Leu Gly Met Ile Gly Val
 275 280 285
 Ala Lys Asn Ala Met Asp Pro Val Gly His Tyr Ser Arg Pro Asp Val
 290 295 300
 His Arg Leu Leu Leu Asn Arg Lys Lys Ala Ala Gln Val Glu His Phe
 305 310 315 320
 Ala Leu Pro Val Asp Ala Ile Asp Ser Glu Pro Gln Ala Thr Thr Ala
 325 330 335
 His

<210> 281

<211> 936

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 281

atgtccaaga	tcgccgtcgt	ccaagagcct	ccggtgctgc	tcgatcgcg	cgccaccctc	60
gagcgcgccg	tctcggccat	cgagcgggcg	gccgacgtgg	gggcgcacct	cgtcgtgttc	120
cccagagacgt	acgtcccggg	gtaccccgcac	tgggtctggc	ggacgcgccc	cgacgacttc	180
aagctcgcg	gcgcgtgca	cgagcgcctc	ctcgcgaacg	cggtcgacct	cgaaaaggac	240
cagctcgcg	cgctccgcga	ggcgcgcgcg	cggcgaggcg	tcaccatcgc	gtgcggcggtg	300
aacgagcgcg	aggggagcca	cgccgcgcgcg	accctctaca	acaccgtcgt	cgtcgtcgga	360
cccgcgcgcg	cgatcctcaa	ccgccaccgc	aagctcgtcc	ccacgaaccc	cgagcgcatg	420
gtctggggcc	cggtgacgc	gagcgggctg	cgctcgtcgc	acacgcgcgc	cgccgcggtg	480
ggggcgctca	tctgctggga	gaactacatg	ccgctcgcg	gcttcgcgct	ctacgcgcag	540
ggcgctcgag	tctacctcgc	gccgacgtgg	gatcacggcg	acacttggtc	cgcctccatg	600

```

cggcacatcg cgcgcgaggc gcgcgcctgg gtcgtctcgg gggccatctg catgcaggcg 660
aaggacgtcc ccgccgactt cccgcagcgc gcggcgatct accccgacga ggaggagtgg 720
ctcaaccccg gcgatgccgt cgtcgtcgat cccaccggcg ccgtcgccgc cggcccgcgtg 780
caccgcgagc gcggcatcct ctacgccgag tgcgatcccg cgcgggcgtc gtcgcccgc 840
cgcacgctcg acgtctccgg gcaactacgga cggcccgcag tctttcacct gcagatcgac 900
cgcacaccgc gcgtgccggc gtcgttccgg gactga 936

```

<210> 282

<211> 311

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 282

```

Met Ser Lys Ile Ala Val Val Gln Glu Pro Pro Val Leu Leu Asp Arg
 1          5          10          15
Ala Ala Thr Leu Glu Arg Ala Val Ser Ala Ile Glu Arg Ala Ala Asp
 20          25          30
Val Gly Ala His Leu Val Val Phe Pro Glu Thr Tyr Val Pro Gly Tyr
 35          40          45
Pro Asp Trp Val Trp Arg Thr Arg Pro Asp Asp Phe Lys Leu Ala Gly
 50          55          60
Ala Leu His Glu Arg Leu Leu Ala Asn Ala Val Asp Leu Glu Lys Asp
 65          70          75          80
Gln Leu Ala Pro Leu Arg Glu Ala Ala Arg Arg Arg Gly Val Thr Ile
 85          90          95
Ala Cys Gly Val Asn Glu Arg Glu Gly Ser His Gly Arg Ala Thr Leu
100          105          110
Tyr Asn Thr Val Val Val Val Gly Pro Asp Gly Ala Ile Leu Asn Arg
115          120          125
His Arg Lys Leu Val Pro Thr Asn Pro Glu Arg Met Val Trp Gly Pro
130          135          140
Gly Asp Ala Ser Gly Leu Arg Val Val Asp Thr Pro Ala Gly Arg Val
145          150          155          160
Gly Ala Leu Ile Cys Trp Glu Asn Tyr Met Pro Leu Ala Arg Phe Ala
165          170          175
Leu Tyr Ala Gln Gly Val Glu Val Tyr Leu Ala Pro Thr Trp Asp His
180          185          190
Gly Asp Thr Trp Leu Ala Ser Met Arg His Ile Ala Arg Glu Ala Arg
195          200          205
Ala Trp Val Val Ser Gly Ala Ile Cys Met Gln Ala Lys Asp Val Pro
210          215          220
Ala Asp Phe Pro Gln Arg Ala Ala Ile Tyr Pro Asp Glu Glu Glu Trp
225          230          235          240
Leu Asn Pro Gly Asp Ala Val Val Val Asp Pro Thr Gly Ala Val Ala
245          250          255
Ala Gly Pro Leu His Arg Glu Arg Gly Ile Leu Tyr Ala Glu Cys Asp
260          265          270
Pro Ala Arg Ala Ser Leu Ala Arg Arg Thr Leu Asp Val Ser Gly His
275          280          285
Tyr Gly Arg Pro Asp Val Phe His Leu Gln Ile Asp Arg Thr Pro Arg
290          295          300
Val Pro Ala Ser Phe Arg Asp
305          310

```

<210> 283

<211> 1017

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 283

```

atgggcatcg aacatccgaa gtacaaggctc gcggtggtgc aggcggcacc ggcttggctc    60
gatctcgacg cgctcgatcga caagaccatc gggctgatcg aggaggccgc ccaaaaaggc    120
gccaagctga ttgcattccc cgaggccttc atccccggtt acccctggca catctggatg    180
gactcgccgg cctgggcgat cggccgcggt ttctgtgcagc gctattttga caattcgctc    240
gcctatgaca gcccgcaggc cgagaaactg cgcgcggcgg ttcgcaaggc aaagctcacg    300
gccgtgatcg ggctgtccga gcgcgacggc ggagctcttt acctcgcgca atggctgatc    360
gggcccgcagc gtgagacccat cgccaagcgc cgcaagctgc ggccgacaca tgcggagcgc    420
acggtatacg gcgagggcga cggcagcgac ctccgcggtt acaaccgtcc ggacattggc    480
cgccttggcg cgctctgctg ctgggagcat ctccagccgc tgcgaaata cgcgatgtac    540
gcgcagaaac agcaggtgca tgcgcggcgc tggccgagct ttctgctgta cgatcccttc    600
gcggtggcgc tcggcgccga agtgaacaac gcggcctcgc gcgtctatgc ggtcgaaggc    660
tcctgcttcg tgcggcgccc gtgcgcgacg gtctcgacag ccatgatcga cgaactctgc    720
gaccggccgg acaagcacgc gctgttgcat gtcggcggcg gttttgccgc gatctacggt    780
cctgacggga gccagatcgg cgacaaactc gctcccacc aggaagggtt gctgatccgc    840
gagatcgatc tcggcgccat cggcgtcgcc aagaatgcgg cggatcccgc cgggcattat    900
tcggggcctg acgtgacgcg actgttgctc aacaagaagc cgtacaagcg cgtcgagcag    960
ttttcgccgc cggccgaggc gtcgagccg acggatatcg cagcagcagc aagctaa    1017

```

<210> 284

<211> 338

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 284

```

Met Gly Ile Glu His Pro Lys Tyr Lys Val Ala Val Val Gln Ala Ala
 1          5          10          15
Pro Ala Trp Leu Asp Leu Asp Ala Ser Ile Asp Lys Thr Ile Gly Leu
 20        25        30
Ile Glu Glu Ala Ala Gln Lys Gly Ala Lys Leu Ile Ala Phe Pro Glu
 35        40        45
Ala Phe Ile Pro Gly Tyr Pro Trp His Ile Trp Met Asp Ser Pro Ala
 50        55        60
Trp Ala Ile Gly Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
 65        70        75        80
Ala Tyr Asp Ser Pro Gln Ala Glu Lys Leu Arg Ala Ala Val Arg Lys
 85        90        95
Ala Lys Leu Thr Ala Val Ile Gly Leu Ser Glu Arg Asp Gly Gly Ser
100       105       110
Leu Tyr Leu Ala Gln Trp Leu Ile Gly Pro Asp Gly Glu Thr Ile Ala
115       120       125
Lys Arg Arg Lys Leu Arg Pro Thr His Ala Glu Arg Thr Val Tyr Gly
130       135       140
Glu Gly Asp Gly Ser Asp Leu Ala Val His Asn Arg Pro Asp Ile Gly
145       150       155       160
Arg Leu Gly Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys
165       170       175
Tyr Ala Met Tyr Ala Gln Asn Glu Gln Val His Val Ala Ala Trp Pro
180       185       190
Ser Phe Ser Leu Tyr Asp Pro Phe Ala Val Ala Leu Gly Ala Glu Val
195       200       205
Asn Asn Ala Ala Ser Arg Val Tyr Ala Val Glu Gly Ser Cys Phe Val
210       215       220
Leu Ala Pro Cys Ala Thr Val Ser Gln Ala Met Ile Asp Glu Leu Cys

```

```

225          230          235          240
Asp Arg Pro Asp Lys His Ala Leu Leu His Val Gly Gly Gly Phe Ala
          245          250          255
Ala Ile Tyr Gly Pro Asp Gly Ser Gln Ile Gly Asp Lys Leu Ala Pro
          260          265          270
Asp Gln Glu Gly Leu Leu Ile Ala Glu Ile Asp Leu Gly Ala Ile Gly
          275          280          285
Val Ala Lys Asn Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp
          290          295          300
Val Thr Arg Leu Leu Leu Asn Lys Lys Pro Tyr Lys Arg Val Glu Gln
305          310          315          320
Phe Ser Pro Pro Ala Glu Ala Leu Glu Pro Thr Asp Ile Ala Ala Ala
          325          330          335
Ala Ser

```

<210> 285
 <211> 918
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 285
atgaatacta atctagtaaa ggctcgcggcg gctcaagttg ctccccattt tctcaatttg      60
agcaatacgg tggaaaaaac ctgcaactta atttctgaag caggcaaaaa tggagcaaag      120
ctaatacgat ttccagaagc cttcatctct gggtatcccg attgggtctg gcttattccc      180
aatgcgaatt ctgcaatgct ggatgattta taccaggaat tgggttgagaa cgcagtaacg      240
atccctgata caacaacaca taaactatgt caggctgcaa aagatgcagg ggtatatgtt      300
gcggtaggta tacatgagag aaattcagaa gcaagtggct tcacgctttt caatacgctt      360
ctatacatca acgatcaagg cgtaatcatc ggaaaacacc gaaaattaat ccctacaggg      420
ggcgaacggc tggctctggg gcagggtaat ggggatacac tttctgcatt cgatacagac      480
ttcgccaaat taggaggatt gctttgttgg gaaaattata tgccactcgc gcgtcaagct      540
atgtattccg ttggaactga agtatatgta gcccacacct gggactccag cgagaatttg      600
ttgttaagca tgcgccatat tgcccagag ggcgggtatg ttgtaattag tgtttgccag      660
gtctccgaa aagacgacat cctgatcag tatgaattta agaaactcta tcctgataat      720
tcagaatgga tcaatagcgg taacagttgc atcatcaacc gcgcgggtga gattattgct      780
ggaccaatct caaaccaaca agaaatactt tatgcagatt tagacctgag ttttaattgca      840
aaatctaaac gtatgttcga tgttactggg cattattccc ggccggatgt gtttagctat      900
gaaatcaaca aaagctag

```

<210> 286
 <211> 305
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 286
Met Asn Thr Asn Leu Val Lys Val Ala Ala Ala Gln Val Ala Pro His
1          5          10          15
Phe Leu Asn Leu Ser Asn Thr Val Glu Lys Thr Cys Asn Leu Ile Ser
          20          25          30
Glu Ala Gly Lys Asn Gly Ala Lys Leu Ile Val Phe Pro Glu Ala Phe
          35          40          45
Ile Ser Gly Tyr Pro Asp Trp Val Trp Leu Ile Pro Asn Ala Asn Ser
          50          55          60
Ala Met Leu Asp Asp Leu Tyr Gln Glu Leu Val Glu Asn Ala Val Thr
65          70          75          80

```

```

Ile Pro Asp Thr Thr Thr His Lys Leu Cys Gln Ala Ala Lys Asp Ala
      85                      90                      95
Gly Val Tyr Val Ala Val Gly Ile His Glu Arg Asn Ser Glu Ala Ser
      100                    105                    110
Gly Phe Thr Leu Phe Asn Thr Leu Leu Tyr Ile Asn Asp Gln Gly Val
      115                    120                    125
Ile Ile Gly Lys His Arg Lys Leu Ile Pro Thr Gly Gly Glu Arg Leu
      130                    135                    140
Val Trp Gly Gln Gly Asn Gly Asp Thr Leu Ser Ala Phe Asp Thr Asp
      145                    150                    155                    160
Phe Gly Lys Leu Gly Gly Leu Leu Cys Trp Glu Asn Tyr Met Pro Leu
      165                    170                    175
Ala Arg Gln Ala Met Tyr Ser Val Gly Thr Glu Val Tyr Val Ala Pro
      180                    185                    190
Thr Trp Asp Ser Ser Glu Asn Trp Leu Leu Ser Met Arg His Ile Ala
      195                    200                    205
Arg Glu Gly Gly Met Phe Val Ile Ser Val Cys Gln Ala Leu Arg Lys
      210                    215                    220
Asp Asp Ile Pro Asp Gln Tyr Glu Phe Lys Lys Leu Tyr Pro Asp Asn
      225                    230                    235                    240
Ser Glu Trp Ile Asn Ser Gly Asn Ser Cys Ile Ile Asn Pro Arg Gly
      245                    250                    255
Glu Ile Ile Ala Gly Pro Ile Ser Asn Gln Gln Glu Ile Leu Tyr Ala
      260                    265                    270
Asp Leu Asp Leu Ser Leu Ile Ala Lys Ser Lys Arg Met Phe Asp Val
      275                    280                    285
Thr Gly His Tyr Ser Arg Pro Asp Val Phe Ser Tyr Glu Ile Asn Lys
      290                    295                    300
Ser
305

```

<210> 287

<211> 936

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 287

```

gtgatcaagg tagcaatcgc ccaggtggca ccggtgggtc tggacaaggc gcgcaccatt      60
gagaagcgg taggaattat tcgcgctgcc gcgcaagagg gcattgagct cctgggtttc      120
ccggagacgt ttatcccgac ctatccagcc tgggtatggc gcttgcgctc gggtagtgat      180
tacggcctga gcgaggaact gcacgcgctc ctgctggata attcggtaga tatggagagc      240
aaggacctgg agccattgca agctgttgct gcagagacca gcatgaccgt ggtaataggt      300
atgaacgagc gagacggccg attcagccgg ggtacaatct acaatgccct ggttgatgc      360
ggtccagggt gcacgatcct gaacaggcac cgcaagctta tgcccaccaa ccccgagcgt      420
atgggttggg gtatgggcca tgccagcggg ctgaaggtag tggaaatgtc ttacgggcgc      480
ctgggtgggc tgatttgctg ggagaatttc atgcctctcg cgcgctatgg cttgtatgcc      540
caggtgtgtg agatttacgt ggcgcccacc tatgaccagg gcgacggctg ggtcggcagc      600
atgcagcata tagcccgga gggtcgttgc tgggtactct cggccgggac ccttttgct      660
ggcagtgatt ttctgccgga ttttccgggc aagaccgagt tatacccca tgaccaggag      720
tgggtgaatc cgggtggctc ggtgatcgtg gcaccggggg gagagattgt ggccggcccc      780
atgtatcgcg acgaaggtct gctgggtctg gagttggatg cgacgcttag tgtccgcggc      840
aagcgctcgc tggatgtggc cggccattac tcccggccgg atttgtttga actggaata      900
gatggcgacc cgctggaacc catagagtgg gattga      936

```

<210> 288

<211> 311

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 288

```

Val Ile Lys Val Ala Ile Ala Gln Val Ala Pro Val Val Leu Asp Lys
 1           5           10           15
Ala Arg Thr Ile Glu Lys Ala Val Gly Ile Ile Arg Ala Ala Gln
 20           25           30
Glu Gly Ile Glu Leu Leu Val Phe Pro Glu Thr Phe Ile Pro Thr Tyr
 35           40           45
Pro Ala Trp Val Trp Arg Leu Arg Pro Gly Thr Asp Tyr Gly Leu Ser
 50           55           60
Glu Glu Leu His Ala Leu Leu Asp Asn Ser Val Asp Met Glu Ser
 65           70           75           80
Lys Asp Leu Glu Pro Leu Gln Ala Val Ala Ala Glu Thr Ser Met Thr
 85           90           95
Val Val Ile Gly Met Asn Glu Arg Asp Gly Arg Phe Ser Arg Gly Thr
 100          105          110
Ile Tyr Asn Ala Leu Val Val Ile Gly Pro Gly Gly Thr Ile Leu Asn
 115          120          125
Arg His Arg Lys Leu Met Pro Thr Asn Pro Glu Arg Met Val Trp Gly
 130          135          140
Met Gly Asp Ala Ser Gly Leu Lys Val Val Glu Met Ser Tyr Gly Arg
 145          150          155          160
Leu Gly Gly Leu Ile Cys Trp Glu Asn Phe Met Pro Leu Ala Arg Tyr
 165          170          175
Gly Leu Tyr Ala Gln Gly Val Glu Ile Tyr Val Ala Pro Thr Tyr Asp
 180          185          190
Gln Gly Asp Gly Trp Val Gly Ser Met Gln His Ile Ala Arg Glu Gly
 195          200          205
Arg Cys Trp Val Leu Ser Ala Gly Thr Leu Leu Arg Gly Ser Asp Phe
 210          215          220
Leu Pro Asp Phe Pro Gly Lys Thr Glu Leu Tyr Pro Asp Asp Gln Glu
 225          230          235          240
Trp Val Asn Pro Gly Gly Ser Val Ile Val Ala Pro Gly Gly Glu Ile
 245          250          255
Val Ala Gly Pro Met Tyr Arg Asp Glu Gly Leu Leu Val Cys Glu Leu
 260          265          270
Asp Ala Thr Leu Ser Val Arg Gly Lys Arg Ser Leu Asp Val Ala Gly
 275          280          285
His Tyr Ser Arg Pro Asp Leu Phe Glu Leu Glu Ile Asp Gly Asp Pro
 290          295          300
Leu Glu Pro Ile Glu Trp Asp
 305          310

```

<210> 289

<211> 921

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 289

```

atggtgacgg tggccgccgt acaggcaacg ccggtgttcc tcgaccgcga ggcgacctcg      60
gacaaggtct gcgccttggt caaggaggcg gccggccacg gggcagaact gatcgtcttc      120
cccgagtcct tcgtccctgc ctatccggac tgggtgtggc gcacccttgc ctggagtgc      180
accgagttcg tgaagcgctt ctacgcgaac gcggtgaccg tccccggcgc gaccctcgag      240
cgcatcggcg cagcggcggc ggaggcggag gcgtacgtcg tgatcggcgt gaccgagatc      300
gacggcggaa ctctctacaa cacccttctc tacctggggc cggacggaca gctgttgcaa      360

```

```

cggcatcgca agctcatgcc caccggtggg gagcggaccg tgtggggaat gggagacggc 420
tctgagctcg acgtcgtgag caccgccgttc ggcgtcgtcg gtgggttggt gtgctgggag 480
aactacatgc cgctcgcccg ggcggcgatc tacgccaccg actgtgacat ctacctggct 540
ccgacatggg acaacagcga cactgtggta gccacgttgc gtcacatcgc caaggagggg 600
cggcagttcg tcatcggcgt cgccccgctg ctgcgcggct ccgacgtacc ggaggacctc 660
cgcggcacgc tctacgggct gtcggacgac tggatgtcgc gcggctacac caccatcgtc 720
gcaccaagcg gcgaggtgat cgccggcccg gtccctggagc gtgaggagat cctcttcgcg 780
gacctcgacc tggccgacgt gcaggagcag agaaggatgt tcgacctgt cgccactac 840
tcacgacccg acgtcttcac gctccacgtc gacgcacgac cgaagagccc ggtcgtcttc 900
gagagggatg caccgacctg a 921

```

<210> 290

<211> 306

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 290

```

Met Val Thr Val Ala Val Gln Ala Thr Pro Val Phe Leu Asp Arg
 1          5          10          15
Glu Ala Thr Ser Asp Lys Val Cys Ala Leu Val Lys Glu Ala Ala Gly
 20          25          30
His Gly Ala Glu Leu Ile Val Phe Pro Glu Ser Phe Val Pro Ala Tyr
 35          40          45
Pro Asp Trp Val Trp Arg Thr Pro Ala Trp Ser Asp Thr Glu Phe Val
 50          55          60
Lys Arg Phe Tyr Ala Asn Ala Val Thr Val Pro Gly Ala Thr Leu Glu
 65          70          75          80
Arg Ile Gly Ala Ala Ala Glu Ala Glu Ala Tyr Val Val Ile Gly
 85          90          95
Val Thr Glu Ile Asp Gly Gly Thr Leu Tyr Asn Thr Leu Leu Tyr Leu
100          105          110
Gly Pro Asp Gly Gln Leu Leu Gln Arg His Arg Lys Leu Met Pro Thr
115          120          125
Gly Gly Glu Arg Thr Val Trp Gly Met Gly Asp Gly Ser Glu Leu Asp
130          135          140
Val Val Ser Thr Pro Phe Gly Val Val Gly Gly Leu Leu Cys Trp Glu
145          150          155          160
Asn Tyr Met Pro Leu Ala Arg Ala Ala Ile Tyr Ala Gln His Cys Asp
165          170          175
Ile Tyr Leu Ala Pro Thr Trp Asp Asn Ser Asp Thr Trp Val Ala Thr
180          185          190
Leu Arg His Ile Ala Lys Glu Gly Arg Gln Phe Val Ile Gly Val Ala
195          200          205
Pro Leu Leu Arg Gly Ser Asp Val Pro Glu Asp Leu Arg Gly Thr Leu
210          215          220
Tyr Gly Leu Ser Asp Asp Trp Met Ser Arg Gly Tyr Thr Thr Ile Val
225          230          235          240
Ala Pro Ser Gly Glu Val Ile Ala Gly Pro Val Leu Glu Arg Glu Glu
245          250          255
Ile Leu Phe Ala Asp Leu Asp Leu Ala Asp Val Gln Glu Gln Arg Arg
260          265          270
Met Phe Asp Pro Val Gly His Tyr Ser Arg Pro Asp Val Phe Thr Leu
275          280          285
His Val Asp Ala Arg Pro Lys Ser Pro Val Val Phe Glu Arg Asp Ala
290          295          300
Pro Thr
305

```

<210> 291
 <211> 1002
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 291
 atgatgaaaa caactgttac cgttgcctgc gttcaggccg cccccgtatt tatggattta 60
 gaaggcacca tagataaaac gatcacccctc atctctgaag ccgcacagaa aggcgcggag 120
 ctcatcgctt ttccggagac ctggataccc ggttaccctg ggttcttatg gctgaactcg 180
 cccgcgacaa atatgcccct ggtttatcaa tatcatcaga actctctggg gctggacagt 240
 gcccaggcga agcgaattgc ggatgctgca cagcagaata acatcactgt cgttctggga 300
 ttcagcgagc gcgatcatgg aagcctctat atctcacagt ggctgattgg cagcgacggg 360
 gaaactattg gcatccggcg caagctcaag gccacacacg tggagcgtag gctgttcggc 420
 gaaagcgacg gctcctccct gaccacctgg gagacacctc tgggtaacgt cggggccctc 480
 tgctgctggg agcacctgca gccgctgtct cgctatgcga tgtattccca gcatgaagag 540
 atccatatcg ctgctgtggc cagcttcagt ctttacacca gcgcaactgc cgcgctcgga 600
 cctgaagtcg acacggcggc ttcacgcctc tatgccgagg aggggcagtg cttcgtgtta 660
 gccccatgtg ccgtggtttc tgatgagatg attgatttac tctgtcctga tgatgaccgg 720
 agagcgttac tcagtgccgg agggggacat gcccgatttt acggacactga tggaagagaa 780
 ctctgcaccc ctctcgggga aaatgaggaa ggactgctta tcgctgagct cgactctgct 840
 gcgatcacct ttgccaaact ggcggcagat cccgtaggcc actattcccg ccctgacgtg 900
 acccgccctc tttttaatcc ttcagccaac aagactgtta ttaaaccgca ttcgcctcct 960
 gagttaattg ccgaacaggc tccggaagaa gaggaggagt ag 1002

<210> 292
 <211> 333
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 292
 Met Met Lys Thr Thr Val Thr Val Ala Cys Val Gln Ala Ala Pro Val
 1 5 10 15
 Phe Met Asp Leu Glu Gly Thr Ile Asp Lys Thr Ile Thr Leu Ile Ser
 20 25 30
 Glu Ala Ala Gln Lys Gly Ala Glu Leu Ile Ala Phe Pro Glu Thr Trp
 35 40 45
 Ile Pro Gly Tyr Pro Trp Phe Leu Trp Leu Asn Ser Pro Ala Thr Asn
 50 55 60
 Met Pro Leu Val Tyr Gln Tyr His Gln Asn Ser Leu Val Leu Asp Ser
 65 70 75 80
 Ala Gln Ala Lys Arg Ile Ala Asp Ala Ala Gln Gln Asn Asn Ile Thr
 85 90 95
 Val Val Leu Gly Phe Ser Glu Arg Asp His Gly Ser Leu Tyr Ile Ser
 100 105 110
 Gln Trp Leu Ile Gly Ser Asp Gly Glu Thr Ile Gly Ile Arg Arg Lys
 115 120 125
 Leu Lys Ala Thr His Val Glu Arg Thr Leu Phe Gly Glu Ser Asp Gly
 130 135 140
 Ser Ser Leu Thr Thr Trp Glu Thr Pro Leu Gly Asn Val Gly Ala Leu
 145 150 155 160
 Cys Cys Trp Glu His Leu Gln Pro Leu Ser Arg Tyr Ala Met Tyr Ser
 165 170 175
 Gln His Glu Glu Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu Tyr
 180 185 190
 Thr Ser Ala Thr Ala Ala Leu Gly Pro Asp Val Asn Thr Ala Ala Ser


```

      195              200              205
Arg Leu Tyr Ala Ala Glu Gly Gln Cys Phe Val Leu Ala Pro Cys Ala
      210              215              220
Val Val Ser Asp Glu Met Ile Asp Leu Leu Cys Pro Asp Asp Asp Arg
      225              230              235              240
Arg Ala Leu Leu Ser Ala Gly Gly Gly His Ala Arg Ile Tyr Gly Pro
      245              250              255
Asp Gly Arg Glu Leu Val Thr Pro Leu Gly Glu Asn Glu Glu Gly Leu
      260              265              270
Leu Ile Ala Glu Leu Asp Ser Ala Ala Ile Thr Phe Ala Lys Leu Ala
      275              280              285
Ala Asp Pro Val Gly His Tyr Ser Arg Pro Asp Val Thr Arg Leu Leu
      290              295              300
Phe Asn Pro Ser Ala Asn Lys Thr Val Ile Lys Arg His Ser Pro Pro
      305              310              315              320
Glu Leu Ile Ala Glu Gln Ala Pro Glu Glu Glu Glu Glu
      325              330

```

<210> 293

<211> 1008

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 293

```

atgaaaaata tcaaaaactc agaaaaaagc agcacagtaa gagtcgctgc ggtacaaatc      60
agtccggtgt tgtacaaccg cgaagctacc gttcaaaaag tagtcaacaa aatccttgaa      120
ctaggaaaac aaggggtaca attcgccact tttccggaac cgatagtgcc ttattatcct      180
tattttcttt ttattcaggc gccttatgcc atgggcaaag aacacctgcg cttgcttgaa      240
caatcagtta ctgttcgcgc agccgcgacc gatgccataa gtgaggcggc aaaggaagcc      300
aatatggtag tgtctattgg tgtcaatgaa cgagacgggtg gtaccattta caatacgcaa      360
ctcctttttg atgctgacgg aacattaatt cagcgcagac gtaaaacttac accaacgtat      420
catgaaagaa tgatttgggg acaagggtgac gcttcaggtc ttcgtgccac agacagcgct      480
gttgggcgta tcgggcagtt ggcttgttgg gaacattaca atccattgtt ccgttatgct      540
ttgattgctg atggagaaca aatccattct gccatgtatc ccggatcatt tttaggtgcg      600
ttgcacgggtg aacaaaccga aatcaatgta cgccaacacg ctttagaatc ggccagcttc      660
gtcgtagtgg ctaccggttg gttggatgcc gatcaacaag cacaaattgc gaaagacacc      720
ggtggaccac tcggaccaat ttcgggaggt tgttttacag ccgttatagg ccctgacgga      780
caactaatcg gggaagccct tacatcaggt gaaggggaag tgattgccga tattgatttg      840
gcacaaattg atgcccgcaa aagattaatg gatgccagtg gtcactacaa ccgtcctgaa      900
ttgttgagct tgcataatga tcacactccg actgctccta tgcataaaa agtagtttac      960
actgagccgg gattagcaaa aagacaaaat gaaaattcat caaattaa      1008

```

<210> 294

<211> 335

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 294

```

Met Lys Asn Ile Lys Asn Ser Glu Lys Ser Ser Thr Val Arg Val Ala
  1              5              10              15
Ala Val Gln Ile Ser Pro Val Leu Tyr Asn Arg Glu Ala Thr Val Gln
      20              25              30
Lys Val Val Asn Lys Ile Leu Glu Leu Gly Lys Gln Gly Val Gln Phe
      35              40              45
Ala Thr Phe Pro Glu Thr Ile Val Pro Tyr Tyr Pro Tyr Phe Ser Phe

```

```

      50              55              60
Ile Gln Ala Pro Tyr Ala Met Gly Lys Glu His Leu Arg Leu Leu Glu
65              70              75              80
Gln Ser Val Thr Val Pro Ser Ala Ala Thr Asp Ala Ile Ser Glu Ala
      85              90              95
Ala Lys Glu Ala Asn Met Val Val Ser Ile Gly Val Asn Glu Arg Asp
      100              105              110
Gly Gly Thr Ile Tyr Asn Thr Gln Leu Leu Phe Asp Ala Asp Gly Thr
      115              120              125
Leu Ile Gln Arg Arg Arg Lys Leu Thr Pro Thr Tyr His Glu Arg Met
      130              135              140
Ile Trp Gly Gln Gly Asp Ala Ser Gly Leu Arg Ala Thr Asp Ser Ala
145              150              155              160
Val Gly Arg Ile Gly Gln Leu Ala Cys Trp Glu His Tyr Asn Pro Leu
      165              170              175
Phe Arg Tyr Ala Leu Ile Ala Asp Gly Glu Gln Ile His Ser Ala Met
      180              185              190
Tyr Pro Gly Ser Phe Leu Gly Ala Leu His Gly Glu Gln Thr Glu Ile
      195              200              205
Asn Val Arg Gln His Ala Leu Glu Ser Ala Ser Phe Val Val Val Ala
      210              215              220
Thr Gly Trp Leu Asp Ala Asp Gln Gln Ala Gln Ile Ala Lys Asp Thr
225              230              235              240
Gly Gly Pro Ile Gly Pro Ile Ser Gly Gly Cys Phe Thr Ala Val Ile
      245              250              255
Gly Pro Asp Gly Gln Leu Ile Gly Glu Ala Leu Thr Ser Gly Glu Gly
      260              265              270
Glu Val Ile Ala Asp Ile Asp Leu Ala Gln Ile Asp Ala Arg Lys Arg
      275              280              285
Leu Met Asp Ala Ser Gly His Tyr Asn Arg Pro Glu Leu Leu Ser Leu
      290              295              300
His Ile Asp His Thr Pro Thr Ala Pro Met His Glu Arg Val Val Tyr
305              310              315              320
Thr Glu Pro Gly Leu Ala Lys Arg Gln Asn Glu Asn Ser Ser Asn
      325              330              335

```

<210> 295

<211> 1134

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 295

```

atggccgcaa aagtacttgg aggacgtgac acagtaaaag tagcagttgt tcaaacacca      60
tcagtcttta tggacaagaa agcctgtctc gaacttgcct gcgataagat tatcgaagcc      120
ggcaaagagg gcgcggagct tggtgttttt cctgaaacct ggattccgac atatccttat      180
tggaacctgg gatgggatac catcgcccat ggcttccatg atgtgatggc ggacctgcag      240
gacaattccg tggtcgtcgg gagcgaagac accgacatat tgggcaaagc cgcccgga      300
gctggcgccct acgtcgtcat gggctgtaat gagctcgatg accgggtcgg cagcaggacc      360
ttgttcaact cgctgggtcta tatggacaaa tatggcggcg tgctcggccg tcaccgtaaa      420
ttaatcccgt cttttatcga acgcatctgg tggggcaatg gggacagccg cgatctcaaa      480
gtttacgaca cggaaattgg gcgcatcggc ggtcaaattc gctgggaaaa tcacattgtg      540
aacatcaccg catggtacat tgcccaaggc gtggatatc atgtctcggg ttggccggga      600
atgtggaact gtggcgagaa agaaggagaa tccttcatat acgccgttca cgacatcaac      660
aaatgtgacc tcatccctgc tacacgcgga cgggcattta cgggtcagtg ttatgtcctc      720
tcagccaaca acctactcgg gatggaagac attcctgacg atttcccgtt ccgggatacc      780
atgaactatg gcggtccggg ccaggaggat ttgtcggat gggcttcggg tggcagccat      840
attgttcgac caacgtctga atttatgtg cgcgcgacgt ttgatataga caccatcatc      900
tatgcagaac ttcaggcgaa atacatcaaa gtggtgaagt cggctcttca ttccctcggc      960

```

```

cactacgcgc ggtgggacct cgtcaacttg accacgccgc caccgccgta tgaacctgaa 1020
accgacgcac cagctctcac ggccgatatc cgtgatcggg tcatcgagag tgtggctaaa 1080
gagttcaagc tcgaaccaga aaaagtggct gaagttgtgc gcaatgccgc ctag 1134

```

<210> 296
 <211> 377
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 296
 Met Ala Ala Lys Val Leu Gly Gly Arg Asp Thr Val Lys Val Ala Val
 1 5 10 15
 Val Gln Thr Pro Ser Val Phe Met Asp Lys Lys Ala Cys Leu Glu Leu
 20 25 30
 Ala Cys Asp Lys Ile Ile Glu Ala Gly Lys Glu Gly Ala Glu Leu Val
 35 40 45
 Val Phe Pro Glu Thr Trp Ile Pro Thr Tyr Pro Tyr Trp Thr Met Gly
 50 55 60
 Trp Asp Thr Ile Ala His Gly Phe His Asp Val Met Ala Asp Leu Gln
 65 70 75 80
 Asp Asn Ser Val Val Val Gly Ser Glu Asp Thr Asp Ile Leu Gly Lys
 85 90 95
 Ala Ala Arg Glu Ala Gly Ala Tyr Val Val Met Gly Cys Asn Glu Leu
 100 105 110
 Asp Asp Arg Val Gly Ser Arg Thr Leu Phe Asn Ser Leu Val Tyr Met
 115 120 125
 Asp Lys Tyr Gly Gly Val Leu Gly Arg His Arg Lys Leu Ile Pro Ser
 130 135 140
 Phe Ile Glu Arg Ile Trp Trp Gly Asn Gly Asp Ser Arg Asp Leu Lys
 145 150 155 160
 Val Tyr Asp Thr Glu Ile Gly Arg Ile Gly Gly Gln Ile Cys Trp Glu
 165 170 175
 Asn His Ile Val Asn Ile Thr Ala Trp Tyr Ile Ala Gln Gly Val Asp
 180 185 190
 Ile His Val Ser Val Trp Pro Gly Met Trp Asn Cys Gly Ala Glu Glu
 195 200 205
 Gly Glu Ser Phe Ile Tyr Ala Gly His Asp Ile Asn Lys Cys Asp Leu
 210 215 220
 Ile Pro Ala Thr Arg Gly Arg Ala Phe Thr Gly Gln Cys Tyr Val Leu
 225 230 235 240
 Ser Ala Asn Asn Leu Leu Arg Met Glu Asp Ile Pro Asp Asp Phe Pro
 245 250 255
 Phe Arg Asp Thr Met Asn Tyr Gly Gly Pro Gly Gln Glu Asp Phe Val
 260 265 270
 Gly Trp Ala Cys Gly Gly Ser His Ile Val Ala Pro Thr Ser Glu Phe
 275 280 285
 Met Val Pro Pro Thr Phe Asp Ile Asp Thr Ile Ile Tyr Ala Glu Leu
 290 295 300
 Gln Ala Lys Tyr Ile Lys Val Val Lys Ser Val Phe Asp Ser Leu Gly
 305 310 315 320
 His Tyr Ala Arg Trp Asp Leu Val Asn Leu Thr Thr Pro Pro Pro Pro
 325 330 335
 Tyr Glu Pro Glu Thr Asp Ala Pro Ala Leu Thr Ala Asp Ile Arg Asp
 340 345 350
 Arg Val Ile Glu Ser Val Ala Lys Glu Phe Lys Leu Glu Pro Glu Lys
 355 360 365
 Val Ala Glu Val Val Arg Asn Ala Ala
 370 375

<210> 297
 <211> 1059
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 297
 atgacacgtt ttcgggacgt cacggtggcg gcggttcagg ccgcacccgt ctatttcgat 60
 cgggaggcct ccacagataa ggcggtgccaa ttgattcacg aagcggcgaa gaaaggcgca 120
 gccctcgcgg cgttcggcga aacgtggttg ccgggatatc cgttctttgc atgggggttc 180
 gcgcacaacc ggagcctggt ctggaatgcg gccgccgagt acatcgccaa tgctgtggag 240
 attccgagtc caacgacgga ccgcctctgc gccgcagcga agatcgccgg gattgacgtg 300
 gtaatcggcg tcgtagaact ggatggacga acgcgagcgt cggtttacag cacactgctg 360
 ttcatcgggg gagagggggc gatcctgggg cgccaccgca aattgaagcc aaccacatg 420
 gagcgaacgg tgtggggtga aggggacgct cacgggctcc gcgttcacga gcgtccgtac 480
 ggccgcctca gcgggctgaa ttgctgggaa cacaacatga tgctgcccgg ctatgtgctt 540
 gccgcgagg gcacgcagtt tcacgtcgcg acatggcctg ggaaagagag gctcacagtt 600
 ccgccgaacg aggcggctta tacgcgccag cttctcctct ctcgcgccta tgcatccag 660
 gcgggcgcgt acgtgatcag cgtcgcgggg ctgctcggac ccgactcgat gccggagcgt 720
 tatcgcgaac tgggacagtc ctatgagttg accggcgaca gcgtcatcat cgatccgcgc 780
 ggcgaggtca tcgcggggcc cgcaagggc gagaccatcc tgctcgcgca atgcagccag 840
 gaagccctct tcgccgcaaa gtccgccatt gacgtcggcg gtcattactc gcgcccgat 900
 atttttcagc tgcgtgtcaa cgatcagcta cagcatcagg tccggagact cgaggcgact 960
 ctacgcccc cagtcgccgt agttgtcggg cctgagggta gctcacatga gcaggagacg 1020
 gccttcgggc catccagcct cctggccacg acaagctag 1059

<210> 298
 <211> 352
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 298
 Met Thr Arg Phe Arg Asp Val Thr Val Ala Ala Val Gln Ala Ala Pro
 1 5 10 15
 Val Tyr Phe Asp Arg Glu Ala Ser Thr Asp Lys Ala Cys Gln Leu Ile
 20 25 30
 His Glu Ala Ala Lys Lys Gly Ala Ala Leu Ala Ala Phe Gly Glu Thr
 35 40 45
 Trp Leu Pro Gly Tyr Pro Phe Phe Ala Trp Gly Phe Ala His Asn Arg
 50 55 60
 Ser Leu Phe Trp Asn Ala Ala Glu Tyr Ile Ala Asn Ala Val Glu
 65 70 75 80
 Ile Pro Ser Pro Thr Thr Asp Arg Leu Cys Ala Ala Ala Lys Ile Ala
 85 90 95
 Gly Ile Asp Val Val Ile Gly Val Val Glu Leu Asp Gly Arg Thr Arg
 100 105 110
 Ala Ser Val Tyr Ser Thr Leu Leu Phe Ile Gly Arg Glu Gly Ala Ile
 115 120 125
 Leu Gly Arg His Arg Lys Leu Lys Pro Thr His Met Glu Arg Thr Val
 130 135 140
 Trp Gly Glu Gly Asp Ala His Gly Leu Arg Val His Glu Arg Pro Tyr
 145 150 155 160
 Gly Arg Leu Ser Gly Leu Asn Cys Trp Glu His Asn Met Met Leu Pro
 165 170 175
 Gly Tyr Val Leu Ala Ala Gln Gly Thr Gln Phe His Val Ala Thr Trp

180 185 190
 Pro Gly Lys Glu Arg Leu Thr Val Pro Pro Asn Glu Ala Ala Tyr Thr
 195 200 205
 Arg Gln Leu Leu Leu Ser Arg Ala Tyr Ala Ser Gln Ala Gly Ala Tyr
 210 215 220
 Val Ile Ser Val Ala Gly Leu Leu Gly Pro Asp Ser Met Pro Glu Arg
 225 230 235 240
 Tyr Arg Glu Leu Gly Gln Ser Tyr Glu Leu Thr Gly Asp Ser Val Ile
 245 250 255
 Ile Asp Pro Arg Gly Glu Val Ile Ala Gly Pro Ala Lys Gly Glu Thr
 260 265 270
 Ile Leu Leu Ala Gln Cys Ser Gln Glu Ala Leu Phe Ala Ala Lys Ser
 275 280 285
 Ala Ile Asp Val Gly Gly His Tyr Ser Arg Pro Asp Ile Phe Gln Leu
 290 295 300
 Arg Val Asn Asp Gln Leu Gln His Gln Val Arg Arg Leu Glu Ala Thr
 305 310 315 320
 Leu Thr Pro Pro Val Ala Val Val Val Gly Pro Glu Gly Ser Ser His
 325 330 335
 Glu Gln Glu Thr Ala Phe Gly Pro Ser Ser Leu Leu Ala Thr Thr Ser
 340 345 350

<210> 299

<211> 987

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 299

atgactgttg	ttaaggccgc	cgcagtgcag	atcagcccg	tgctctacag	ccgtgcagga	60
accgtcgaga	aggtcgtgaa	gaagatcgac	gagctgggcc	agaagggtgt	cgagtttgcc	120
gtcttccttg	aaaccgttgt	cccctactac	ccctacttct	ccttcgtgca	gccccctac	180
aaactggcca	cggagcacct	gcgcctgctt	gaggagtcgg	tgaccgtgcc	ctctgccgag	240
acggacgcca	tcggcgacgc	cgcccgaag	gccaacatgg	tcgtctcgat	cggtgtcaac	300
gaacgtgatg	gcggcaccat	ttacaacacc	caactcctgt	tcgacgccga	cggaaccctg	360
atccagcgcc	gccgcaagat	cacgcccagc	taccacgagc	ggatgatctg	gggacaggga	420
gacggatcag	gcttgcgcgc	ggtcgacagc	gtcgtcggcc	gcatcggcc	gctcgcctgc	480
tgggagcact	accagccgct	ggcccgttac	gctctcatcg	ccgacggcga	gcagatccac	540
gccgcgatgt	accccggcgc	cttcgggggc	gatctgttcg	cagagcagat	cgaagtcaat	600
gtccgtcagc	acgctctgga	atcggccagt	ttcgtcgtca	gcgccaccgc	ctggctcgac	660
gccgaccagc	aggcccagat	tcggaaggac	accggcgccc	ccgtacaggc	gatctccggc	720
ggcttcttca	cagccatcat	cgaccccagc	ggccgcatca	tcggcggaacc	gatcacctcc	780
ggcgaaggcg	aagtcacgcg	tgacctcgac	tttgcgtcca	tcgaccgccg	caagcgctcg	840
atggacgcca	gcggccacta	cagccgcccc	gaactgtcca	gcctgcagat	cgaccggacg	900
ccggcaccgc	ccgtccacga	tcgcaatcgc	caggggtcct	caagcgctcc	ggcaactgaa	960
aagggccgct	cagccgaggc	caagtga				987

<210> 300

<211> 328

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 300

Met	Thr	Val	Val	Lys	Ala	Ala	Ala	Val	Gln	Ile	Ser	Pro	Val	Leu	Tyr
1			5					10					15		
Ser	Arg	Ala	Gly	Thr	Val	Glu	Lys	Val	Val	Lys	Lys	Ile	Asp	Glu	Leu

<210>	301
<211>	1032
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

[illegible]

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agcctcgagt ggatcaacgc cgggaacagc atcgtcgtcg atccggacgg cgcggtggtc 780
gcgggaccgc tggcgcgggc gcacgacacg ctctacgtcg agatcgatcc gggccgcgcc 840
gccggtcccc gatggatctt cgacgccgcc ggtcactatc accgtcccga cctgttccat 900
ttcgcgatgc gcgcgccggt ggcgccagag accgcgccgg ttgtgcgga gcgcggccgg 960
cggctagcct cggccccggc gcggaagcca cggaaacggc cggcgcgtcc caccgaagg 1020
aggactcgat ga 1032

```

<210> 302

<211> 335

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 302

```

Met Thr Thr Pro Ala Pro Phe Thr Ala Ala Val Val Gln Ala Ser Pro
1      5      10      15
Val Phe Leu Asp Arg Asp Ala Thr Val Asp Lys Ala Cys Ala Leu Ile
20     25     30
Thr Ala Ala Gly Ala Arg Gly Ala Lys Leu Val Val Leu Pro Glu Thr
35     40     45
Phe Val Pro Ala Tyr Pro Ala Trp Val Trp Tyr Leu Pro Leu Thr Arg
50     55     60
Arg Pro Asp Val Ala Lys Leu Tyr Arg Ala Leu Val Glu Asn Ala Ile
65     70     75     80
Asp Val Pro Gly Pro Glu Thr Glu Arg Leu Gly Arg Ala Ala Arg Asp
85     90     95
Ala Gly Ala Trp Val Ala Ile Gly Val Asn Glu Arg Asn Ala Lys Ala
100    105    110
Ser Arg Thr Ser Leu Tyr Asn Thr Val Leu Leu Phe Asp Asp Gln Gly
115    120    125
Thr Leu Val Glu Ser Arg Arg Lys Leu Met Pro Thr Gly Gly Glu Arg
130    135    140
Leu Val Trp Thr Pro Gly Glu Pro Val Pro Leu Arg Val His Asp Thr
145    150    155    160
Pro Leu Gly Arg Val Gly Ala Leu Ile Cys Trp Glu Asn Tyr Met Pro
165    170    175
Leu Ala Arg Phe Ala Leu Tyr Glu Gln Gly Val Gln Ile Tyr Leu Ala
180    185    190
Pro Thr Trp Asp Tyr Ser Glu Ala Trp Leu Ala Ser Met Arg His Val
195    200    205
Ala Arg Glu Gly Arg Thr Trp Val Ile Gly Cys Ser Gln Ala Val Arg
210    215    220
Arg Asp Glu Ile Pro Asp His Leu Pro Phe Lys Asp Ala Ile Pro Glu
225    230    235    240
Ser Leu Glu Trp Ile Asn Ala Gly Asn Ser Ile Val Val Asp Pro Asp
245    250    255
Gly Ala Val Val Ala Gly Pro Leu Ala Arg Ala His Asp Thr Leu Tyr
260    265    270
Val Glu Ile Asp Pro Gly Arg Ala Ala Gly Ser Arg Trp Ile Phe Asp
275    280    285
Ala Ala Gly His Tyr His Arg Pro Asp Leu Phe His Phe Ala Met Arg
290    295    300
Ala Pro Val Ala Pro Glu Thr Ala Pro Val Val Arg Lys Arg Gly Arg
305    310    315    320
Arg Leu Ala Ser Ala Pro Ala Arg Lys Pro Arg Lys Arg Pro Ala
325    330    335

```

<210> 303

<211> 1011

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 303

```

atgggcatcg ttcaccccaa gtacaaagtc gctgtcgttc aggctgcccc tgtatggcta      60
gacctggagg ccactgttga taaatgcatt cagttgattg aagaagcagc cagcaagggc      120
tgcaagctca tcgccttccc tgagaccttc attcccggat acccttggtg tatctggatg      180
ggaacgcctg cctggactat tcagcgcggc tttgtacagc gctattttga taattctctg      240
tcttatgaca gtccgcaagc ggagaagcta aggcaggcag tcaaaaaggc tgagatcacg      300
gccgtactag gtctttctga gcgcagcggc ggtagcttgt acattgcaca atggaccatt      360
ggccctgacg gagaaaccat acacaaacgc agaaaagtgc gtccaacgca tggtagcggt      420
acgggtattg gcgacggtga cggtagtgat cttgcggtgc acgatacccc cctggggcgg      480
ctgggcgcgc ttgcgtgctg ggagaacata ctgtcactga acaagtatgc gatgtattca      540
cagaatgagc aggtgcacgt agccgcttgg cctagcttct cgggtctacga gcctttcgcc      600
catgcattgg gttgggaggt caataacgca gtcagcaagg tttacgcggt agaaggcggc      660
tgttttgtat tggcgccttg cgcagtggtc tccgaggaaa tgatcgaagc actgtgcgat      720
acacccgata agcaccaact ggctcatgca ggtggagggc atgctgtcat ttacggacca      780
gatggcagtc ctctggcaga taagttaacc gaaggagagg aggggctatt aattgcagaa      840
attgatctcg gtctcatcag cttggcgaaa aatgccatgg acccggtggg gcattactct      900
cgacctgacg tacatcgctt gctattgaat cgcaatccag caaagcgggt tgaggaattt      960
tctctgccca ttgatttggc agagacaact ccgccaatat taggcacgta g      1011

```

<210> 304

<211> 336

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 304

```

Met Gly Ile Val His Pro Lys Tyr Lys Val Ala Val Val Gln Ala Ala
1      5      10      15
Pro Val Trp Leu Asp Leu Glu Ala Thr Val Asp Lys Cys Ile Gln Leu
20     25     30
Ile Glu Glu Ala Ala Ser Lys Gly Cys Lys Leu Ile Ala Phe Pro Glu
35     40     45
Thr Phe Ile Pro Gly Tyr Pro Trp Tyr Ile Trp Met Gly Thr Pro Ala
50     55     60
Trp Thr Ile Gln Arg Gly Phe Val Gln Arg Tyr Phe Asp Asn Ser Leu
65     70     75     80
Ser Tyr Asp Ser Pro Gln Ala Glu Lys Leu Arg Gln Ala Val Lys Lys
85     90     95
Ala Glu Ile Thr Ala Val Leu Gly Leu Ser Glu Arg Ser Gly Gly Ser
100    105    110
Leu Tyr Ile Ala Gln Trp Thr Ile Gly Pro Asp Gly Glu Thr Ile His
115    120    125
Lys Arg Arg Lys Val Arg Pro Thr His Gly Glu Arg Thr Val Phe Gly
130    135    140
Asp Gly Asp Gly Ser Asp Leu Ala Val His Asp Thr Pro Leu Gly Arg
145    150    155    160
Leu Gly Ala Leu Ala Cys Trp Glu Asn Ile Leu Ser Leu Asn Lys Tyr
165    170    175
Ala Met Tyr Ser Gln Asn Glu Gln Val His Val Ala Ala Trp Pro Ser
180    185    190
Phe Ser Val Tyr Glu Pro Phe Ala His Ala Leu Gly Trp Glu Val Asn
195    200    205
Asn Ala Val Ser Lys Val Tyr Ala Val Glu Gly Gly Cys Phe Val Leu

```



```

      210              215              220
Ala Pro Cys Ala Val Val Ser Glu Glu Met Ile Glu Ala Leu Cys Asp
225              230              235              240
Thr Pro Asp Lys His Gln Leu Ala His Ala Gly Gly Gly His Ala Val
      245              250              255
Ile Tyr Gly Pro Asp Gly Ser Pro Leu Ala Asp Lys Leu Pro Glu Gly
      260              265              270
Glu Glu Gly Leu Leu Ile Ala Glu Ile Asp Leu Gly Leu Ile Ser Leu
      275              280              285
Ala Lys Asn Ala Met Asp Pro Val Gly His Tyr Ser Arg Pro Asp Val
      290              295              300
His Arg Leu Leu Leu Asn Arg Asn Pro Ala Lys Arg Val Glu Glu Phe
305              310              315              320
Ser Leu Pro Ile Asp Leu Ala Glu Thr Thr Pro Pro Ile Leu Gly Thr
      325              330              335

```

<210> 305

<211> 1068

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 305

```

atgacgatgc aacatcccaa gtttcgcgct gctgccgtgc aggcggcacc ggtcttcctt      60
gaccttgatg cgtcgataga taaagccatc gacctgatcg cgcaagccgc caaaggcggc      120
gcgcaattga ttgcctttcc ggaaacctgg ctgcccggct accccttttt catctggctc      180
gattcgccgg cctggggcat gcaattcatc cagcgctacc atgacaattc cctgggtctac      240
ggcacaccgc aggcgcgagc catcgcgagc gctgcgaaaa agcatcgcat catggtcgtc      300
atggggcaca gcgagcggga tcatggaagt ctgtacatcg ctcaagtggat catcggtgcc      360
gatggggaaa cggttgcgac acgtcgtaag ctcaaaccga ctcatgccga gcgcaccttg      420
tttgggggaa gcgatggcag tgacctgagc gtgttcgata caccgctggg aagggttggc      480
gcactatgct gctgggagca cctccagccc ctgtcgaaat acgcgctata cgcacagaat      540
gagcaggtcc acattgcttc ctggccaagc ttttccctgt atcgcggggg cgccctacgcg      600
ctcggcgccg aagtgaacaa tgccggccagc cagatttatg ctgtcgaagg ccagtgtttt      660
gtgatcgcgc cgtgcggggg cgtcacgaaa gaaatgctgg acgtgctgtg caccgacgaa      720
atgaaaaagc agttgttggg tgaaggcggc gggttcgcgc gaatttacgc gcccgatgga      780
cagatgatgc acgcgcgct ggccgaaaac gaagagggcc tgggtgatgc cgtatctcgac      840
ctgggcatga tctcgctggc caaagtagtc gccgaccggc ccgggcatta tgcgcggccc      900
gacgtaaccc ggttactgct ggacaagact ccgggagacc gcgtcatgct ggcgagccgt      960
cgcgccaagg aggtcagccg cgctggtaac gacgagccgc aagtgtgtgt ctgcgcgaac      1020
gacacgctga cctcgccgaa gccagcgtct tcgcgcaaag caagctga      1068

```

<210> 306

<211> 355

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 306

```

Met Thr Met Gln His Pro Lys Phe Arg Ala Ala Ala Val Gln Ala Ala
 1              5              10              15
Pro Val Phe Leu Asp Leu Asp Ala Ser Ile Asp Lys Ala Ile Asp Leu
      20              25              30
Ile Ala Gln Ala Ala Lys Gly Gly Ala Gln Leu Ile Ala Phe Pro Glu
      35              40              45
Thr Trp Leu Pro Gly Tyr Pro Phe Phe Ile Trp Leu Asp Ser Pro Ala
      50              55              60

```

Trp Gly Met Gln Phe Ile Gln Arg Tyr His Asp Asn Ser Leu Val Tyr
 65 70 75 80
 Gly Thr Pro Gln Ala Glu Arg Ile Ala Gln Ala Ala Lys Lys His Arg
 85 90 95
 Ile Met Val Val Met Gly His Ser Glu Arg Asp His Gly Ser Leu Tyr
 100 105 110
 Ile Ala Gln Trp Ile Ile Gly Ala Asp Gly Glu Thr Val Ala Thr Arg
 115 120 125
 Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Leu Phe Gly Glu Gly
 130 135 140
 Asp Gly Ser Asp Leu Ser Val Phe Asp Thr Pro Leu Gly Arg Val Gly
 145 150 155 160
 Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr Ala Leu
 165 170 175
 Tyr Ala Gln Asn Glu Gln Val His Ile Ala Ser Trp Pro Ser Phe Ser
 180 185 190
 Leu Tyr Arg Gly Gly Ala Tyr Ala Leu Gly Ala Glu Val Asn Asn Ala
 195 200 205
 Ala Ser Gln Ile Tyr Ala Val Glu Gly Gln Cys Phe Val Ile Ala Pro
 210 215 220
 Cys Gly Val Val Thr Lys Glu Met Leu Asp Val Leu Cys Thr Asp Glu
 225 230 235 240
 Met Lys Lys Gln Leu Val Glu Gly Gly Phe Ala Arg Ile Tyr
 245 250 255
 Ala Pro Asp Gly Gln Met Met His Ala Pro Leu Ala Glu Asn Glu Glu
 260 265 270
 Gly Leu Val Tyr Ala Asp Leu Asp Leu Gly Met Ile Ser Leu Ala Lys
 275 280 285
 Val Val Ala Asp Pro Ala Gly His Tyr Ala Arg Pro Asp Val Thr Arg
 290 295 300
 Leu Leu Leu Asp Lys Thr Pro Gly Asp Arg Val Met Leu Ala Ser Arg
 305 310 315 320
 Arg Gly Lys Glu Val Ser Arg Ala Gly Asn Asp Glu Pro Gln Val Leu
 325 330 335
 Val Ser Arg Asn Asp Thr Leu Thr Ser Pro Lys Pro Ala Ser Ser Arg
 340 345 350
 Lys Ala Ser
 355

<210> 307

<211> 942

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 307

atggctgaac	cggaatcctt	tatcgtcgct	gctgtacagg	ctacaccgat	ctttcttgac	60
cgccaggcaa	cccttgagaa	agcgtgcgac	ctgattgccg	aagctggcag	caatggcgca	120
aaactcgttc	ttttccoga	agcctttatc	cccacctatc	ctgattggat	atgggcggtg	180
acaggctcac	aatctgcgct	gctcgacgaa	ctttatgtgg	aactactgga	aaactccgtg	240
accatccccg	acgcgaccac	tgagcaactt	tgtgaagcag	cacgtaacgc	cggtctctac	300
gtcgtcatgg	gagtgaatga	gcgcaacgcc	gagggcgagca	acgccacact	ctataacacc	360
ctgctctata	ttgacgatca	gggcaaaatt	ctcggcaagc	atcgcaaaatt	ggtcccgacc	420
gccctggagc	gaatcgtctg	gggctatggc	gatggcagca	cgcttgacgc	ctttgaaacg	480
ccgctgggca	agattggcgg	gctgatctgt	tgggaaaatt	acatgccact	ggcgcgccaa	540
acactttatg	cctggggggg	gcaaaatttac	ttggccgcaa	cgtgggatcg	cggcgaagtt	600
tggcaggcga	ccatgcgccca	tattgccagg	gaaggcgggc	tctatgtagt	cgctcctgt	660
attccatttc	acatcaaaga	cattcctgac	cacatgcctg	aaatccgcaa	tctctatgca	720
ccggggacag	actggatcaa	cgtcggccaa	agctgcatca	tcaacccag	cgcgactat	780

```

attgcaggcc ctgtcgagtg tcgcgaggag attctttatg ccgaggtaaa tctgcgccag      840
agtgcggcgg caaacgtat gttggatgtg gcgggccatt atggacgccc tgatgtcttt      900
cacctaccg tcaaccgcac gcccaatccg catattcgat aa                          942

```

<210> 308

<211> 313

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 308

```

Met Ala Glu Pro Glu Ser Phe Ile Val Ala Ala Val Gln Ala Thr Pro
 1           5           10           15
Ile Phe Leu Asp Arg Gln Ala Thr Leu Glu Lys Ala Cys Asp Leu Ile
      20           25           30
Ala Glu Ala Gly Ser Asn Gly Ala Lys Leu Val Leu Phe Pro Glu Ala
      35           40           45
Phe Ile Pro Thr Tyr Pro Asp Trp Ile Trp Ala Val Thr Gly Ser Gln
      50           55           60
Ser Ala Leu Leu Asp Glu Leu Tyr Val Glu Leu Leu Glu Asn Ser Val
      65           70           75           80
Thr Ile Pro Asp Ala Thr Thr Glu Gln Leu Cys Glu Ala Ala Arg Asn
      85           90           95
Ala Gly Leu Tyr Val Val Met Gly Val Asn Glu Arg Asn Ala Glu Ala
      100          105          110
Ser Asn Ala Thr Leu Tyr Asn Thr Leu Leu Tyr Ile Asp Asp Gln Gly
      115          120          125
Lys Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Ala Leu Glu Arg
      130          135          140
Ile Val Trp Gly Tyr Gly Asp Gly Ser Thr Leu Asp Ala Phe Glu Thr
      145          150          155          160
Pro Leu Gly Lys Ile Gly Gly Leu Ile Cys Trp Glu Asn Tyr Met Pro
      165          170          175
Leu Ala Arg Gln Thr Leu Tyr Ala Trp Gly Val Gln Ile Tyr Leu Ala
      180          185          190
Ala Thr Trp Asp Arg Gly Glu Val Trp Gln Ala Thr Met Arg His Ile
      195          200          205
Ala Arg Glu Gly Gly Val Tyr Val Val Ala Ser Cys Ile Pro Phe His
      210          215          220
Ile Lys Asp Ile Pro Asp His Met Pro Glu Ile Arg Asn Leu Tyr Ala
      225          230          235          240
Pro Gly Thr Asp Trp Ile Asn Val Gly Gln Ser Cys Ile Ile Asn Pro
      245          250          255
Ser Gly Asp Tyr Ile Ala Gly Pro Val Glu Cys Arg Glu Glu Ile Leu
      260          265          270
Tyr Ala Glu Val Asn Leu Arg Gln Ser Ala Ala Ala Lys Arg Met Leu
      275          280          285
Asp Val Ala Gly His Tyr Gly Arg Pro Asp Val Phe His Leu Thr Val
      290          295          300
Asn Arg Thr Pro Asn Pro His Ile Arg
      305          310

```

<210> 309

<211> 951

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

```

<400> 309
ttgaccgact gtctcaaaat agccgccgcc caaatcactc cggctcttct cgaccgcgtt      60
gcgaccacga agaaggtcgt cgaaaccatc gaaaaagcgg ccgccggcgg tgcgcggctg      120
gtcgcattcg gcgaagcgct gttgcccgcc tatccattgt ggctgacgcg caccgacgcc      180
gcgcggttca attccgacgt gcaaaaaaac ttgcacgcga tctatctcaa gcaatccgtc      240
tcgatagcag gcggtcacct atctccgatt tgcaaaatcg caagcgaacg caagattgcc      300
gtcatcctcg gcatcgccga gcgcgcgacc gaccggggcg accacaccat ttactgctcg      360
tgcgtgttca tcgatgccga cggccgaatc gcgtcgggtcc atcgcaagct gatgccgaca      420
tacgaagaac gcctcagttg gggattcggc gacgggtgcgg gactcgtcac gcatccggtc      480
gggcccgttca cggtgggcgc gttgaactgc tgggaaaact ggatgccctt cgcgcgcacc      540
gcgctgtatg ccggcggaga agatttgacg gttgcgatct ggcccggcgg atcgggtgctc      600
acggaagaca tcacgcgctt catcgcacgc gagtcgcgct cgttcgtcct gtccgtcagc      660
ggcatcattc gcgaaagcga catccccagc ggggtcccct atcgcatga aatgtgtgct      720
aaaggcgaaa ccatctacaa cggcggaagc tgcatcgccg gaccgcgcg tcagtggatc      780
atcgcgcccc taaccgaccg tgaagagttg atcttcgcgg agatcgacca cgaacacgtc      840
cgccgcgagc ggcagaattt cgaccgggcc gggcattacg cgcggcccga tgtgttgcaa      900
ataaccgttg atcgtcgacg acaaacagcg gcgaatttta ttgatgacta a              951

```

```

<210> 310
<211> 316
<212> PRT
<213> Unknown

```

```

<220>
<223> Obtained from an environmental sample

```

```

<400> 310
Leu Thr Asp Cys Leu Lys Ile Ala Ala Ala Gln Ile Thr Pro Val Phe
 1          5          10          15
Leu Asp Arg Val Ala Thr Thr Lys Lys Val Val Glu Thr Ile Glu Lys
 20          25          30
Ala Ala Ala Gly Gly Ala Arg Leu Val Ala Phe Gly Glu Ala Leu Leu
 35          40          45
Pro Ala Tyr Pro Leu Trp Leu Thr Arg Thr Asp Ala Ala Arg Phe Asn
 50          55          60
Ser Asp Val Gln Lys Asn Leu His Ala Ile Tyr Leu Lys Gln Ser Val
 65          70          75          80
Ser Ile Ala Gly Gly His Leu Ser Pro Ile Cys Lys Ile Ala Ser Glu
 85          90          95
Arg Lys Ile Ala Val Ile Leu Gly Ile Ala Glu Arg Ala Thr Asp Arg
100          105          110
Gly Asp His Thr Ile Tyr Cys Ser Cys Val Phe Ile Asp Ala Asp Gly
115          120          125
Arg Ile Ala Ser Val His Arg Lys Leu Met Pro Thr Tyr Glu Glu Arg
130          135          140
Leu Ser Trp Gly Phe Gly Asp Gly Ala Gly Leu Val Thr His Pro Val
145          150          155          160
Gly Pro Phe Thr Val Gly Ala Leu Asn Cys Trp Glu Asn Trp Met Pro
165          170          175
Leu Ala Arg Thr Ala Leu Tyr Ala Gly Gly Glu Asp Leu His Val Ala
180          185          190
Ile Trp Pro Gly Gly Ser Val Leu Thr Glu Asp Ile Thr Arg Phe Ile
195          200          205
Ala Arg Glu Ser Arg Ser Phe Val Leu Ser Val Ser Gly Ile Ile Arg
210          215          220
Glu Ser Asp Ile Pro Ser Gly Val Pro Tyr Arg Asp Glu Met Cys Ala
225          230          235          240
Lys Gly Glu Thr Ile Tyr Asn Gly Gly Ser Cys Ile Ala Gly Pro Asp
245          250          255
Gly Gln Trp Ile Ile Ala Pro Val Thr Asp Arg Glu Glu Leu Ile Phe

```

260 265 270
 Ala Glu Ile Asp His Glu His Val Arg Arg Glu Arg Gln Asn Phe Asp
 275 280 285
 Pro Ala Gly His Tyr Ala Arg Pro Asp Val Leu Gln Ile Thr Val Asp
 290 295 300
 Arg Arg Arg Gln Thr Ala Ala Asn Phe Ile Asp Asp
 305 310 315

<210> 311

<211> 1011

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 311

```

atgtcagaaa agcgaataat cagagcagct gcagttcaga tcacacctga atttgactca      60
gcagatggaa cagttaagaa ggtatgcaag gtaatcgatg aagcaggcgc aaagggtgta      120
caaattatag tattccccga aaccttcatt ccgtattacc catacttctc attcattacc      180
ccccagttt ctgctggcgc tgagcatttg aagctttatg aaaaaagtgt cgtgatacct      240
ggtcctgtca ctcaagcgaat cgccgagaga gctagagtga atcaaatggt cgtcgtactc      300
ggtgtaaacg agagagataa cggtagcctc tataacactc aactgatctt cgataccaat      360
ggtgagttga tgtgaagag aagaaaaatc actcctacat atcatgagcg catgatctgg      420
ggacaagggtg atgcttcagg cttaaaagta gttgaaacga gcattgcccg ggtaggtgct      480
ctagcttgct ggaacatta caaccgctg gccagatatt ctctcatgac acagcatgaa      540
gaaattcact gcgcacaatt cccaggttct atggttgcc aaatatttgc cgaccaaatg      600
gatgtcacta tcagacatca cgcattggaa tctggctgtt tcgtcattaa tgccaccggc      660
tggctcacag acgagcaaat ccagtccatt acagatgacc caaaaatgca gaaagcatta      720
cgtggcggct gcaacacagc aatcatttct cccgaagggtg tgcacttaac agagccctta      780
cgtgaagggtg aaggcatttt gattgctgac ctggacatgt cactcatcac aaaacgaaaa      840
agaatgatgg attcagtagg tcattattca agacctgaac tattaagtct ggcgatcaat      900
gacaagccag caacaacaaa attttcaatg actgagggtg gtactcaaac tgagcaattt      960
cgaatcgtag aggagttgaa aaatgacgac aagcttagca ccggaaacta a      1011

```

<210> 312

<211> 336

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 312

```

Met Ser Glu Lys Arg Ile Ile Arg Ala Ala Ala Val Gln Ile Thr Pro
1      5      10      15
Glu Phe Asp Ser Ala Asp Gly Thr Val Lys Lys Val Cys Lys Val Ile
20      25      30
Asp Glu Ala Gly Ala Lys Gly Val Gln Ile Ile Val Phe Pro Glu Thr
35      40      45
Phe Ile Pro Tyr Tyr Pro Tyr Phe Ser Phe Ile Thr Pro Pro Val Ser
50      55      60
Ala Gly Ala Glu His Leu Lys Leu Tyr Glu Lys Ser Val Val Ile Pro
65      70      75      80
Gly Pro Val Thr Gln Ala Ile Ala Glu Arg Ala Arg Val Asn Gln Met
85      90      95
Val Val Val Leu Gly Val Asn Glu Arg Asp Asn Gly Ser Leu Tyr Asn
100      105      110
Thr Gln Leu Ile Phe Asp Thr Asn Gly Glu Leu Met Leu Lys Arg Arg
115      120      125
Lys Ile Thr Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly Asp

```

```

      130              135              140
Ala Ser Gly Leu Lys Val Val Glu Thr Ser Ile Ala Arg Val Gly Ala
145              150              155              160
Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ser Leu Met
      165              170              175
Thr Gln His Glu Glu Ile His Cys Ala Gln Phe Pro Gly Ser Met Val
      180              185              190
Gly Gln Ile Phe Ala Asp Gln Met Asp Val Thr Ile Arg His His Ala
      195              200              205
Leu Glu Ser Gly Cys Phe Val Ile Asn Ala Thr Gly Trp Leu Thr Asp
      210              215              220
Glu Gln Ile Gln Ser Ile Thr Asp Asp Pro Lys Met Gln Lys Ala Leu
225              230              235              240
Arg Gly Gly Cys Asn Thr Ala Ile Ile Ser Pro Glu Gly Val His Leu
      245              250              255
Thr Glu Pro Leu Arg Glu Gly Glu Gly Ile Leu Ile Ala Asp Leu Asp
      260              265              270
Met Ser Leu Ile Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His
      275              280              285
Tyr Ser Arg Pro Glu Leu Leu Ser Leu Ala Ile Asn Asp Lys Pro Ala
      290              295              300
Thr Thr Lys Phe Ser Met Thr Glu Gly Cys Thr Gln Thr Glu Gln Phe
305              310              315              320
Arg Ile Ala Glu Glu Leu Lys Asn Asp Asp Lys Leu Ser Thr Gly Asn
      325              330              335

```

<210> 313
 <211> 987
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 313
atggcggccg ttcaggctgc gccggttccg tttgatgctg aggcttcggt ggataaggcc      60
tgctcgcttaa ttcaagaagc tgcagccaaa ggcgcagata tagttgcttt cggtgaggca      120
tggctaccgc gctaccoccta ttttgccctg ttaccccaag taacaccaga gtggtatagt      180
gcggtcgccg attatcttgc cagctctgtt gatatccctg gcccgatcac cgataaactt      240
tgccaggctg cccgtcgtgc atcggttgaa ctcacatggt gtgtggtaga acgcagcaag      300
tctcaggga ccacattatt cagccttctt tttattagca aggatggcga aataattggc      360
aagcaccgca agctgaagcc cactactgcc gaacgaaccg tctggggtga aggcgatgcc      420
agcggactga ggggtcacga tcggcctatt gccagaatca gtgggctctc ctgctgggag      480
aacaaaatga tgctgccagg ttacgcactg atggcgagg gtacgcagggt gcatgtctcc      540
gcctggccag ggatcccaga ggattacccc atggagggtgc ctgcacaccc ccgtcaaaaag      600
ctgctttccc aagcctttgc actgcaaggc ggggtgctatg ttatttctcc ctccattgtc      660
cttagggcag aagatgtgcc cgagaaacac gccgctctac tgatgggaga ccaagtgggc      720
ggtagctata tcattgacct ctgcggaaaa gtgatcgccg aggccggtgc gggtgagact      780
atcctgattg ccaaaggcaa ccttgacctc gtaagggccg ccaaaaatggc cagtgatgta      840
gggggggtctt attcacgccc ggatcttttg cagttgatga tcaataaccg accactcgaa      900
cagctgattg agttcagtg tgaaggtgca ggtaggggga atctagtatc caactcacc      960
gaggtgtcag aacaagaagg tgagtaa                                     987

```

<210> 314
 <211> 328
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 314

```

Met Ala Ala Val Gln Ala Ala Pro Val Pro Phe Asp Ala Glu Ala Ser
 1          5          10          15
Val Asp Lys Ala Cys Arg Leu Ile Gln Glu Ala Ala Lys Gly Ala
 20          25          30
Asp Ile Val Ala Phe Gly Glu Ala Trp Leu Pro Gly Tyr Pro Tyr Phe
 35          40          45
Ala Trp Leu Pro Gln Val Thr Pro Glu Trp Tyr Ser Ala Ala Ala Asp
 50          55          60
Tyr Leu Ala Ser Ser Val Asp Ile Pro Gly Pro Ile Thr Asp Lys Leu
 65          70          75          80
Cys Gln Ala Ala Arg Arg Ala Ser Val Glu Leu Ile Met Gly Val Val
 85          90          95
Glu Arg Ser Lys Ser Gln Gly Thr Thr Tyr Cys Thr Leu Leu Phe Ile
100          105          110
Ser Lys Asp Gly Glu Ile Ile Gly Lys His Arg Lys Leu Lys Pro Thr
115          120          125
Leu Ala Glu Arg Thr Val Trp Gly Glu Gly Asp Ala Ser Gly Leu Arg
130          135          140
Val His Asp Arg Pro Ile Ala Arg Ile Ser Gly Leu Ser Cys Trp Glu
145          150          155          160
Asn Lys Met Met Leu Pro Gly Tyr Ala Leu Met Ala Gln Gly Thr Gln
165          170          175
Val His Val Ser Ala Trp Pro Gly Ile Pro Glu Asp Ser Pro Met Glu
180          185          190
Val Pro Ala His Pro Arg Gln Lys Leu Leu Ser Gln Ala Phe Ala Leu
195          200          205
Gln Gly Gly Cys Tyr Val Ile Ser Pro Ser Ile Val Leu Arg Ala Glu
210          215          220
Asp Val Pro Glu Lys His Ala Ala Leu Leu Met Gly Asp Gln Val Gly
225          230          235          240
Gly Ser Tyr Ile Ile Asp Pro Cys Gly Lys Val Ile Ala Glu Ala Gly
245          250          255
Ala Gly Glu Thr Ile Leu Ile Ala Lys Gly Asn Leu Asp Leu Val Arg
260          265          270
Ala Ala Lys Met Ala Ser Asp Val Gly Gly Ser Tyr Ser Arg Pro Asp
275          280          285
Leu Leu Gln Leu Met Ile Asn Asn Arg Pro Leu Glu Gln Leu Ile Glu
290          295          300
Phe Ser Ala Glu Gly Ala Gly Arg Gly Asn Leu Val Ser Asn Ser Pro
305          310          315          320
Glu Val Ser Glu Gln Glu Gly Glu
325

```

<210> 315

<211> 960

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 315

```

atgacaatgc ttaagaccaa attccgggtt gctgcggtgc aggcagcgcc tgtattcctg      60
gacgagagg ctacgctgga gaaagcctgc ggactgattg aggaggcggg tcgcaacggg      120
gccagcctgg tggctcttcc tgagtcgttc attccggcct atcccgattg ggtctgggct      180
gtgccggcgg gtgaagaagc ttactttaat gaactgtatg ctcaactgct ggccaacgcc      240
gttgaaattc ccagcccggc caccgaacgc ttgagccagg cagcgaaaaa ggctaaagtc      300
catgtggtta tgggcctgac cgaacgcaac agcgaggcca gcggcggcag cctctacaat      360
accttgctct atcttgacc acagggccaa attctgggca aacatcgcaa gctggtgccc      420
accggcgggc agcggctggt ttgggcccag ggcgacggca gtaccctgca agtctacgag      480

```

```

accccccttgg gtaaaactcag cggcttgatt tgctgggaaa attatatgcc gctggcccg 540
tacgcgctct atgcctgggg tacgcaaata tatatcgccg ccacctggga tgcaggcgag 600
ccgtggcttt cgacgctgcg gcatatcgcc aaagagggcc ggggtgttgt catcggtgt 660
ggcatggcct tgcgtaaggc tgatattccc gaccattttg aattcaagca gcgcttttat 720
caaaatgccg gcgagtggat caatggaggc gacagcgcca ttgtcaatcc tgaggggtgaa 780
tttattgctg gacccctgag cgagcaggaa ggtattttgt acgccgagat tgatcctggc 840
cagatggccg gacaaaatg gatgctcgat gtggccgggc actatgctcg cccggatgtc 900
tttgaactga ccgtccagac cgtagctcgg cccatgatta cctctactca gccgcgatag 960

```

<210> 316

<211> 319

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 316

```

Met Thr Met Leu Lys Thr Lys Phe Arg Val Ala Ala Val Gln Ala Ala
1      5      10      15
Pro Val Phe Leu Asp Arg Glu Ala Thr Leu Glu Lys Ala Cys Gly Leu
20     25     30
Ile Glu Glu Ala Gly Arg Asn Gly Ala Ser Leu Val Val Phe Pro Glu
35     40     45
Ser Phe Ile Pro Ala Tyr Pro Asp Trp Val Trp Ala Val Pro Ala Gly
50     55     60
Glu Glu Ala Leu Leu Asn Glu Leu Tyr Ala Gln Leu Leu Ala Asn Ala
65     70     75     80
Val Glu Ile Pro Ser Pro Ala Thr Glu Arg Leu Ser Gln Ala Ala Lys
85     90     95
Lys Ala Lys Val His Val Val Met Gly Leu Thr Glu Arg Asn Ser Glu
100    105    110
Ala Ser Gly Gly Ser Leu Tyr Asn Thr Leu Leu Tyr Leu Asp Pro Gln
115    120    125
Gly Gln Ile Leu Gly Lys His Arg Lys Leu Val Pro Thr Gly Gly Glu
130    135    140
Arg Leu Val Trp Ala Gln Gly Asp Gly Ser Thr Leu Gln Val Tyr Glu
145    150    155    160
Thr Pro Leu Gly Lys Leu Ser Gly Leu Ile Cys Trp Glu Asn Tyr Met
165    170    175
Pro Leu Ala Arg Tyr Ala Leu Tyr Ala Trp Gly Thr Gln Ile Tyr Ile
180    185    190
Ala Ala Thr Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Leu Arg His
195    200    205
Ile Ala Lys Glu Gly Arg Val Phe Val Ile Gly Cys Gly Met Ala Leu
210    215    220
Arg Lys Ala Asp Ile Pro Asp His Phe Glu Phe Lys Gln Arg Phe Tyr
225    230    235    240
Gln Asn Ala Gly Glu Trp Ile Asn Gly Gly Asp Ser Ala Ile Val Asn
245    250    255
Pro Glu Gly Glu Phe Ile Ala Gly Pro Leu Ser Glu Gln Glu Gly Ile
260    265    270
Leu Tyr Ala Glu Ile Asp Pro Gly Gln Met Ala Gly Pro Lys Trp Met
275    280    285
Leu Asp Val Ala Gly His Tyr Ala Arg Pro Asp Val Phe Glu Leu Thr
290    295    300
Val Gln Thr Val Ala Arg Pro Met Ile Thr Ser Thr Gln Pro Arg
305    310    315

```

<210> 317

<211> 993

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 317

```

atgaccattg taaaagccgc tgccgtccaa ataagccctg tcctttacag ccgcgaaggg      60
accgtggaca aggttggtcca gaagatcctc gaactcggca agcaaggcgt ccagttcgcc      120
actttcccgg agacgggtggt cccctactac ccctacttct ccttcgtcca gtcgggctac      180
gcccctcaagg tgggcaagga acatctgcgc ttgctcgaac agtcggtcac cgtgccatcg      240
gccaccacgc tcgccatcgg cgaagcctgc aagcaggcgg ggatgggtgt gtccatcggc      300
gtcaacgaac gcgacggcag cacgatctac aacacgcagc tgctcttcga tgccgacggc      360
accttgattc agcgcgcgcg aaagatcagc ccgaccttcc atgaacgcat ggtctggggc      420
caggggcgacg gctccgggct gcgcgcggtc gacagcggg tcggggcgcat cggccagttg      480
gcgtgctggg agcactacaa cccgctggcc cgctacgcca tgatggccga cggcgagcag      540
atccactcgg cgatgtaccc cggttccttc gcaggcgacg ccttctccga acagatccag      600
gtcaacatcc gccagcacgc attggaagcc ggctgcttcg tcgtgaacgc caccgcgtgg      660
ctggacgcgc atcagcaggc gcagatcatg caggacaccg gttgcgccat cggcccgatc      720
tccagtgggt gcttcaccgc catcgtttcg ccggacggcg tggtgctggg cgagcctctg      780
cggtcgggtg agggcgaggt gattgcccgt ctcgacttca cgctgatcga caagcgcaag      840
cagatgatgg attcacgcgg gcactatgcg cgcccgaat tgctcagcct gttgatcgac      900
cgcacggcga ccgcgcgtgt gcatgagcgc agcgcgcac cgaaggcgac tgccgagcag      960
gcggacggtc catccgccgt gaatgcgcag taa                                993

```

<210> 318

<211> 330

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 318

```

Met Thr Ile Val Lys Ala Ala Ala Val Gln Ile Ser Pro Val Leu Tyr
 1          5          10          15
Ser Arg Glu Gly Thr Val Asp Lys Val Val Gln Lys Ile Leu Glu Leu
      20          25          30
Gly Lys Gln Gly Val Gln Phe Ala Thr Phe Pro Glu Thr Val Val Pro
      35          40          45
Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Ser Gly Tyr Ala Leu Lys Val
      50          55          60
Gly Lys Glu His Leu Arg Leu Leu Glu Gln Ser Val Thr Val Pro Ser
      65          70          75          80
Ala Thr Thr Leu Ala Ile Gly Glu Ala Cys Lys Gln Ala Gly Met Val
      85          90          95
Val Ser Ile Gly Val Asn Glu Arg Asp Gly Ser Thr Ile Tyr Asn Thr
      100          105          110
Gln Leu Leu Phe Asp Ala Asp Gly Thr Leu Ile Gln Arg Arg Arg Lys
      115          120          125
Ile Ser Pro Thr Phe His Glu Arg Met Val Trp Gly Gln Gly Asp Gly
      130          135          140
Ser Gly Leu Arg Ala Val Asp Ser Ala Val Gly Arg Ile Gly Gln Leu
      145          150          155          160
Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Met Met Ala
      165          170          175
Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Phe Ala Gly
      180          185          190
Asp Ala Phe Ser Glu Gln Ile Gln Val Asn Ile Arg Gln His Ala Leu
      195          200          205
Glu Ala Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp

```

```

      210              215              220
Gln Gln Ala Gln Ile Met Gln Asp Thr Gly Cys Ala Ile Gly Pro Ile
225              230              235              240
Ser Ser Gly Cys Phe Thr Ala Ile Val Ser Pro Asp Gly Val Leu Leu
      245              250              255
Gly Glu Pro Leu Arg Ser Gly Glu Gly Glu Val Ile Ala Asp Leu Asp
      260              265              270
Phe Thr Leu Ile Asp Lys Arg Lys Gln Met Met Asp Ser Arg Gly His
      275              280              285
Tyr Ala Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Ala Thr
      290              295              300
Ala His Val His Glu Arg Ser Ala His Pro Lys Ala Thr Ala Glu Gln
305              310              315              320
Ala Asp Gly Pro Ser Ala Val Asn Ala Gln
      325              330

```

<210> 319
 <211> 1017
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 319
atgacgaccc cgcgtatcgt ccgcgtcgcc gcggtgcaga tggcgcccga cctggaatcc      60
gcacacggca cggtagacaa ggtctgccgc gccattcttg aggccggcga aaaagcgcg      120
cgcatggtgg tctttcccga gaccttcgtg ccctactacc cctacttctc cttcatccag      180
ccggcggtga cgatggggcg cgcacacctc gagctctacg agcgcgcggt gacggtgccc      240
ggcccggtca ccctggccgt gggcgaagcg gcgcggcggg cgggcgcggt cgctcgtgctc      300
ggcgtcaatg aacgcgacca cggctcgctc tacaacaccc agctgatctt cgacgagacc      360
ggcgcgctgg tgctcaagcg ccgcaagctc accccgacct atcacgagcg catggtgtgg      420
ggccagggcg atggcagcgg tctcaagggt gtggacaccg gcatcggccg catcggcgcg      480
ctggcctgct gggagcacta caaccgctc gcccgctaca ccctgatggc gcagcatgaa      540
gagatccacg ccgcgcagtt ccccggttcc atggtcggcc agatctttgc cgaccagatg      600
gcggtgacca tccgccacca cgcgctggaa tccggtgctg tcgtggtgaa cgccaccggc      660
tggtcaccg atgcgagat caccgccatc acccccgacc cggccatgca gcgcgcgctg      720
cgcgcgcggt gccacaccgc catcgtgtcg ccggaaggca gctacgtctg cgaaccgctc      780
accgagggcg aaggcatgct ggtggccgac ctcgacatgc ggctggtcac caagcgcaag      840
cggatgatgg attcggctcg ccaactacgc cggccggagc tgctttcgct caacgccgat      900
cttgccccc agccggcgct gcacacacag ccggtgcgt ccctccctct ctccttcag      960
gcaggagccg accatgtcga cgacgaccgc accgcgtccg caacagctga tctctga      1017

```

<210> 320
 <211> 338
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 320
Met Thr Thr Pro Arg Ile Val Arg Val Ala Ala Val Gln Met Ala Pro
1              5              10              15
Asp Leu Glu Ser Ala His Gly Thr Val Asp Lys Val Cys Arg Ala Ile
      20              25              30
Leu Glu Ala Gly Glu Lys Gly Ala Arg Met Val Val Phe Pro Glu Thr
      35              40              45
Phe Val Pro Tyr Tyr Pro Tyr Phe Ser Phe Ile Gln Pro Ala Val Thr
      50              55              60
Met Gly Ala Ala His Leu Glu Leu Tyr Glu Arg Ala Val Thr Val Pro

```

[illegible]

ggctccgagg atgtgttcga ggctcgcat taa

993

<210> 322

<211> 330

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 322

```

Met Arg Val Val Lys Ala Ala Ala Val Gln Leu Ser Pro Val Leu His
 1           5           10           15
Ser Arg Asp Gly Thr Val Glu Lys Val Val Arg Lys Ile His Glu Leu
 20           25           30
Ala Glu Glu Gly Val Glu Phe Ala Thr Phe Pro Glu Thr Val Val Pro
 35           40           45
Tyr Tyr Pro Tyr Phe Ser Phe Val Gln Thr Pro Leu Gln Gln Ile Phe
 50           55           60
Gly Thr Glu Tyr Leu Arg Leu Leu Asp Gln Ala Val Thr Val Pro Ser
 65           70           75           80
Ala Ala Thr Asp Ala Ile Gly Glu Ala Ala Arg Trp Ala Gly Leu Val
 85           90           95
Val Ser Ile Gly Val Asn Glu Arg Asp Gly Gly Thr Leu Tyr Asn Thr
100          105          110
Gln Leu Leu Phe Asp Ala Asp Gly Ser Leu Ile Gln Arg Arg Lys
115          120          125
Ile Thr Pro Thr His Tyr Glu Arg Met Ile Trp Gly Gln Gly Asp Gly
130          135          140
Ser Gly Leu Arg Ala Val Asp Ser Lys Ala Gly Arg Ile Gly Gln Leu
145          150          155          160
Ala Cys Trp Glu His Asn Asn Pro Leu Ala Arg Tyr Ala Leu Met Ala
165          170          175
Asp Gly Glu Gln Ile His Ser Ala Met Tyr Pro Gly Ser Met Phe Gly
180          185          190
Asp Ser Phe Ser Gln Lys Thr Glu Ile Asn Ile Arg Gln His Ala Leu
195          200          205
Glu Ser Ala Cys Phe Val Val Asn Ala Thr Ala Trp Leu Asp Ala Asp
210          215          220
Gln Gln Ala Gln Ile Met Lys Asp Thr Gly Cys Gly Ile Gly Pro Ile
225          230          235          240
Ser Gly Gly Cys Phe Thr Ala Ile Val Ala Pro Asp Gly Ser Leu Leu
245          250          255
Gly Glu Pro Ile Arg Ser Gly Glu Gly Val Val Val Ala Asn Leu Asp
260          265          270
Phe Thr Leu Ile Asp Arg Arg Lys Gln Val Met Asp Ser Arg Gly His
275          280          285
Tyr Ser Arg Pro Glu Leu Leu Ser Leu Leu Ile Asp Arg Thr Pro Thr
290          295          300
Ala His Val His Glu Arg Ala Thr His Pro Thr Thr Gly Ala Glu Gln
305          310          315          320
Gly Ser Glu Asp Val Phe Glu Ala Arg Ile
325          330

```

<210> 323

<211> 951

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 323
 atgagcaacg tgaagtcgc ggtcgtgcaa cgcgcgccgg tgttcggcaa ccgcgccgcc 60
 accctcgatc gcgcgctcgc cgcgctggcc gaagcggcgc agcagggggc gaagctggtc 120
 gtgatgcccg agcacttcat ccccggtac cgcgctgga tctggcgctt gcgtccgggc 180
 accgacctgc gattgtgcga acagctgcac gcgatgctgc gcgccaacgc cgtgaggctg 240
 gatgacggtg acctggcccc gttgaccgag gccgcgcagc ggcatgcgct caccgtggtc 300
 tgcggcgctt gcgagatcga caccgaattc agtcgcggca ccctgtacaa caccgtggtc 360
 gtgatcgggc ccgacggcac gctgctcaac cggcatcgca agctgatgcc caccaacccc 420
 gagcgcatgg tctggggcat gggcgacgcc accgggctga aggtggctga cagccctgc 480
 gggcgcatcg gcacgtgat ttgctgggag aactacatgc cattcgcacg cgccgcgctg 540
 tacgcgcagg gggctgaggt cctggttgca ccgacctacg acgaaggccc ggtatggctg 600
 gcgtcgatgc agcacatcgc ccgcgaaggc ggctgctggg tggtagggcaa cggctgcgca 660
 ttccagggcc gcgacatgcc ggacaccttg ccgggcaagg ccagctgtt tcccagggcc 720
 gacgcctggg tcaacgccgg ggactcggtc atcgtcgcgc caggcgcccg gacagtggcg 780
 ggtccgttgc acgaggcgtt cgggctgttc accgccgaga tcgacctctc ccgggtcgga 840
 atggcccgcc gcagcctgga tgtggccggg cactatggac ggcccagcat cttctgcctg 900
 caggtcaacg cccgggcgca gccgccggtt gaggtgacgc accatggctg a 951

<210> 324
 <211> 316
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 324
 Met Ser Asn Val Lys Val Ala Val Val Gln Arg Ala Pro Val Phe Gly
 1 5 10 15
 Asn Arg Ala Ala Thr Leu Asp Arg Ala Val Ala Ala Leu Ala Glu Ala
 20 25 30
 Ala Gln Gln Gly Ala Lys Leu Val Val Met Pro Glu His Phe Ile Pro
 35 40 45
 Gly Tyr Pro Ala Trp Ile Trp Arg Leu Arg Pro Gly Thr Asp Leu Arg
 50 55 60
 Leu Cys Glu Gln Leu His Ala Met Leu Arg Ala Asn Ala Val Arg Leu
 65 70 75 80
 Asp Asp Gly Asp Leu Ala Pro Leu Thr Glu Ala Ala Gln Arg His Ala
 85 90 95
 Leu Thr Val Val Cys Gly Val Cys Glu Ile Asp Thr Glu Phe Ser Arg
 100 105 110
 Gly Thr Leu Tyr Asn Thr Val Val Val Ile Gly Pro Asp Gly Thr Leu
 115 120 125
 Leu Asn Arg His Arg Lys Leu Met Pro Thr Asn Pro Glu Arg Met Val
 130 135 140
 Trp Gly Met Gly Asp Ala Thr Gly Leu Lys Val Val Asp Thr Pro Cys
 145 150 155 160
 Gly Arg Ile Gly Thr Leu Ile Cys Trp Glu Asn Tyr Met Pro Phe Ala
 165 170 175
 Arg Ala Ala Leu Tyr Ala Gln Gly Val Glu Val Leu Val Ala Pro Thr
 180 185 190
 Tyr Asp Glu Gly Pro Val Trp Leu Ala Ser Met Gln His Ile Ala Arg
 195 200 205
 Glu Gly Gly Cys Trp Val Val Gly Asn Gly Cys Ala Phe Gln Gly Arg
 210 215 220
 Asp Met Pro Asp Thr Leu Pro Gly Lys Ala Gln Leu Phe Pro Glu Ala
 225 230 235 240
 Asp Ala Trp Val Asn Ala Gly Asp Ser Val Ile Val Ala Pro Gly Gly
 245 250 255
 Arg Thr Val Ala Gly Pro Leu His Glu Ala Phe Gly Leu Phe Thr Ala

260 265 270
 Glu Ile Asp Leu Ser Arg Val Gly Met Ala Arg Arg Ser Leu Asp Val
 275 280 285
 Ala Gly His Tyr Gly Arg Pro Asp Ile Phe Cys Leu Gln Val Asn Ala
 290 295 300
 Arg Ala Gln Pro Pro Val Glu Val Thr His His Gly
 305 310 315

<210> 325

<211> 1077

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 325

```

atgactgcaa aaaagattgt ccgcgccgcc gctgtccagc tcaatcccgt gctggacagc      60
gccgacggca cccttgtgaa agtgttgacg gcgattgccg acgccgcagc gcagggcggtg      120
caactgatcg tctttcccgga gacgggtggtg ccctactatc cttacttttc cttcgtcacg      180
cctgcggttt cgatggggcg ggcgcatctg aaactgtacg aacaatcgcc cacggtgcca      240
ggtccactga ccgacgccgt cgccgcagcc gcgcggggcac atcagatggt ggttgtgtctc      300
ggcgtcaacg agcgcgatca cggcacgctc tacaacacgc aactgatctt cgacgccgac      360
ggcacgctcc cactgaagcg tcgcaagatc acgccgacct atcacgagcg catggtctgg      420
ggcatgggag atggctccgg cctgcgcacg gtgaagaccg aggtcggaac cgttggcgcg      480
ctggcctgct gggaaacact caaccgcgtg gcacgctacg cgctgatggc gcagcacgaa      540
gagatccatt gcagccagtt ccccggtctg ctggtcggcc cgatcttttc cgagcagatg      600
gaaatcacca tgcgtcatca cgcgctgga tccggctgct tcgctcgtaa cgccactgca      660
tggtgacgac ctgagcaggt gcgatcacag gcgccaacac cggcaatgga aaaagccttc      720
tccggtggtt gctacaccgc gatcatttgc ccggaaggaa aacatctggg cgaacctctt      780
cgcgacggcg aaggcatggt catcgccgat cttgatcttg atctcatcac caagcgcaag      840
cgaatgatgg attcggttgg cactacgca cggccggaat tgttgagcct gcagctcgac      900
aaccgatcaa ctgcaccgct gacaacgctc ccggtggccg ccgcagcgcc gtcgcttgca      960
gagatggaag cacagcgctt gtcacgttat ctcgatgcca gctccggcag cgccgcacaa     1020
ggcatcgaag ccgcctacat caatgccctc agctcttttt caggaaaacc ctcatga     1077
  
```

<210> 326

<211> 358

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 326

```

Met Thr Ala Lys Lys Ile Val Arg Ala Ala Val Gln Leu Asn Pro
 1          5          10          15
Val Leu Asp Ser Ala Asp Gly Thr Leu Val Lys Val Leu Gln Ala Ile
 20          25          30
Ala Asp Ala Ala Gln Gly Val Gln Leu Ile Val Phe Pro Glu Thr
 35          40          45
Val Val Pro Tyr Tyr Pro Tyr Phe Ser Phe Val Thr Pro Ala Val Ser
 50          55          60
Met Gly Ala Ala His Leu Lys Leu Tyr Glu Gln Ser Pro Thr Val Pro
 65          70          75          80
Gly Pro Leu Thr Asp Ala Val Ala Ala Ala Arg Ala His Gln Met
 85          90          95
Val Val Val Leu Gly Val Asn Glu Arg Asp His Gly Thr Leu Tyr Asn
100          105          110
Thr Gln Leu Ile Phe Asp Ala Asp Gly Thr Leu Pro Leu Lys Arg Arg
115          120          125
  
```

Lys Ile Thr Pro Thr Tyr His Glu Arg Met Val Trp Gly Met Gly Asp
 130 135 140
 Gly Ser Gly Leu Arg Thr Val Lys Thr Glu Val Gly Thr Val Gly Ala
 145 150 155 160
 Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met
 165 170 175
 Ala Gln His Glu Glu Ile His Cys Ser Gln Phe Pro Gly Ser Leu Val
 180 185 190
 Gly Pro Ile Phe Ser Glu Gln Met Glu Ile Thr Met Arg His His Ala
 195 200 205
 Leu Glu Ser Gly Cys Phe Val Val Asn Ala Thr Ala Trp Leu Thr Pro
 210 215 220
 Glu Gln Val Arg Ser Gln Ala Pro Thr Pro Ala Met Glu Lys Ala Phe
 225 230 235 240
 Ser Gly Gly Cys Tyr Thr Ala Ile Ile Ser Pro Glu Gly Lys His Leu
 245 250 255
 Gly Glu Pro Leu Arg Asp Gly Glu Gly Met Val Ile Ala Asp Leu Asp
 260 265 270
 Phe Asp Leu Ile Thr Lys Arg Lys Arg Met Met Asp Ser Val Gly His
 275 280 285
 Tyr Ala Arg Pro Glu Leu Leu Ser Leu Gln Leu Asp Asn Arg Ser Thr
 290 295 300
 Ala Pro Leu Thr Thr Ser Pro Val Ala Ala Ala Pro Ser Leu Ala
 305 310 315 320
 Glu Met Glu Ala Gln Arg Leu Ser Arg Tyr Leu Asp Ala Ser Ser Gly
 325 330 335
 Ser Ala Ala Gln Gly Ile Glu Ala Ala Tyr Ile Asn Ala Leu Ser Ser
 340 345 350
 Phe Ser Gly Lys Pro Ser
 355

<210> 327

<211> 975

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 327

atggttgatc	aaataacttaa	cgatcgttct	gaattattaa	cagttgggtt	ggcgcagatt	60
gctccaatct	ggctgaaccg	cgaaaaaaca	cttgcgaaag	tggttgagaa	agtaaatcaa	120
gctgcaaagc	aagattgtca	tcttgttgct	tttgggtgaag	ctttgggtccc	cggatatccc	180
ttttggattg	aacttacaga	tggcgcgcga	ttcaactcca	atgttcacaaa	agaaattcac	240
gcgcactata	tggatcaggc	agtacagata	gagaatggtc	atttaaaagc	gctttgtgaa	300
acatcggccg	caaacaagat	tgccgtgatc	gttgggtgca	ttgaacgcgc	agccgatcgc	360
ggcgggcaca	gcttatatgc	ttcattggtt	tttattaatc	ctcaagggca	aatcggatcg	420
gtgcatcgca	aacttatgcc	aacttatgaa	gaacgtttta	cctgggtcacc	tggcgatgga	480
catggtttgc	gaacgcatca	actaggtgct	ttcactgttg	gcggcttgaa	ttgttgggaa	540
aactggatgc	cattgccacg	cgccgcattg	tacgcacaag	gtgaagactt	tcatgtcgca	600
atctggccgg	gaagcattca	caatacgcaa	gatattacgc	gctatattgc	gaaggaaatcc	660
agatcgtttg	taatgtctac	ttccgggttc	atgcgtaaaag	aagactttcc	atctgatacg	720
cctcaacttag	acaaaatact	tgcaaaactct	ccgaatgtac	ttgcaaatgg	tggtacctgt	780
ctcgccggac	cggacggtca	gtggatcggt	gaaccatttg	tgaatgagga	aaaattagtt	840
gttgcgactg	tgaaccacaa	gcagggtccgt	gaagaaagac	aaaattttga	tccggtcgga	900
cactattccc	gtcctgatgt	cacgcagttg	attgtgaaca	gacaaagaca	atcaacaatc	960
aagctcaacg	attaa					975

<210> 328

<211> 324

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 328

```

Met Val Asp Gln Ile Leu Asn Asp Arg Ser Glu Leu Leu Thr Val Gly
 1           5           10           15
Leu Ala Gln Ile Ala Pro Ile Trp Leu Asn Arg Glu Lys Thr Leu Ala
 20           25           30
Lys Val Val Glu Lys Val Asn Gln Ala Ala Lys Gln Asp Cys His Leu
 35           40           45
Val Ala Phe Gly Glu Ala Leu Val Pro Gly Tyr Pro Phe Trp Ile Glu
 50           55           60
Leu Thr Asp Gly Ala Arg Phe Asn Ser Asn Val Gln Lys Glu Ile His
 65           70           75           80
Ala His Tyr Met Asp Gln Ala Val Gln Ile Glu Asn Gly His Leu Lys
 85           90           95
Ala Leu Cys Glu Thr Ser Ala Ala Asn Lys Ile Ala Val Ile Val Gly
100           105           110
Cys Ile Glu Arg Ala Ala Asp Arg Gly Gly His Ser Leu Tyr Ala Ser
115           120           125
Leu Val Phe Ile Asn Pro Gln Gly Gln Ile Gly Ser Val His Arg Lys
130           135           140
Leu Met Pro Thr Tyr Glu Glu Arg Leu Thr Trp Ser Pro Gly Asp Gly
145           150           155           160
His Gly Leu Arg Thr His Gln Leu Gly Ala Phe Thr Val Gly Gly Leu
165           170           175
Asn Cys Trp Glu Asn Trp Met Pro Leu Pro Arg Ala Ala Leu Tyr Ala
180           185           190
Gln Gly Glu Asp Phe His Val Ala Ile Trp Pro Gly Ser Ile His Asn
195           200           205
Thr Gln Asp Ile Thr Arg Tyr Ile Ala Lys Glu Ser Arg Ser Phe Val
210           215           220
Met Ser Thr Ser Gly Phe Met Arg Lys Glu Asp Phe Pro Ser Asp Thr
225           230           235           240
Pro His Leu Asp Lys Ile Leu Ala Asn Ser Pro Asn Val Leu Ala Asn
245           250           255
Gly Gly Ser Cys Leu Ala Gly Pro Asp Gly Gln Trp Ile Val Glu Pro
260           265           270
Phe Val Asn Glu Glu Lys Leu Val Val Ala Thr Val Asn His Lys Gln
275           280           285
Val Arg Glu Glu Arg Gln Asn Phe Asp Pro Val Gly His Tyr Ser Arg
290           295           300
Pro Asp Val Thr Gln Leu Ile Val Asn Arg Gln Arg Gln Ser Thr Ile
305           310           315           320
Lys Leu Asn Asp

```

<210> 329

<211> 1023

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 329

```

gtgccggcca aagtacgcgc cgccgccgtg cagctcagcc ccgtgctctt cagccgtgaa      60
ggcacgacca gcaaggtctg cgacaagatt gccgaggcgg cggcgaggg cgccgagctg      120
gtggtgtttc ccgaaaccgt agtgccgtat taccgtatt tctcgttcat caaggctccg      180

```



```

gccgtgatcg ggcgcgagca cttactcttg ctcgaacaag ccgtcacggt gcccgggccc 240
agcgtcgaag ccacgcgaga agccgctcgc aaggcgggcg cgggtggttc gatcggcgctc 300
aacgaacgcg atcacggcac gctgtacaac acccagctgt tgttcgacgc cgacggtcgg 360
ttggcgcaag cccgcccga gacaccccc acgtatcacg agcggatgat ctgggggcag 420
ggcgatggct cgggcttggt ggcggtggat acgcgagtcg gcaggattgg ctccctggcg 480
tgctgggagc actacaaccc gctggctcgc tatgcgctga tggccgacca cgagcaaatt 540
cacgtggcca tgttccttg ctcgctcgtg ggcgacatct tccgcgagca aatcgaggtc 600
acgattcggc accacgcgct cgagtcgggc tgcttcgctg tcaacgcgac gggctacctg 660
agcgacgcgc aggtgacgca gatcgcgggc gacaccaagc tcgaccgcgc cctgcgcggc 720
ggttgcttca ccgccatcgt atcgcccag ggcacgctgc tggcgccacc gctcaccgac 780
ggtgagggca tggtcattgc cgacctcgat ctgtcgctca tcgccaacac caaacgcatg 840
atggacagcg tcggccatta cagccggccc gagctgctca gcgtgctgat cgaccgctcg 900
ccgcagccgc atttgcgcga gaaaactgcc tctttaccgc aacctcggat gtcccatgaa 960
tcgctcgctc ccgatagtaa cggcctccgc gacgctgacg cgaaagcctc gaccctctcc 1020
tga 1023

```

<210> 330

<211> 340

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 330

```

Val Pro Ala Lys Val Arg Ala Ala Val Gln Leu Ser Pro Val Leu
1      5      10      15
Phe Ser Arg Glu Gly Thr Thr Ser Lys Val Cys Asp Lys Ile Ala Glu
20     25     30
Ala Ala Ala Gln Gly Ala Glu Leu Val Val Phe Pro Glu Thr Val Val
35     40     45
Pro Tyr Tyr Pro Tyr Phe Ser Phe Ile Lys Ala Pro Ala Val Ile Gly
50     55     60
Ala Glu His Leu Leu Leu Leu Glu Gln Ala Val Thr Val Pro Gly Pro
65     70     75     80
Ser Val Glu Ala Ile Ala Glu Ala Ala Arg Lys Ala Gly Ala Val Val
85     90     95
Ser Ile Gly Val Asn Glu Arg Asp His Gly Thr Leu Tyr Asn Thr Gln
100    105    110
Leu Leu Phe Asp Ala Asp Gly Arg Leu Ala Gln Ala Arg Arg Lys Ile
115    120    125
Thr Pro Thr Tyr His Glu Arg Met Ile Trp Gly Gln Gly Asp Gly Ser
130    135    140
Gly Leu Val Ala Val Asp Thr Arg Val Gly Arg Ile Gly Ser Leu Ala
145    150    155    160
Cys Trp Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met Ala Asp
165    170    175
His Glu Gln Ile His Val Ala Met Phe Pro Gly Ser Leu Val Gly Asp
180    185    190
Ile Phe Arg Glu Gln Ile Glu Val Thr Ile Arg His His Ala Leu Glu
195    200    205
Ser Gly Cys Phe Val Val Asn Ala Thr Gly Tyr Leu Ser Asp Ala Gln
210    215    220
Val Thr Gln Ile Ala Gly Asp Thr Lys Leu Asp Arg Ala Leu Arg Gly
225    230    235    240
Gly Cys Phe Thr Ala Ile Val Ser Pro Glu Gly Thr Leu Leu Ala Pro
245    250    255
Pro Leu Thr Asp Gly Glu Gly Met Val Ile Ala Asp Leu Asp Leu Ser
260    265    270
Leu Ile Ala Lys Arg Lys Arg Met Met Asp Ser Val Gly His Tyr Ser
275    280    285

```

Arg Pro Glu Leu Leu Ser Val Leu Ile Asp Arg Ser Pro Gln Pro His
 290 295 300
 Leu Arg Glu Lys Thr Ala Ser Leu Pro Glu Pro Arg Met Ser His Glu
 305 310 315 320
 Ser Leu Ala Pro Asp Ser Asn Gly Leu Arg Asp Ala Asp Ala Lys Ala
 325 330 335
 Ser Thr Leu Ser
 340

<210> 331

<211> 1041

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 331

```

atgtccggaa caggacctat cggaccgggc gtgaaggctc ccgtcgtaca agccgcgcca      60
tgtctgctcg atcttgatgc gggcgctcgag aaggcgatcg ccttgatcga ccaagcgggc      120
aaggctggcg cgcggctcat caattttccc gaaatttggc tgccggggtta tccttggtgg      180
atctggctga atccaccgcg catcaacatg cagtatgtcg cgccttacat gaacaactcc      240
attgtcgcag gcagcaagca tgaccacgca cttcgggccc ccgcgcgcgc caacaatatt      300
cacgtcgtga tcggtgtctc cgagcgcgcc ggcggcagtc tgtacatggc tcagtggcac      360
tatgggcccc agggcgaggt gatctcgcgt cgtcgtaagc taaaaccac ccatgtcgaa      420
cgcagcgtct ttggcgaagg cgacggcagc gacatgatcg ttactcagac cgatttcggg      480
cgcgtcggcg cgctatgctg ttgggaacac ctgcaaccgc tgtcgaaata cgcgctcttt      540
tcccaggacg agcagattca ttgcgcggcg tggcccgctt tcagcctcta tgcaaaactc      600
tcgaagccct tcagccccga agtcagcgtc aacgtgaacc aaatctacgc cgtagaaggg      660
caatgcttcg tcctgtcgtc gtgctcgggt atcgatcagg cgatctacga caggttggtg      720
cagaacgaat tgaccagaaa gttcctcgag gtggcggggg gctacagccg aatcttcggg      780
ccgaacggtg cggaaattcg tgagaatctc ccaccgata gggaaggcct ggtggttgcc      840
gatatcgatc tcggcctgat ctgcactcc aagagtgccg ctgatccggc tggtcactac      900
gcgaggggccc acgctctggc gctcatgcat aaccgtaatc cccgccgtcc ggttatcggt      960
ttcggcgagg cgacgcgcaa gggtgccgac gcactgccta aaggcgcgga acccgcgga      1020
gcgctcgaag cggccgagtg a                                     1041

```

<210> 332

<211> 346

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 332

```

Met Ser Gly Thr Gly Pro Ile Gly Pro Val Val Lys Val Ala Val Val
  1      5      10      15
Gln Ala Ala Pro Cys Leu Leu Asp Leu Asp Ala Gly Val Glu Lys Ala
  20      25      30
Ile Ala Leu Ile Asp Gln Ala Gly Lys Ala Gly Ala Arg Leu Ile Asn
  35      40      45
Phe Pro Glu Ile Trp Leu Pro Gly Tyr Pro Trp Trp Ile Trp Leu Asn
  50      55      60
Pro Pro Ala Ile Asn Met Gln Tyr Val Ala Pro Tyr Met Asn Asn Ser
  65      70      75      80
Ile Val Ala Gly Ser Lys His Asp His Ala Leu Arg Ala Ala Ala Arg
  85      90      95
Arg Asn Asn Ile His Val Val Ile Gly Val Ser Glu Arg Ala Gly Gly
  100     105     110
Ser Leu Tyr Met Ala Gln Trp His Tyr Gly Pro Glu Gly Glu Val Ile

```

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 334

```

Met Ala Ile Glu His Pro Arg Tyr Arg Val Ala Ala Val Gln Ala Ala
 1          5          10          15
Pro Glu Phe Leu Asn Leu Glu Ala Thr Val Asp Lys Thr Ile Ala Leu
 20          25          30
Ile Glu Glu Ala Ala Arg Gly Gly Ala Ser Leu Ile Ala Phe Pro Glu
 35          40          45
Thr Trp Ile Pro Gly Tyr Pro Trp Phe Ala Trp Leu Gly Ala Pro Ile
 50          55          60
Trp Gly Met Lys Phe Ile Gln Ala Tyr His Asp Asn Ser Met Val Ile
 65          70          75          80
Asp Gly Ala Gln Phe Glu Arg Ile Ala Gln Ala Ala Ser Arg Cys Asn
 85          90          95
Ile Thr Val Val Leu Gly Phe Ser Glu Lys Asp Ala Gly Ser Leu Tyr
100          105          110
Ile Ala Gln Ala Ile Leu Ser Pro Glu Gly Lys Thr Ile Ala Thr Arg
115          120          125
Arg Lys Leu Lys Pro Thr His Val Glu Arg Ala Ile Phe Gly Glu Gly
130          135          140
Asp Gly Ser Asp Leu Ala Val His Asp Thr Lys Leu Gly Arg Val Gly
145          150          155          160
Ala Leu Cys Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr Ala Met
165          170          175
Tyr Ala Gln Asn Glu Gln Val His Ile Ala Ala Trp Pro Ser Phe Ser
180          185          190
Leu Tyr Val Asp Ala Ala Tyr Ala Leu Gly Pro Glu Val Asn Asn Ala
195          200          205
Ala Ser Arg Leu Tyr Ala Val Glu Gly Gln Cys Phe Val Val Ala Pro
210          215          220
Cys Ala Thr Val Ser Gln Lys Met Ile Asp Met Leu Cys Glu Thr Pro
225          230          235          240
Glu Gln Gln Ala Leu Leu Lys Pro Gly Gly Gly His Ala Gln Ile Tyr
245          250          255
Gly Pro Asp Gly Arg Ser Leu Ala Asp Pro Leu Pro Pro Asp Ala Glu
260          265          270
Gly Leu Leu Tyr Ala Asp Ile Asp Leu Ala Ala Ile Thr Leu Ala Lys
275          280          285
Ala Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val Thr Gln
290          295          300
Leu Leu Leu Asp Arg Asn Pro Lys Pro Arg Val Val His Ala Lys Pro
305          310          315          320
Gly Gln Ser Ala Asn Asn Ser Ser Pro Gly Met Arg Ala Val Glu His
325          330          335
Thr Glu Leu Glu Gly Glu Gln Ala
340          345

```

<210> 335

<211> 1053

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 335

atgactacgc gcgtgattaa agtcgctgcc gcgcagctgt ctccggtgct ggcaactgca

60

```

tcggagcaca gccgcgagga cacgattgcg aaagtgatcg acgccatcgc tgcggcgctcg      120
caacagggcg cgcaactgat tgtgtttccg gaaacagtcg ttccgtatta cccgtatttt      180
tcatttatca cgcccgcggt aacgatgggt gccgaacatt tgaaattgta cgaacaggca      240
gtgacgggtac ccagcgcagc gacagatgct gtcgctgcgg cggcaaaaaa ttatggcatg      300
gtagtgggtgc tcggaattaa tgaacgcgat cacggctcgc tgtacaacgc gcaattaatt      360
ttcgacgccg atggtgagct gctattaaag cgtcgaaaaa ttacgccgac ttatcacgaa      420
cgcatgggtgt ggggacaagg cgacggcagc ggtttaaaag ttgtcgatac tgctgccggc      480
cgtgtcggcg cgctcgcgtg ctgggaacat tacaaccgcg tcgcgcgtta cagcctgatg      540
gcacaacacg aagaaattca ttgcagtcaa tttccgggat cgttggtcgg ccctattttc      600
gccgaacaaa tggaaatcac catgcgtcat cacgcactcg aatccggctg ttttgtggtg      660
aatgcaacgg cctggccttag cgatacacia atccaatcaa ttacccccga taaagccatg      720
cagaaagcac tgcgcggcgg ttgctacacc gcaatcatct cgcccgaagg caaacatctg      780
tgcccaccgc tgtatgacgg agaaggaata attgtggcgg aattggactt cgcgttaaat      840
accaaacgta aacgcatgat ggattccgtc ggccattacg cgcgaccaga actactttct      900
ttgctcctcg atgatcgct aactgcgcgg ctcaaaaact tacagacgac gatggcctct      960
gccaaatccg ctgaagatgg ttttccttta ttgcagacg ttttatatcc agacagtctt     1020
ttcattgaga cgtcgaaatt cgcgagtgca tga                                     1053

```

<210> 336

<211> 350

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 336

```

Met Thr Thr Arg Val Ile Lys Val Ala Ala Ala Gln Leu Ser Pro Val
 1          5          10          15
Leu Ala Thr Ala Ser Glu His Ser Arg Glu Asp Thr Ile Ala Lys Val
          20          25          30
Ile Asp Ala Ile Ala Ala Ala Ser Gln Gln Gly Ala Gln Leu Ile Val
          35          40          45
Phe Pro Glu Thr Val Val Pro Tyr Tyr Pro Tyr Phe Ser Phe Ile Thr
          50          55          60
Pro Ala Val Thr Met Gly Ala Glu His Leu Lys Leu Tyr Glu Gln Ala
65          70          75          80
Val Thr Val Pro Ser Ala Ala Thr Asp Ala Val Ala Ala Ala Lys
          85          90          95
Asn Tyr Gly Met Val Val Val Leu Gly Ile Asn Glu Arg Asp His Gly
          100          105          110
Ser Leu Tyr Asn Ala Gln Leu Ile Phe Asp Ala Asp Gly Glu Leu Leu
          115          120          125
Leu Lys Arg Arg Lys Ile Thr Pro Thr Tyr His Glu Arg Met Val Trp
          130          135          140
Gly Gln Gly Asp Gly Ser Gly Leu Lys Val Val Asp Thr Ala Ala Gly
145          150          155          160
Arg Val Gly Ala Leu Ala Cys Trp Glu His Tyr Asn Pro Leu Ala Arg
          165          170          175
Tyr Ser Leu Met Ala Gln His Glu Glu Ile His Cys Ser Gln Phe Pro
          180          185          190
Gly Ser Leu Val Gly Pro Ile Phe Ala Glu Gln Met Glu Ile Thr Met
          195          200          205
Arg His His Ala Leu Glu Ser Gly Cys Phe Val Val Asn Ala Thr Ala
          210          215          220
Trp Leu Ser Asp Thr Gln Ile Gln Ser Ile Thr Pro Asp Lys Ala Met
225          230          235          240
Gln Lys Ala Leu Arg Gly Gly Cys Tyr Thr Ala Ile Ile Ser Pro Glu
          245          250          255
Gly Lys His Leu Cys Pro Pro Leu Tyr Asp Gly Glu Gly Ile Ile Val
          260          265          270

```

Ala Glu Leu Asp Phe Ala Leu Ile Thr Lys Arg Lys Arg Met Met Asp
 275 280 285
 Ser Val Gly His Tyr Ala Arg Pro Glu Leu Leu Ser Leu Leu Leu Asp
 290 295 300
 Asp Arg Val Thr Ala Pro Leu Lys Asn Leu Gln Thr Thr Met Ala Ser
 305 310 315 320
 Ala Lys Ser Ala Glu Asp Gly Phe Pro Leu Phe Ala Asp Val Leu Tyr
 325 330 335
 Pro Asp Ser Ser Phe Ile Glu Thr Ser Lys Phe Ala Glu Ser
 340 345 350

<210> 337

<211> 957

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 337

```

atgaagggag tgtgtgccat gtcgacgaaa gttgccatcg tccaggcgcc gccggtcctg      60
ctgcatcgcg acaggacgat tgcgaagggtg cgttcgtcga tcgaggatgc cgccaatgcg      120
ggcgctcgcg tgatcgtatt tcccgaagct tatgtaccgc gctatccgag ttggatctgg      180
cgtctcaggc ccggaggcga catgggactg tcgtctgaga ttcacgcaag attgcgggaa      240
aatgccgttg atctcgcgaa cggaggcctg gcgcattgcc agggggctgc agcaaaattc      300
ggcgcgactg tcgttatcgg catcaatgaa ctcgacagcg agttcagcgg aacgacattg      360
ttcaacaccg tgggtgtcat cggccccgac ggaacgcgcc tcaacaggca tcgaaaatta      420
atgccgacca acccgagcg catggtgtgg ggcacgggcg atgcctcggg tctgctgtgc      480
atcgatacgc cggcgggacg gctgggaacc atgatctgct gggagagcta catgccgctg      540
gcgcgctatg ctctctatgc gcaaggcatc gagatatacg tcgctcccac gtgggacgca      600
ggcgagagct ggattgctac gatcgccac atcgccaagg aggccggctg ctgggtgatc      660
ggcacggcaa ccgtcatcca gggcagcgat gttccggacg atttcccgga acgcgacaag      720
ctcttcaagc cggaggagtg gatcaacgac ggcgatgcgg tcgtggtcaa gcccattggc      780
gcgattgctg ccggaccgca caatcgacag aaaagcatac tctacgccga catcgaccgg      840
gaggccgcgc ggcgagcccg ccggtcgctc gatgtctgtg gccactattc ccgccagacg      900
gttttctctt tctcgggtcaa ccgaaagcca ttccgccctg ccgactttgt gggttga      957

```

<210> 338

<211> 313

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 338

Met Lys Gly Val Cys Ala Met Ser Thr Lys Val Ala Ile Val Gln Ala
 1 5 10 15
 Pro Pro Val Leu Leu His Arg Asp Gly Arg Leu Arg Arg Cys Val Arg
 20 25 30
 Arg Ser Arg Met Pro Pro Met Arg Ala Pro Arg Ser Tyr Phe Pro Ala
 35 40 45
 Tyr Val Pro Gly Tyr Pro Ser Trp Ile Trp Arg Leu Arg Pro Gly Gly
 50 55 60
 Asp Met Gly Leu Ser Ser Glu Ile Thr Gln Asp Cys Gly Lys Met Pro
 65 70 75 80
 Leu Ile Ser Arg Thr Glu Ala Trp Arg Met Ser Arg Gly Leu Gln Gln
 85 90 95
 Asn Ser Ala Arg Leu Ser Leu Ser Ala Ser Met Asn Ser Thr Ala Ser
 100 105 110
 Ser Ala Glu Arg His Cys Ser Thr Val Val Val Ile Gly Pro Asp Gly

```

      115      120      125
Thr Arg Leu Asn Arg His Arg Lys Leu Met Pro Thr Asn Pro Glu His
      130      135      140
Gly Val Gly His Gly Arg Cys Leu Gly Ser Ala Cys His Arg Tyr Ala
145      150      155      160
Gly Gly Thr Ala Gly Asn His Ile Cys Trp Glu Ser Tyr Met Pro Leu
      165      170      175
Ala Arg Tyr Ala Leu Tyr Ala Gln Gly Ile Glu Ile Tyr Val Ala Pro
      180      185      190
Thr Trp Asp Ala Gly Glu Ser Trp Ile Ala Thr Met Arg His Ile Ala
195      200      205
Lys Glu Ala Gly Cys Trp Val Ile Gly Thr Ala Thr Val Ile Gln Gly
210      215      220
Ser Asp Val Pro Asp Asp Phe Pro Glu Arg Asp Lys Leu Phe Lys Pro
225      230      235      240
Arg Ser Gly Ser Thr Thr Ala Met Arg Ser Trp Ser Ser Pro Trp Ala
      245      250      255
Arg Leu Leu Pro Asp Arg Thr Ile Asp Arg Lys Ala Tyr Ser Thr Pro
      260      265      270
Thr Ser Thr Gly Arg Pro Arg Gly Glu Pro Ala Gly Arg Ser Met Cys
      275      280      285
Gly His Tyr Ser Arg Pro Asp Val Phe Ser Phe Ser Val Asn Arg Lys
290      295      300
Pro Phe Arg Pro Ala Asp Phe Val Gly
305      310

```

<210> 339
 <211> 1020
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 339
atgtcaggat cattcaaagt tgcagcagtg caggcggctc cggccttcct caatctcgat      60
gcgggcatcg acaaggcggg ggcgctgac gagcaagccg ccgcgcagga cggttcagctc      120
atcgcccttc ccgagacctg gttgcccgga taccctgggt ggatctggct cgatgcaccc      180
gccgttacca tgggctatgt cgttccctac aatctcaatt cactagaggc gggcagcccg      240
caggacaagc gtctggcaaa tgccgcgctg gagaacaaca tccaggtggg gatgggtctg      300
tctgaacgcc atgacggcac gctctacatc gcgcagtggc actatggtga agatggcgag      360
gtgatctcgc gacggcgcaa gctcaagccg acccatgtcg aacgcacggg gttcggggaa      420
ggcgacggca gcgacatggt ggtcaaggac acaagtctgg gacgggtcgg cgctctgtgc      480
tgttggaac acctgcagcc gctcaacaaa tacgcgatgt actcccagaa cgagcagatc      540
cacatcggtt cctggcccag cttcagcctc tacaaggcgg gcgcctatgc gcttggggca      600
gacctcaaca cggcggcaag ccagatgtat gcggccgagg gccagtgtt tgttctggct      660
gcctgcgcca cggtcagtca ggacatgttc gacatgctct gcgacacgga aatgaagcag      720
cagttcctga ccaccggtgg cggattcgcc cgcattttcg gacctgacgg ctgcgccatg      780
ggcaatgtgc ttgaagaaca tgaagaaggg ctggtgatcg ccgaaatcga tctcaccatg      840
attgcgatcg ccaaggcggc ggctgacccg tgcgggcact attcccggcc cgatgtgttc      900
cgactgatgt tcaaccagaa gccaaagccc gtggtgatgc cattcgaaaa cgacgtggcc      960
cgcgagattg tcgaggccgc cgaggatcag gtcagcgcaa accggctcgc agcggaatga      1020

```

<210> 340
 <211> 329
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 340

```

Met Ser Gly Ser Phe Lys Val Ala Ala Val Gln Ala Ala Pro Ala Phe
 1          5          10          15
Leu Asn Leu Asp Ala Gly Ile Asp Gly Gly Gly Ala Asp Arg Ala Ser
 20          25          30
Arg Arg Ala Gly Arg Ser Ala His Arg Leu Ser Arg Asp Leu Val Ala
 35          40          45
Gly Tyr Pro Trp Trp Ile Trp Leu Asp Ala Pro Ala Val Thr Met Gly
 50          55          60
Tyr Val Val Pro Tyr Asn Leu Asn Ser Arg Gly Gly Gln Pro Ala Gly
 65          70          75          80
Gln Ala Ser Gly Lys Cys Arg Ala Glu Gln His Pro Gly Gly Asp Gly
 85          90          95
Leu Ser Glu Arg His Asp Gly Thr Leu Tyr Ile Ala Gln Trp His Tyr
100          105          110
Gly Glu Asp Gly Glu Val Ile Ala Thr Ala Gln Ala Gln Ala Asp Pro
115          120          125
Cys Arg Thr His Gly Val Arg Gly Arg Arg Arg Gln Arg His Val Val
130          135          140
Lys Asp Thr Ser Leu Gly Arg Val Gly Ala Leu Cys Cys Trp Glu His
145          150          155          160
Leu Gln Pro Leu Asn Lys Thr Arg Cys Thr Pro Arg Thr Ser Arg Ser
165          170          175
Thr Ser Val Pro Gly Pro Ala Ser Ala Ser Thr Arg Ala Ala Leu Cys
180          185          190
Ala Trp Gly Arg Pro Gln His Gly Gly Lys Pro Asp Val Cys Gly Arg
195          200          205
Gly Pro Val Leu Cys Ser Leu Pro Ala Pro Arg Ser Val Arg Thr Cys
210          215          220
Ser Thr Cys Ser Ala Thr Arg Lys Ser Ser Ser Thr Gly Gly Gly
225          230          235          240
Phe Ala Arg Ile Phe Gly Pro Asp Gly Ser Pro Met Gly Asn Val Leu
245          250          255
Glu Glu His Glu Arg Ala Gly Asp Arg Arg Asn Arg Ser His His Asp
260          265          270
Cys Asp Arg Gln Gly Gly Gly Pro Val Arg Ala Leu Phe Pro Ala Arg
275          280          285
Cys Val Pro Thr Asp Val Gln Pro Glu Ala Lys Pro Gly Gly Asp Ala
290          295          300
Ile Arg Lys Thr Trp Pro Ala Arg Leu Ser Arg Pro Pro Arg Ile Arg
305          310          315          320
Ser Ala Gln Thr Gly Ser Gln Arg Asn
325

```

<210> 341

<211> 1056

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 341

```

atggcactga ccaacccaaa atataaagtc gccgccgtcc aggccgcgcc agcgttcctc      60
gatctggatg cgtccgtcga aaaagcggtc cggctgatcg acgaggcccg cgccaagggc      120
gcgcgcctca ttgcgttccc ggaaacctgg atccccggct atccctggtg gatctggctc      180
ggcgcgcccg cctgggcgat catgaaaggt ttgtctcgg cctatttcga caattcgctc      240
acctatgaca gtccggccgc ggacaaaattg cgccaggccg ccaagcgcaa cgatatcgtc      300
gtggtgctcg gcctgtcggg gcgcgacggc ggcagtctct atatcgcgca atggatcatc      360
ggcccggacg gcgaaactgt cgcccagcgc cgcaagctca agccgaccca tgctgagcgt      420
tcggtgttcg gcgagggcga tggcagcgac cttgccgtgc atgagctcgc gatcgggcgc      480

```

```

gtcggcgcg c tgtgctgctg ggagcatctg caaccgctgt cgaatacgc catgtatgcg 540
cagaacgagc aggttcacgt ggcggcctgg ccgagctttt cgctgtacga tccgttcgcc 600
catgccctcg gtgcggaggt caacaacgcc gccagcaaga tctacgcggt cgagggatcg 660
tgcttcgctg tggcaccctg cgccaccgtt tcaaaggaaa tgatecgacct gttgtgcgac 720
acgccggaca agcacggtct gctgcacgcc ggcggcggtt ttgccgcgat ctacggccct 780
gacggctcgc cgatcggcga ccgctggcg cccgaccagg aaggtctgat ctatgccgat 840
gtcgatctcg gcatgatctc ggtcgcgaag gccgcccgg atccggccgg acattatgcg 900
cggccggatg tcacaaggtt gctgctcaac aaacgcccgg gcaatcgtgt cgaggcgctg 960
gcacttccgg tggatcaggt tgcggcaggt gaggagatcc cctcgatatc gcgatcggcc 1020
agaggggttg ccgaactgcc aaacgcccgc gaatag 1056

```

<210> 342
 <211> 342
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 342

Met	Ala	Leu	Thr	Asn	Pro	Lys	Tyr	Lys	Val	Ala	Ala	Val	Gln	Ala	Ala
1				5					10					15	
Pro	Ala	Phe	Leu	Asp	Leu	Asp	Ala	Pro	Ser	Lys	Lys	Arg	Ser	Gly	Ser
			20					25					30		
Thr	Arg	Pro	Ala	Pro	Arg	Ala	Arg	Ala	Ser	Leu	Arg	Ser	Arg	Thr	Trp
		35					40					45			
Ile	Pro	Gly	Tyr	Pro	Trp	Trp	Ile	Trp	Leu	Gly	Ala	Pro	Ala	Trp	Ala
	50					55					60				
Ile	Met	Lys	Gly	Phe	Val	Ser	Pro	Ile	Ser	Thr	Ile	Arg	Ser	Pro	Met
65					70					75				80	
Thr	Val	Arg	Pro	Arg	Thr	Asn	Cys	Ala	Arg	Pro	Pro	Ser	Ala	Thr	Tyr
				85					90					95	
Arg	Arg	Gly	Ala	Arg	Pro	Val	Gly	Ala	Arg	Arg	Arg	Gln	Ser	Leu	Tyr
			100					105					110		
Arg	Ala	Met	Asp	His	Arg	Pro	Thr	Ala	Lys	Leu	Ser	Pro	Ser	Ala	Ala
		115					120					125			
Ser	Ser	Ser	Arg	Pro	Met	Ser	Ser	Val	Arg	Cys	Ser	Ala	Arg	Ala	Met
	130					135					140				
Ala	Ala	Thr	Leu	Pro	Cys	Met	Ser	Ser	Arg	Ser	Gly	Ala	Ser	Ala	Arg
145					150					155					160
Cys	Ala	Ala	Gly	Ser	Ile	Cys	Thr	Ala	Val	Glu	Ile	Arg	His	Val	Cys
			165						170					175	
Ala	Glu	Arg	Ala	Gly	Ser	Arg	Gly	Gly	Leu	Ala	Glu	Leu	Phe	Ala	Thr
		180						185					190		
Ile	Arg	Ser	Pro	Met	Pro	Ser	Val	Arg	Arg	Ser	Thr	Thr	Pro	Pro	Ala
		195					200					205			
Arg	Ser	Thr	Arg	Ser	Arg	Asp	Arg	Ala	Ser	Ser	Trp	His	Pro	Ala	Pro
	210					215					220				
Pro	Phe	Gln	Arg	Lys	Ser	Thr	Cys	Cys	Ala	Thr	Arg	Arg	Thr	His	Gly
225					230					235					240
Leu	Leu	His	Ala	Gly	Gly	Gly	Phe	Ala	Ala	Ile	Tyr	Gly	Pro	Asp	Gly
			245						250					255	
Ser	Pro	Ile	Gly	Asp	Arg	Trp	Arg	Pro	Thr	Arg	Lys	Val	Ser	Met	Pro
		260						265					270		
Met	Ser	Ile	Ser	Ala	Ser	Arg	Ser	Arg	Arg	Pro	Pro	Asp	Pro	Ala	Gly
		275					280					285			
His	Tyr	Ala	Arg	Pro	Asp	Val	Thr	Arg	Leu	Leu	Leu	Asn	Lys	Arg	Pro
	290					295					300				
Gly	Asn	Arg	Val	Arg	Arg	Trp	His	Phe	Arg	Trp	Ile	Arg	Leu	Arg	Gln
305					310					315					320
Val	Arg	Arg	Ser	Pro	Arg	Tyr	Arg	Asp	Arg	Pro	Glu	Gly	Cys	Arg	Thr

325
Ala Lys Arg Gly Arg Ile
340

330

335

<210> 343
<211> 942
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 343
atgaagtcaa aaattgcggt tattcagcga cctcctgtat tgttagacct tcaggcttca 60
atcgcccggt ccattacttc tggtagaggaa gcggcaggca agggatctga gctccttggt 120
tttcccagaga catttctgcc tggttatccg tcctggatct ggcgctctca gccgggcgga 180
gacatggtgc tgacatctga aatccacgca aaatatcgcg cgaactctgt tgatgttgag 240
cgcgggggtc tggccccttt atgcgaagcg gcggcgaaac acggcgtcac aattgtcatg 300
gggctcagtg aaattgatgg gcgctacagc gggactacac tctttaatac agtggtgacc 360
attggcgcgg aaggagagct ccttaataga caccgcaagc tcatgccgac aaaccagag 420
cgtatggtct gggggcaagg ggatgcctct ggtctgcggg ttgtcgacac gcccggtggg 480
cgcgctcgga cgctgatctg ctgggaaaac tacatgccgc tatcgcgcta tgcgctttat 540
tctcaaaaaca ttgacatcta tgtggcgccg acctgggacg cgggcgagag ctggatcgcc 600
tccatgcagc atatcgccaa agaaggtggc tgctgggtga tcggcacggc caccgcatg 660
gagggctctg atgtccacgc cgacttccct cagcgggagg tgcttttccc tgatagcagc 720
gaatggatca atgacggtga cgctgtagtg gttaaaccca tgggggcgat tgtcgcgggt 780
ccgcatcacc gggataagag tattctctat gctgagattg acgtcgaagt ggcacgcaat 840
gcgcggcgct cgctcgatgt ggcggggcat tactcccggc cggatatattt ttcctttggc 900
gtggatcgcc ggcctttgcc gccggttacg tttgaggatt ga 942

<210> 344
<211> 303
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 344
Met Lys Ser Lys Ile Ala Val Ile Gln Arg Pro Pro Val Leu Leu Asp
1 5 10 15
Leu Gln Ala Ser Ile Ala Arg Ala Ile Thr Leu Leu Arg Lys Arg Gln
20 25 30
Ala Arg Asp Leu Ser Ser Leu Phe Phe Pro Arg His Phe Cys Leu Val
35 40 45
Ile Arg Pro Gly Ser Gly Val Ser Ser Arg Ala Glu Thr Trp Cys His
50 55 60
Leu Lys Ser Thr Gln Asn Ile Ala Arg Thr Leu Asp Val Glu Arg Gly
65 70 75 80
Asp Leu Ala Pro Leu Cys Glu Ala Ala Ala Lys His Gly Val Thr Ile
85 90 95
Val Met Gly Gln Asn Trp Ala Leu Gln Arg Asp Tyr Thr Leu Tyr Ser
100 105 110
Gly Asp His Trp Arg Gly Arg Arg Leu Leu Asn Arg His Arg Lys Leu
115 120 125
Met Pro Thr Asn Pro Glu Arg Met Val Trp Gly Gln Gly Asp Ala Ser
130 135 140
Val Cys Gly Leu Ser Thr Arg Pro Trp Ala Ala Ser Ala Arg Ser Ala
145 150 155 160
Gly Lys Thr Thr Cys Arg Tyr Arg Tyr Ala Leu Tyr Ser Gln Asn Ile
165 170 175

```

Asp Ile Tyr Val Ala Pro Thr Trp Asp Ala Gly Glu Ser Trp Ile Ala
      180      185      190
Ser Met Gln His Ile Ala Lys Glu Gly Gly Cys Trp Val Ile Gly Thr
      195      200      205
Ala Thr Ala Met Glu Gly Ser Asp Ser Gln Pro Thr Ser Leu Ser Gly
      210      215      220
Arg Cys Phe Ser Leu Ile Ala Ala Asn Gly Ser Met Thr Val Thr Leu
      225      230      235      240
Trp Leu Asn Pro Trp Gly Arg Leu Ser Arg Val Arg Ile Thr Gly Ile
      245      250      255
Arg Val Phe Ser Met Leu Arg Leu Thr Arg Ser Gly Thr Gln Cys Ala
      260      265      270
Ala Leu Ala Arg Cys Gly Gly Ala Leu Leu Pro Ala Gly Tyr Phe Phe
      275      280      285
Leu Trp Val Asp Arg Arg Pro Leu Pro Pro Val Thr Phe Glu Asp
      290      295      300

```

<210> 345

<211> 1011

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 345

```

atgaaagcga tcaaggccgc tgccgtgcag gcagcaccgg tattcctgaa cctcgacgca      60
tcgatcacca aggcggaaac attcgtcgcc gaggcgcgag cgaatggtgc caagctggtg      120
gcgtttccgg aaacctggct gccgggctat ccctgggttca tctggctcgg tgcgcccggc      180
gaaggcatgc agttcatccc gcgctatcac gaaaacagca tggagctccg ctcgcccggag      240
atgcgccgct tgcaggcgat cgcgcgcaag tatgaagtga cgctcgtcac gggctattcc      300
gagcgcgatg gtggcagccg ctacatgtcc caggtcatta ttggcgatca gggcgacatc      360
cttctcaatc gccgtaaatt gaagccaacc catgtcgagc ggacggtctt cggcgaaggc      420
gacggttcgg acctgggtgt ggtcgaaacg gcattcggca ggctcggtgc gctcaattgc      480
tgggaaacata tccagccgct cgtcaagatg tcgatgtatg cccagcatga ggaaatccat      540
gtcgcggggtt ggccgagctt ctgctgtctac cgcgatctcg cctatgccct gggaccggaa      600
gtcaacaatg ccgtcagtca ggtctatgcc gtggagggtg gcgcctatgt tctggcaccg      660
tgtgcgatcg taagccagga gatgttcgac attctggccg acaagcctga aaaggccttt      720
ctcctcaatc cccgcacatc caagcccggc ggtggcttca cgcagatcta tgcgcccggat      780
ggtcgaccgc tttgcgagcc gcttgccgac gatgtggaag gcatectcta tgcgcatctc      840
gatccggcaa cgatcgccgt cgcgaaaggc gccgcccgat ctgcggggca ctattcgcgg      900
ccggacgcac tctcgctggt gatcaatcgc gaaaagcgcg cgggtgatggc tgaaatcaac      960
gcgccggcga cgccgacctt caccgccatc tccctggacg ctgcccagta g      1011

```

<210> 346

<211> 329

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 346

```

Met Lys Ala Ile Lys Ala Ala Ala Val Gln Ala Ala Pro Val Phe Leu
  1           5           10           15
Asn Leu Asp Ala Ser Ile Thr Lys Ala Glu Thr Phe Val Ala Glu Ala
      20      25      30
Ala Ala Asn Gly Ala Lys Leu Val Ala Phe Pro Glu Thr Trp Leu Pro
      35      40      45
Gly Tyr Pro Trp Phe Ile Trp Leu Gly Ala Pro Ala Glu Gly Met Gln
      50      55      60

```

<210> 348
 <211> 297
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 348
 Met Lys Val Ala Ala Ile Gln Ala Ala Pro Val Tyr Leu Asp Arg Gln
 1 5 10 15
 Ala Thr Leu Glu Lys Ala Leu Ser Trp Met Lys Arg Pro Gln Thr Ala
 20 25 30
 Pro Lys Ser Ala Pro Ser Leu Arg Pro Ser Ser Arg Ala Ile Pro Trp
 35 40 45
 Met Asp Leu Thr Asp Gly Ala Lys Trp Asn Asp Asp Lys Gln Lys Ala
 50 55 60
 Ala Tyr Ala Cys Tyr Val Asp Ala Ala Val Glu Ala Asp Gly Pro Glu
 65 70 75 80
 Leu Gln Ala Ile Ala Lys Lys Ser Lys Ala Leu Gly Leu Phe Thr Ile
 85 90 95
 Trp Ala Trp Ser Asn Ala Arg Arg Arg Pro Gly Gln Tyr Ile Val Pro
 100 105 110
 Ser Leu Pro Ser Ile Pro Thr Arg Val Ser Ser Ala Tyr Thr Glu Asn
 115 120 125
 Ser Cys Pro Pro Thr Pro Ser Ala Ser Cys Gly Ala Lys Ala Thr Asp
 130 135 140
 Thr Asp Ser Arg Cys Met Asn Ser Pro Ala Ser Lys Ser Ala Arg Thr
 145 150 155 160
 Ala Gly Lys Ile Gly Cys Pro Ala Arg Tyr Ala Met Tyr Ala Gln Gly
 165 170 175
 Glu Gln Leu His Val Ala Thr Trp Pro Gly Ser Pro Trp Leu Thr Lys
 180 185 190
 Asp Ile Thr Arg Phe Ile Ala Leu Glu Gly Arg Ile Tyr Val Met Ser
 195 200 205
 Val Gly Gly Val Leu Ser Ala Asn Asp Ile Pro Asp Ser Phe Pro Leu
 210 215 220
 Lys Thr Asp Leu Leu Lys Ile Arg Asp Arg Tyr Leu Ser Gly Gly Thr
 225 230 235 240
 Asp Ser Arg Pro Arg Arg His His Pro Arg Arg Pro Arg Gln Lys Arg
 245 250 255
 Arg Asp His Thr Leu Arg Gly Leu Asp Leu Asn Thr Val Leu Gln Glu
 260 265 270
 Arg Gln Asn Phe Asp Pro Ala Gly His Tyr Ala Arg Pro Asp Val Ser
 275 280 285
 Asn Trp Lys Ser Thr Lys Ile Asp Asp
 290 295

<210> 349
 <211> 1002
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 349
 atgacgtccc ctgttcaaac caagtacaaa gtcgcctgtg ttcaggcggc gcccgagttt 60
 ctcgatctcg acaaaggcgt tgccaaagcg gtgcgcctga tcgaagaagc cgccacccaa 120
 aaggcctcgc tgatcgcgtt tcccgaagtc tggctcccgc gctatccgtg gtggatctgg 180
 ctcgactcgc cggcctgggg cttgcagttc gtccagcgct acttcgaaaa cgctctggtc 240

```

gtcggcagcc cccaatggga gcgcttggtc aaggccgccc cgcacaaca tatccatggt 300
gtgctcggat tctccgaacg ggacggcagc acgctgtacc tcgcacaggc catcatcgat 360
aacaccggga aggtgatcgc cagcggcgc aaactcaagc caacacacgc cgaacgcacg 420
gttttcggcg aaggcgacgg gagccacatc gcggtgcatg aaaccacttt gggccgcatg 480
gggtgactct gctgcgccga gcacatccag ccactgacca agtacgccat gtactcgag 540
cacgagcaga ttcacattgc cgcattggccc agcttctcgg tctaccgagg agcagcggtc 600
cagctgagcg ccgaagccaa caacgccggc agccaggtct atgccctgga gggcagttgc 660
tacgtggtgg ccccttgccg gacggtgtcc aaggagatgt tggacatgct ggctgattcg 720
ccgcaaaaga agcagctcct gctggaaggc ggtggctacg ccatgattta tgggcccgac 780
gccaagcccc tgtgcgagcc cattccagag acagaagaag gcattcttta cgcagatgtg 840
gacctgggct tcatcggtgt caccaaggca gcgtatgacc ccgccgggtca ctattcacgc 900
cccgacgtgc tgcgcctttt gttcaatcgg aagcctgccc ctcggttca cgatttcgat 960
cctgaataca cggccaccga gcagaagaca gacgcggcct ga 1002

```

<210> 350

<211> 333

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 350

```

Met Thr Ser Pro Val Gln Thr Lys Tyr Lys Val Ala Cys Val Gln Ala
1      5      10      15
Ala Pro Glu Phe Leu Asp Leu Asp Lys Gly Val Ala Lys Ala Val Arg
20     25     30
Leu Ile Glu Glu Ala Ala Thr Gln Lys Ala Ser Leu Ile Ala Phe Pro
35     40     45
Glu Val Trp Leu Pro Gly Tyr Pro Trp Trp Ile Trp Leu Asp Ser Pro
50     55     60
Ala Trp Gly Leu Gln Phe Val Gln Arg Tyr Phe Glu Asn Ala Leu Val
65     70     75     80
Val Gly Ser Pro Gln Trp Glu Arg Leu Cys Lys Ala Ala Asp Asn
85     90     95
Asn Ile His Val Val Leu Gly Phe Ser Glu Arg Asp Gly Ser Thr Leu
100    105    110
Tyr Leu Ala Gln Ala Ile Ile Asp Asn Thr Gly Lys Val Ile Ala Thr
115    120    125
Arg Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly Glu
130    135    140
Gly Asp Gly Ser His Ile Ala Val His Glu Thr Thr Leu Gly Arg Met
145    150    155    160
Gly Ala Leu Cys Cys Ala Glu His Ile Gln Pro Leu Thr Lys Tyr Ala
165    170    175
Met Tyr Ser Gln His Glu Gln Ile His Ile Ala Ala Trp Pro Ser Phe
180    185    190
Ser Val Tyr Arg Gly Ala Ala Phe Gln Leu Ser Ala Glu Ala Asn Asn
195    200    205
Ala Ala Ser Gln Val Tyr Ala Leu Glu Gly Ser Cys Tyr Val Val Ala
210    215    220
Pro Cys Ala Thr Val Ser Lys Glu Met Leu Asp Met Leu Ala Asp Ser
225    230    235    240
Pro Gln Lys Lys Gln Leu Leu Glu Gly Gly Gly Tyr Ala Met Ile
245    250    255
Tyr Gly Pro Asp Ala Lys Pro Leu Cys Glu Pro Ile Pro Glu Thr Glu
260    265    270
Glu Gly Ile Leu Tyr Ala Asp Val Asp Leu Gly Phe Ile Gly Val Thr
275    280    285
Lys Ala Ala Tyr Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val Leu
290    295    300

```

Arg Leu Leu Phe Asn Arg Lys Pro Ala Pro Arg Val His Asp Phe Asp
 305 310 315 320
 Pro Glu Tyr Thr Ala Thr Glu Gln Lys Thr Asp Ala Ala
 325 330

<210> 351

<211> 936

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 351

```

atgattacag caggcatcgc agtcgccgct cgggtggtgt tggacaaaac aaaaaccatt 60
gagaaagccg ttggcattat tcacgaggca gccggtaagg gtgtgaacct gcttgtgttt 120
cccgaggcat ttattccctc ctatcccgcc tggggttgcc gcctgcgtcc cggtgagat 180
ttcgggttgt gcgaggagt gcacgccctg ttgcttgata attcggtaaa ttgcaagg 240
gatgacctgg accctgtccg gggcgctgca gccgagcatt caatgaccgt ggtgatggga 300
ttgaatgagc gcgaaggcca gttcggtcgg gctaccctgt ttaacgccat ggtatattatc 360
ggtccggacg gcagcatcct gaaccatcat cggaaactta tgccaaccaa tcatgagcgt 420
acgattcatg gcttcggcga tgcgcgggga ttgaaagtgg tggatacccc gtgcggtcgc 480
gtgggtggtc tgatttgctg ggagaatttc atgccctggt ctcgctacgg cctgtatgcc 540
cagggcgtag aagtgtatgt tgcgccacc tacgaccagg gtgatgggtg gataggatcc 600
atgcagcata ttcccggga aggacggtgc tgggtgttat cggccggaac accgctacgc 660
ggcagtgatt ttcccgcgga catgccgggc aaggctcaac tgtttcccga tgacgatgaa 720
tgggtgaatc ccggtgggtc agtggttatc gcaccgggtg gggaattagt ggctggaccg 780
cttttccgtg aggagggcat ccttgtctgt gaattggatc cggcgaaaag tgctcatgcc 840
aagcggtcct ttgacgtggc cggtcattac gccaggccag atattttcga gttggaata 900
gaccgtgatc cacaggatcc cgtcgagtgg gactga 936

```

<210> 352

<211> 301

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 352

```

Met Ile Thr Ala Gly Ile Ala Val Ala Ala Pro Val Val Leu Asp Lys
 1           5           10           15
Thr Lys Thr Ile Glu Lys Ala Val Ala Leu Phe Thr Arg Gln Arg Val
 20           25           30
Arg Val Thr Cys Leu Cys Phe Pro Arg His Leu Phe Pro Pro Ile Pro
 35           40           45
Pro Gly Val Gly Ala Cys Val Pro Val Glu Ile Ser Gly Cys Ala Arg
 50           55           60
Ser Cys Thr Pro Cys Cys Leu Ile Ile Arg Asn Leu Gln Gly Asp Asp
 65           70           75           80
Leu Asp Pro Val Arg Gly Ala Ala Ala Glu His Ser Met Thr Val Val
 85           90           95
Met Gly Glu Ala Arg Arg Pro Val Arg Ser Gly Tyr Pro Val Arg His
100           105           110
Gly Ile Tyr Arg Ser Gly Arg Gln His Pro Glu Pro Ser Ser Glu Thr
115           120           125
Tyr Ala Asn Gln Ser Ala Tyr Asp Ser Trp Leu Arg Arg Cys Ala Gly
130           135           140
Ile Glu Ser Gly Gly Tyr Pro Val Arg Ser Arg Gly Trp Ser Asp Leu
145           150           155           160
Leu Gly Glu Phe His Ala Pro Gly Ser Leu Gly Leu Tyr Ala Gln Gly

```

```

                165                170                175
Val Glu Val Tyr Val Ala Pro Thr Tyr Asp Gln Gly Asp Gly Trp Ile
                180                185                190
Gly Ser Ala Ala Tyr Cys Pro Gly Arg Thr Val Leu Gly Val Ile Gly
                195                200                205
Arg Asn Thr Ala Thr Arg Gln Phe Ser Arg Thr Cys Arg Ala Arg Leu
                210                215                220
Asn Cys Phe Pro Met Thr Met Asn Gly Ile Pro Val Gly Gln Trp Leu
                225                230                235
Ala Pro Gly Gly Glu Leu Val Ala Gly Pro Leu Phe Arg Glu Glu Gly
                245                250                255
Ile Leu Val Cys Glu Leu Asp Pro Ala Lys Ser Ala His Ala Lys Arg
                260                265                270
Ser Phe Asp Val Ala Gly His Tyr Ala Arg Pro Asp Ile Phe Glu Leu
                275                280                285
Glu Ile Asp Arg Asp Pro Gln Asp Pro Val Glu Trp Asp
                290                295                300

```

<210> 353

<211> 1035

<212> DNA

<213> *Psuedomonas putida* ATCC 700801

<400> 353

```

atgaatgctt caaaaacaca ttataaagtt gcagctgtgc aagccgctcc tgaattcctg      60
gatttgagca aagggggttg taaggctata cgcctcatta aagaagcagc tgataacgga      120
gcatcgctgg ttgcctttcc ggaagtattat cttccagggt atccgtggtg gatctggctt      180
ggctctcccc catggggaat gcagtttggt cagcgctacg tagaaaactc gcttgattta      240
aaaagcgagc agttcgagcg actgtgcaaa gcggctgcta cttaccgtat tcacgttgta      300
atgggttaca gcgaacgctc gtttggcacc ctctacctcg gtcaagcaat tatcgatgac      360
agcgggaaag taattggtac gcgccgtaag ctcaagccca cccatgctga gcgtactgtt      420
tacggtgagg gtaacggcag tgacctcagg gttttcaatt cgcaacttgg aagggtaggt      480
gcactctgct gcgcagagca cgtacaacca ctctcgaagt ttgcatgta cagccagcat      540
gagcagttgc acattgcctc ttggccgagc ttctcggtat atcgcggtgg cgcatatcaa      600
ctgagcgctg aggctaactg cgcgccacc caagtctatg ctcttgaagg ccagtgttc      660
gtaatttcag catgcgcaat cgtatctaaa gacatgctaa acgttctcat cgacaccct      720
gacaagggta acctgttgca ggatggcggt ggcttcgcga tgatttatgg ccccgatggc      780
gcaccgctgt gtgaaccctt gggcgaaacat gaagaaggca tcctttatgc cgacgtcgat      840
ttggcgccca tttccgtagc taaagcgcca ctgcaccgg ttggccatta ctgcgggcca      900
gatgttttgc gtctgctttt caacgatcaa ccgacacctt gcgtggaggc gttcaatccg      960
gtcctgtctg gtactgatgc tccagggtaca gaccttcagg gtgatgagcc cgatgcgcaa      1020
ccgatattctg aataa                                     1035

```

<210> 354

<211> 312

<212> PRT

<213> *Psuedomonas putida* ATCC 700801

<400> 354

```

Met Asn Ala Ser Lys Thr His Tyr Lys Val Ala Ala Val Gln Ala Ala
  1                5                10                15
Pro Glu Phe Leu Asp Leu Asp Lys Gly Val Asp Lys Ala Ile Arg Leu
  20                25                30
Ile Lys Glu Ala Ala Asp Asn Gly Ala Ser Leu Val Ala Phe Pro Glu
  35                40                45
Val Tyr Ser Arg Val Ser Val Val Asp Leu Ala Trp Leu Ser Arg Met
  50                55                60
Gly Asn Ala Val Cys Ser Ala Leu Arg Arg Lys Arg Leu Ile Lys Ala
  65                70                75                80
Ser Ser Ser Ser Asp Cys Ala Lys Arg Leu Leu Leu Thr Val Phe Thr
  85                90                95

```

```

Leu Trp Leu Gln Arg Thr Leu Val Trp His Pro Leu Pro Arg Ser Ser
      100      105      110
Asn Tyr Arg Gln Arg Glu Ser Asn Trp Tyr Ala Pro Ala Gln Ala His
      115      120      125
Pro Cys Ala Tyr Cys Leu Arg Gly Arg Gln Pro Gln Gly Phe Gln Phe
      130      135      140
Ala Thr Trp Lys Gly Arg Cys Thr Leu Leu Arg Arg Ala Arg Thr Thr
      145      150      155      160
Thr Leu Glu Val Cys Asp Val Gln Pro Ala Ala Val Ala His Cys Leu
      165      170      175
Leu Ala Glu Leu Leu Gly Ile Ser Arg Trp Arg Ile Ser Thr Glu Arg
      180      185      190
Gly Leu Arg Gly His Pro Ser Leu Cys Ser Arg Pro Val Leu Arg Asn
      195      200      205
Phe Ser Met Arg Asn Val Ser Lys Asp Met Leu Asn Val Leu Ile Asp
      210      215      220
Thr Pro Asp Lys Gly Asn Leu Leu Gln Asp Gly Gly Gly Phe Ala Met
      225      230      235      240
Ile Tyr Gly Pro Asp Gly Ala Pro Leu Cys Glu Pro Leu Gly Glu His
      245      250      255
Glu Glu Gly Ile Leu Tyr Arg Arg Phe Gly Arg His Phe Arg Ser
      260      265      270
Ser Gly Thr Arg Pro Gly Trp Pro Leu Leu Ala Ala Arg Cys Leu Arg
      275      280      285
Leu Leu Phe Asn Asp Gln Pro Thr Pro Cys Val Glu Ala Phe Asn Pro
      290      295      300
Ala Pro Val Gly Thr Asp Ala Pro
      305      310

```

<210> 355

<211> 1014

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 355

```

atggccgtct ctaaagacgg tactgtttca ggaaagtcgc ctatccgatt gcatgtcgcc      60
gcgatacaga tgggtccaaa gctgggtgac gcgcaggcga acgtgaatca ggcagaagcc      120
cttattcgga aggtctcttg gctgggtgag cggttgatcg tggtaccaga gatgtttacc      180
tccggtgcgg cgtttcatcc cgacatgctc aaagccattc agccattcga tggcgcccca      240
ctccagttgc tgaaagacct ttctcgcaag ggcaatgctg tcatcgggcg ctcgtttctc      300
gccaaagcgt ggcaacaagt attcaatacc ttcgttttgg ttctccgga cgggtcagtc      360
gtaacgcatg acaaggattc accgacctat tgggaaaatt gctattaccg gggcggtacc      420
gatgatggcg tggtgtctac gccattggc cgggtcggct ccgtcctctg ttgggaattt      480
atccgctcaa gaaccgcgag acggctggcg aacaaggcca agatggctcg gggaggctcc      540
tgttggtgga cgctccccga tgatgctgat ccagacagcc cgcgcagagc cgtgaacctc      600
aagatgctgc aagaagcgcc ggttcgcatg gcgcggatgc tgggtgttcc ggtaatacat      660
ggctccacg cgggcagctt cgaaggattc ttcagtcagg aacttgcgga tgttccctat      720
aactcgacgt acctgggcga gacaatgatt gtcgacgcgg gtggccgggt acttgccccg      780
agagcgcaag atgcaggcga aggcgtggtg acggcagaag tggttttgcc cgacaagtcc      840
gtaccaagcg aacctatccc ggagacttgc tggattccca aggaaatgcc ggtgattgg      900
aaagaagcct gggagcgttg gttcgatacc ggtgcggatt actacgagat ggtgaccgcg      960
ccctttatca agacgggtgt gataaacgag tacacaccgg aatatcttag gtag      1014

```

<210> 356

<211> 325

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 356

```

Met Ala Val Ser Lys Asp Gly Thr Val Ser Gly Lys Ser Pro Ile Arg
 1          5          10          15
Leu His Val Ala Ala Ile Gln Met Val Gln Ser Trp Val Thr Arg Arg
          20          25          30
Arg Thr Ile Arg Gln Lys Pro Leu Phe Gly Arg Leu Leu Gly Trp Val
          35          40          45
Arg Val Gly Ser Cys Tyr Gln Arg Cys Leu Pro Pro Val Arg Arg Phe
          50          55          60
Ile Pro Thr Cys Ser Lys Pro Phe Ser Phe Asp Gly Ala Pro Leu Gln
          65          70          75          80
Leu Leu Lys Asp Leu Ser Arg Lys Gly Asn Ala Val Ile Gly Gly Ser
          85          90          95
Phe Leu Gln Ala Trp Ala Thr Ser Ile Gln Tyr Leu Arg Phe Gly Phe
          100          105          110
Ser Gly Arg Val Ser Arg Asn Ala Gln Gly Ser Pro Thr Tyr Trp Glu
          115          120          125
Asn Cys Tyr Tyr Arg Gly Gly Thr Asp Asp Gly Val Leu Ser Thr Pro
          130          135          140
Ile Gly Pro Ser Ala Pro Ser Ser Val Gly Asn Leu Ser Ala Gln Glu
          145          150          155          160
Pro Arg Asp Gly Trp Arg Thr Arg Ser Arg Trp Val Gly Gly Ser Cys
          165          170          175
Trp Trp Thr Leu Pro Asp Asp Ala Asp Pro Asp Ser Pro Arg Arg Ala
          180          185          190
Val Asn Leu Arg Cys Cys Lys Lys Arg Arg Phe Ala Trp Arg Gly Cys
          195          200          205
Trp Val Phe Arg Tyr Met Ala Pro Thr Arg Gln Leu Arg Arg Ile Leu
          210          215          220
Gln Ser Gly Thr Cys Gly Cys Ser Leu Leu Asp Val Pro Gly Arg Asp
          225          230          235          240
Asn Asp Val Asp Ala Gly Gly Arg Val Leu Ala Arg Arg Ala Gln Asp
          245          250          255
Ala Gly Glu Gly Val Val Thr Ala Glu Gly Phe Ala Arg Gln Val Arg
          260          265          270
Thr Lys Arg Thr His Pro Gly Asp Phe Leu Asp Ser Gln Gly Asn Ala
          275          280          285
Gly Ile Gly Lys Lys Pro Gly Ser Val Gly Ser Ile Pro Val Arg Ile
          290          295          300
Thr Thr Arg Trp Pro Arg Pro Leu Ser Arg Arg Val Thr Ser Thr His
          305          310          315          320
Arg Asn Ile Leu Gly
          325

```

<210> 357

<211> 951

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 357

```

atgacaaaac tagccatcgt acaaaaaccg ccagtctttc tggataagca aaaaaccatt      60
gagctggccg tcgccaacat tgaagaggcc gccgccaagg gtgccgatct cgtggtgttt      120
tctgaagctt tcattcccgg ctatcctgcc tggatctggc gtctacgccc cggcggtgac      180
tgggggcttt cagaagagtt gcaccagcgt ttgctgcgca atgccgtcaa tgtggactcc      240
gatgatctgg ctccgttggt tgaggtcgcc cgcaagcacg aactcaccat cgtttgcggt      300

```



```

atcgaggagc gtgacaacaa actaagtcaa acaaccttat ataacaccgt catcacgatt 360
gggtcccgatg gatcggttact gaacaaacat cgcaagctta tgcccaccaa cccggagcga 420
atgggtgtggg ggtttggtga cgcatccggt ttaaaagtcg ttgataccaa tgctggtcga 480
attggctcat taatgtgctg ggaaaattac atgccgctgg ctgctatgc cctatatgca 540
caaggtgtcg agatctatat cgcaccgacc tacgacagcg gtgatggctg gataggcagc 600
atgcagcaca tcgcacgtga agggggctgt tgggtggtgg gatgtgggtg tctcatgaaa 660
ggcagtgata ttccagatga ttcccggag aaatccacgt tgtatccaga tgcagatgaa 720
tgggtgaacc cgggtgattc tgtagtata gcacccggcg gtgaaattat ggccggccca 780
atgaacagag agtccggtat tttgtatcac gagctagaca gagaaaaagt cagcaacgct 840
aaacgagcat tcgatgttgc cgggcattat tcacgtcccg atatctttca gctgcatgta 900
aatacacagg agcagtcacc ctgcgtattc gaaaataatt ccataactta a 951

```

<210> 358

<211> 300

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 358

```

Met Thr Lys Leu Ala Ile Val Gln Lys Pro Pro Val Phe Leu Asp Lys
1      5      10      15
Gln Lys Thr Ile Glu Leu Ala Val Pro Thr Leu Lys Arg Pro Pro Pro
20     25     30
Arg Val Pro Ile Ser Trp Cys Phe Leu Lys Leu Ser Phe Pro Ala Ile
35     40     45
Leu Trp Ile Trp Arg Leu Arg Pro Gly Gly Asp Trp Gly Leu Ser Glu
50     55     60
Glu Leu His Gln Arg Leu Leu Arg Asn Ala Val Asn Val Asp Ser Asp
65     70     75     80
Asp Leu Ala Pro Leu Phe Glu Val Ala Arg Lys His Glu Leu Thr Ile
85     90     95
Val Cys Gly Arg Gly Ala Gln Gln Thr Lys Ser Asn Asn Leu Ile His
100    105    110
Arg His His Asp Trp Ser Arg Trp Ile Tyr Thr Asn Ile Ala Ser Leu
115    120    125
Cys Pro Pro Thr Arg Ser Glu Trp Cys Gly Gly Leu Val Thr His Pro
130    135    140
Leu Lys Val Val Asp Thr Asn Ala Gly Arg Ile Gly Ser Leu Met Cys
145    150    155    160
Trp Glu Asn Tyr Met Pro Leu Ala Arg Tyr Ala Leu Tyr Ala Gln Gly
165    170    175
Val Glu Ile Tyr Ile Ala Pro Thr Tyr Asp Ser Gly Asp Gly Trp Ile
180    185    190
Gly Ser Ala Ala His Arg Thr Arg Gly Leu Leu Gly Gly Gly Met Trp
195    200    205
Val Ser His Glu Arg Gln Tyr Ser Met Ile Ser Arg Arg Asn Pro Arg
210    215    220
Cys Ile Gln Met Gln Met Asn Gly Thr Arg Val Ile Leu Thr Arg Arg
225    230    235    240
Asn Tyr Gly Arg Pro Asn Glu Gln Arg Val Arg Tyr Phe Val Ser Arg
245    250    255
Ala Arg Gln Arg Lys Val Ser Asn Ala Lys Arg Ala Phe Asp Val Ala
260    265    270
Gly His Tyr Ser Arg Pro Asp Ile Phe Gln Leu His Val Ile His Arg
275    280    285
Ser Ser His Pro Ala Tyr Ser Lys Ile Ile Pro Leu
290    295    300

```

<210> 359

<211> 1029
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 359
 atggcaaacg tcgttcgtgc tgcggccgta cagttgagcc ctgttttggg tagtcgcgag 60
 ggtacggtag agaaggtagt tgctgcgac cgtgacgcc cctcgaggg cgcacagctg 120
 tgcgttttcc cggagacggt tggtccctat tatccgtatt tctcgttcat tcggccgccc 180
 gcgccatgg gcaaagacca catgcagctg tacgagcaag ctgtggtcgt gccttctccc 240
 agcacgaacg cgattgccgc ggcggccaaa caacactcga tcgtcgtttc aatcggcgtc 300
 aatgaacgag atcacggtac gatatacaac acgcagttgt tgttcgatgc cgacgggaca 360
 ctcgtgcaac ggcgtcgcaa gataaccccc acgttccacg agcgtatggt gtggggtcaa 420
 ggtgatgggt cgggttttgcg ctgtgtcgac acacaaatcg ggcgcacggt tagcctggct 480
 tggtgggaac attacaatcc cttggcgcg ctcgcattga tggccgatca cgaagagatc 540
 cagtcgcca tgtttccggg ttcgatggtg ggtcagatct tcgccgatca aattcaggta 600
 accattcgcc accacgcgct cgaaagcggc tgtttcgtcg tcaacgctac ggggtatctg 660
 agcaaggaac aggtcgccca gttgtcaca ggacgcgcgc tcgacgcggc gttgaccggt 720
 gggtgttaca ccgcgattgt atcgcctgaa ggcgtcgta tgggcgaacc gctcaccgac 780
 ggcgaaggca tggtcgtggc ggatatggat ctgagcctca tcaccaaacg caaacgcgatg 840
 atggatagcg tcgggcacta cagtcgccc gaattgctgt ctctgctgat caatcgaacg 900
 ccaaccaca cggcggtcga cgtcgaattc aactccaatt ccgagtctca tcatgtcagc 960
 aatacacgaa caccaaagcg cacaactggc ccacgttcga accttcaagt tgccgctgat 1020
 cgcgagtaa 1029

<210> 360
 <211> 335
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 360
 Met Ala Asn Val Val Arg Ala Ala Ala Val Gln Leu Ser Pro Val Leu
 1 5 10 15
 Gly Ser Arg Glu Gly Thr Val Glu Lys Val Val Ala Ala Ile Arg Asp
 20 25 30
 Ala Ala Ser Gln Gly Ala Gln Leu Cys Val Phe Pro Glu Thr Val Val
 35 40 45
 Pro Tyr Ser Val Phe Leu Val His Ser Ala Ala Arg Gly His Gly Gln
 50 55 60
 Arg Pro His Ala Ala Val Arg Ala Ser Cys Gly Arg Ala Phe Ser Gln
 65 70 75 80
 His Glu Arg Asp Cys Arg Gly Gly Gln Thr Leu Asp Arg Arg Phe
 85 90 95
 Asn Arg Arg Met Asn Ala Ile Thr Val Arg Tyr Thr Thr Arg Ser Cys
 100 105 110
 Cys Ser Met Pro Thr Gly His Ser Cys Asn Gly Arg Lys Ile Thr Pro
 115 120 125
 Thr Phe His Glu Arg Met Val Trp Gly Gln Gly Asp Gly Ser Gly Leu
 130 135 140
 Arg Cys Val Asp Thr Gln Ile Gly Arg Ile Gly Ser Leu Ala Cys Trp
 145 150 155 160
 Glu His Tyr Asn Pro Leu Ala Arg Tyr Ala Leu Met Ala Asp His Glu
 165 170 175
 Glu Ile His Val Ala Met Phe Pro Gly Ser Met Val Gly Gln Ile Phe
 180 185 190
 Ala Asp Gln Ile Gln Val Pro Phe Ala Thr Thr Arg Ser Lys Ala Ala

```

      195              200              205
Val Ser Ser Ser Thr Leu Arg Gly Ile Ala Arg Asn Arg Ala Gln Leu
      210              215              220
Ser Gln Gly Thr Ser Leu Asp Ala Ala Leu Thr Gly Gly Cys Tyr Thr
      225              230              235              240
Ala Ile Val Ser Pro Glu Gly Val Val Leu Gly Glu Pro Leu Thr Asp
      245              250              255
Gly Glu Gly Met Val Val Ala Asp Met Asp Leu Ser Leu Ile Pro Asn
      260              265              270
Ala Asn Ala Trp Ile Ala Ser Gly Thr Thr Val Ala Arg Asn Cys Cys
      275              280              285
Leu Cys Ser Ile Thr Pro Thr His Thr Ala Val Asp Val Glu Phe Asn
      290              295              300
Ser Asn Ser Glu Ser His Val Ser Asn Thr Arg His Gln Ser Ala
      305              310              315              320
Gln Leu Ala His Val Arg Thr Phe Lys Leu Pro Leu Ile Ala Ser
      325              330              335

```

<210> 361

<211> 951

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 361

```

atgctaaaacg agaacaatgg cgctactttc aagggttgctg ccgtgcaggc ttcaccggta      60
tttcttgatc gcgctgctac aatcgacaag gcttgcgatt taattgctac ggccggacgc      120
gaggggggctc gcctgatcgt ctttccagaa gcgttcgtcc cggcctatcc tgattgggta      180
tgggcgattc ccgcgggtga tgagggcatg ctcaatgagc tgtatgcaga attacttgcc      240
aatgctgtca ccattcccag cgatgcgacc gagaggttgt gtcgcgcggc gcggcttgct      300
aatgctttacg tgggtgatgg gatgagcgaa cgcaatgccg aagcgagtgg cgccagcctg      360
tataatacgc tgtgtatat tgatgcacag ggacaaatcc tgggaaagca ccggaagctg      420
gttccaacgg gcggcgagcg cctggtatgg gcacagggag atggcagcac cctggaggtt      480
tacgatactc ctttgggaaa actcgggtggc ttaatctgct gggagaatta tatgccgtg      540
gcacgctata ctatgtatgc ctggggcacg caaatctaca ttgcagcgac gtgggatcgc      600
gggcagccat ggctatccac tttgcgacac attgctaaag agggcagagt atatgtgatc      660
ggctgttgta ttgctatgcg caaagatgat atcccagacc attacgcgat gaaggagaag      720
tattacgcgg aagaagacga gtggatcaat attggcgata gcgcaatcgt caatccagaa      780
ggggtattta ttgccgggcc agtgcgtaag caagaagaaa tcctctacgc cgagggttgac      840
ccgcgaatga tgcaggggcc aaagtggatg ctcgacgtgg caggacatta cgcgcgcccc      900
gatgtattcc agttgacggt gcacacggag aggcggcaga tgatccacta g      951

```

<210> 362

<211> 302

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 362

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Met Leu Asn Glu Asn Asn Gly Ala Thr Phe Lys Val Ala Ala Val Gln
  1              5              10              15
Ala Ser Pro Val Phe Leu Asp Arg Ala Tyr Asn Arg Gln Gly Leu Arg
      20              25              30
Phe Asn Cys Tyr Gly Arg Thr Arg Gly Gly Ser Pro Asp Arg Leu Ser
      35              40              45
Arg Ser Val Arg Pro Gly Leu Ser Leu Gly Met Gly Asp Ser Arg Gly
      50              55              60

```

Gly His Ala Gln Ala Val Cys Glu Leu Leu Ala Asn Ala Val Thr Ile
 65 70 75 80
 Pro Ser Asp Ala Thr Glu Arg Leu Cys Arg Ala Ala Arg Leu Ala Asn
 85 90 95
 Ala Tyr Val Val Met Gly Met Ser Glu Arg Asn Ala Glu Ala Ser Gly
 100 105 110
 Ala Ser Leu Tyr Asn Thr Leu Leu Tyr Cys Thr Gly Thr Asn Pro Gly
 115 120 125
 Lys Ala Pro Glu Ala Gly Ser Asn Gly Arg Arg Ala Pro Gly Met Gly
 130 135 140
 Thr Gly Arg Trp Gln His Pro Gly Gly Leu Arg Tyr Ser Phe Gly Lys
 145 150 155 160
 Thr Arg Trp Leu Asn Leu Leu Arg Ile Ile Cys Arg Trp His Ala Ile
 165 170 175
 Leu Cys Met Pro Gly Ala Arg Lys Ser Thr Leu Gln Arg Arg Gly Ile
 180 185 190
 Ala Gly Ser His Gly Tyr Pro Leu Cys Asp Thr Leu Leu Lys Arg Ala
 195 200 205
 Glu Tyr Met Ser Ala Val Val Leu Tyr Ala Gln Arg Tyr Pro Arg Pro
 210 215 220
 Leu Arg Asp Glu Gly Glu Val Leu Arg Gly Arg Arg Val Asp Gln
 225 230 235 240
 Tyr Trp Arg Arg Asn Arg Gln Ser Arg Arg Gly Ile Tyr Cys Arg Ala
 245 250 255
 Ser Ala Ala Arg Arg Ile Leu Tyr Ala Glu Val Asp Pro Arg Met Met
 260 265 270
 Gln Gly Pro Lys Trp Met Leu Asp Val Ala Gly His Tyr Arg Ala Arg
 275 280 285
 Met Tyr Ser Ser Arg Cys Thr Arg Arg Gly Gly Arg Ser Thr
 290 295 300

<210> 363

<211> 1053

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 363

atgccgaaaa agtcgaccgt ccgggtcgca gccgtccaga ttgcgccgga tctgacatcg 60
 cgggaaaaaga cgggtggcacg cgtgatcgag gcgatcgccc aggcattccgc caaagggtgcg 120
 gagcttgtgg tttttcccga gacctttgtg ccgtggtatc cttattttctc gttcgtgttg 180
 cccccgggtct tgtcgggcaa ggagcacctg cggtcttacg aagaggcggt tgcggtgcca 240
 agtgcgccca caagaagcgt agcggctgcc gctcgcgaaac atggcatcgt cgtggcgctt 300
 ggcgtcaacg agcgcgacta tggcacgctc tacaatacgc aactgctttt cgatgccgat 360
 ggcagttctga tcctgaagcg gcgcaagatc accccgactt tccacgagcg gatgatctgg 420
 ggccaggggcg atgcctcagg cctgaagggt gtcgacagcg ccattggccg catcggcgcg 480
 ctggcctgct gggaacacta caatccgcta gcccgctatg cgctgatggc gcagcacgag 540
 gaaatccaca ttgcgcagtt tcccggtccc atggtcgggc cgatctttgc cgatcagatg 600
 gaggtgacga tccgccatca cgcgctggaa agcggctgct tcgtcgtcaa tgccacggga 660
 tggctgacgg atgatcagat cgtctcgatc acaccggata ccggcctgca aaaagcgctg 720
 cggggtggct gcatgacggc gatcatttcc cccgaaggca agcatctcgt gccgccgctc 780
 accgaagggtg agggtatcct cgtcgccgat ctcgacatga gcctcattct caagcgcaag 840
 cgcatgatgg attcgggtcgg ccactatgcc cggcccagat tgctgcacct cgtcatggac 900
 gcccgcccg ctgcgccgat gaggaatcg tccatgccca ctgccttccc cggcgaaaca 960
 ttgacaaccg acatgaccga tggagaacag gatgcgtctt tcgacggaaa cgctgatcaa 1020
 cgaattgcag tccttcggag cccggctggt tga 1053

<210> 364

<211> 335

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 364

```

Met Pro Lys Lys Ser Thr Val Arg Val Ala Ala Val Gln Ile Ala Pro
 1          5          10          15
Asp Leu Thr Ser Arg Glu Lys Gly Gly Thr Arg Asp Arg Gly Asp Arg
      20          25          30
Pro Gly Ile Arg Gln Arg Cys Gly Ala Cys Gly Phe Ser Arg Asp Leu
      35          40          45
Cys Arg Gly Ile Leu Ile Ser Arg Ser Cys Cys Pro Arg Ser Cys Arg
      50          55          60
Ala Arg Ser Thr Cys Gly Ser Thr Lys Arg Arg Leu Arg Cys Gln Val
 65          70          75          80
Pro Pro Gln Glu Ala Arg Leu Pro Leu Ala Asn Met Ala Ser Ser Trp
      85          90          95
Arg Leu Ala Ser Thr Ser Ala Thr Met Ala Arg Ser Thr Ile Arg Asn
      100          105          110
Cys Phe Ser Met Pro Met Ala Val Ser Ser Gly Ala Arg Ser Pro Arg
      115          120          125
Leu Ser Thr Ser Gly Ser Gly Ala Arg Ala Met Pro Gln Ala Glu Gly
      130          135          140
Cys Arg Gln Arg His Trp Pro His Arg Arg Ala Gly Leu Leu Gly Thr
 145          150          155          160
Leu Gln Ser Ala Ser Pro Tyr Ala Leu Met Ala Gln His Glu Glu Ile
      165          170          175
His Ile Ala Gln Phe Pro Gly Ser Met Val Gly Pro Ile Phe Ala Asp
      180          185          190
Gln Met Glu Val Thr Ile Arg His His Ala Leu Glu Ser Gly Cys Phe
      195          200          205
Val Val Asn Ala Thr Gly Trp Arg Met Ile Arg Ser Ser Arg Ser His
      210          215          220
Arg Ile Pro Ala Cys Lys Lys Arg Cys Gly Val Ala Ala Gly Asp His
 225          230          235          240
Phe Pro Arg Arg Gln Ala Ser Arg Ala Ala Ala His Arg Arg Gly Tyr
      245          250          255
Pro Arg Arg Arg Ser Thr Ala Ser Phe Ser Ser Ala Ser Ala Trp Ile
      260          265          270
Arg Ser Ala Thr Met Pro Gly Pro Ser Cys Cys Thr Ser Ser Trp Thr
      275          280          285
Pro Gly Arg Leu Arg Arg Gly Asn Arg Pro Cys Pro Leu Pro Ser Pro
      290          295          300
Ala Lys Ile Asp Asn Arg His Asp Arg Trp Arg Thr Gly Cys Val Phe
 305          310          315          320
Arg Arg Lys Arg Ser Thr Asn Cys Ser Leu Arg Ser Pro Ala Gly
      325          330          335

```

<210> 365

<211> 975

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 365

```

atgacaaagc tagccatcgt tcaaaaaccc cccgtctttc tggataaaga aaaaaccata    60
gcgaagacgg ttgattccat aaaagaggcc gcgacacaaa atgccgactt ggtcatcttc    120

```

```

accgaagcct tcatcccggg ctaccccacc tggatatggc gacttaggcc aggcgctgat 180
tggggcctct cagaagagct gcacgagcag ttattgcgta acgcggtgag tatgggatcg 240
accgacctgg atccgcttta tgaagccgcc caacagcata acgtcactat tgtttgccgc 300
atcgtagaaa gagaccacca actcagccaa tcaaccctct acaacagcat ggtcgtcatt 360
gacacagacg gaacccttct caacaagcac cgcaactca tgccaactaa tcccgaacgc 420
atggtgtggg gctttggcga cgcctcagga ctcaaagccg ttgcaacacc tgcaggccgc 480
atcagcacgt tgttgtgttg ggagaactac atgccattgg cccgatatgc tctgtatgca 540
caaggcgtgg aaatctatat cgcgccaaact tacgacagtg gtgcgggttg gataggaagc 600
ttgcaacaca tagcacgca aggtcgatgc tgggtcgtgg gctgtggcaa cctgattcag 660
gccagtgatc tgcctgaaga cttcccggac aaggacaacc tctaccgga cgcagaagag 720
tgggtgaacc cgggtgactc catagtcatt gcaccagacg gtgagattgt ggccggtcca 780
atgcacaaag agacaggaat tttgtactgc gagatagatc tggagaaagt cagaattgca 840
aaacgagcat tagacgtgac cgggcattat tcgcgaccgg acgttttcaa actgcatgtg 900
aataccgac ctcaatcacc tgtggaattt gaaggtcagg agaccaacaa tccaacaaca 960
ggagaaagct catga 975

```

<210> 366

<211> 315

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 366

```

Met Thr Lys Leu Ala Ile Val Gln Lys Pro Pro Val Phe Leu Asp Lys
1      5      10      15
Glu Lys Thr Ile Ala Lys Thr Val Ile Pro Lys Arg Pro Arg His Lys
20     25     30
Met Pro Thr Trp Ser Ser Ser Pro Lys Pro Ser Ser Arg Ala Thr Thr
35     40     45
Trp Ile Trp Arg Leu Arg Pro Gly Ala Asp Trp Gly Leu Ser Glu Glu
50     55     60
Leu His Glu Gln Leu Leu Arg Arg Gly Glu Tyr Gly Ile Asp Arg Pro
65     70     75     80
Gly Ser Ala Leu Ser Arg Pro Thr Ala Arg His Tyr Cys Leu Arg His
85     90     95
Arg Arg Lys Arg Pro Pro Thr Gln Pro Ile Asn Pro Leu Gln Gln His
100    105    110
Gly Arg His His Arg Arg Asn Pro Ser Gln Gln Ala Pro Gln Thr His
115    120    125
Ala Asn Ser Arg Thr His Gly Val Gly Leu Trp Arg Ala Ser Gly Leu
130    135    140
Lys Ala Val Ala Thr Pro Ala Gly Arg Ile Ser Thr Leu Leu Cys Trp
145    150    155    160
Glu Asn Tyr Met Ile Gly Pro Ile Cys Ser Val Cys Thr Arg Arg Gly
165    170    175
Asn Leu Tyr Arg Ala Asn Leu Arg Gln Trp Cys Gly Leu Asp Arg Lys
180    185    190
Leu Ala Thr His Ser Thr Arg Arg Ser Met Leu Gly Arg Gly Leu Trp
195    200    205
Gln Pro Asp Ser Gly Ser Asp Leu Pro Glu Asp Phe Pro Asp Lys Asp
210    215    220
Asn Leu Tyr Pro Asp Ala Glu Glu Trp Val Asn Pro Gly Asp Ser Ile
225    230    235    240
Val Ile Ala Pro Asp Gly Glu Ile Val Ala Gly Pro Met His Lys Glu
245    250    255
Thr Gly Ile Leu Tyr Arg Asp Arg Ser Gly Glu Ser Gln Asn Cys Lys
260    265    270
Thr Ser Ile Arg Arg Asp Arg Ala Leu Phe Ala Thr Gly Arg Phe Gln
275    280    285

```

Thr Ala Cys Glu Tyr Pro Thr Ser Ile Thr Cys Gly Ile Arg Ser Gly
 290 295 300
 Asp Gln Gln Ser Asn Asn Arg Arg Lys Leu Met
 305 310 315

<210> 367

<211> 981

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 367

```

atgactgccc actttgccga taccctgacc gttgccgtgg cccagatcgc gccggtgtgg      60
ctacagcgcg aagctaccct gcaaaagatg ctggtctggg tggagcgcg cgcgcgcgaa      120
ggcgcgggcc tggtcgcctt cagtgaaggc ctgctgcctg gctaccctt ctggattgaa      180
cacacggacg gcgcccgtt cgagtcgccc ttacagaagc gcctgtacgc ccactactgc      240
gatcagtcgg tccagatcaa tgctgggcac ctgcaccac tctgcgctgc cgcggccaga      300
caccagattt ggtggtctg cggcgatcgc gagcgcgaca gcgcacgcgg actcagcgtg      360
tttgcaccaa tggtcaccaa cgatgccgaa ggcgcgatcc gcagtgtgca ccgcaagctg      420
atgccgacct acgaagaacg cctggtgtgg tcgcccggcg acgcgcacgg actgcgctgc      480
catccgctcg gccagttccg cctcggcagc ctcaattgct gggagaactg gatgccgctg      540
gcgcgcgcgg ccctgtacgc ccagggcgag tctttgcatg ttgcatcctg gcccggcagt      600
cgccgcaaca ccgagaccat tactcccttc atcgcccgcg aaggccgcag ttacgcgctg      660
tccgccagtt ccgtgctgca ccgggatgat ctgcccgact ccgttccggc gctgtcgggtg      720
ctgcgcgact gcctgccgga cgtgatggcc gacggcggct cctgcgtcgc cggccccgac      780
ggacatttcc tgatcgagcc ggtcgtcggc cgggaagagc tgctgctcgc gcagatcgat      840
catgcccggg tacgcgagga acgtcagaac ttcgaccctc tcggccacta ctgcggccg      900
gaactcctgt cgctggtggt ggatacgcgc cgggcgagcg gagtgcagat agtgaatgct      960
gaccatggct ttaagccctg a                                     981

```

<210> 368

<211> 317

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 368

```

Met Thr Ala His Phe Ala Asp Thr Leu Thr Val Ala Val Ala Gln Ile
  1          5          10          15
Ala Pro Val Trp Leu Gln Arg Glu Tyr Pro Ala Lys Asp Ala Gly Leu
  20          25          30
Gly Gly Ala Arg Arg Ala Arg Arg Arg Gly Pro Gly Arg Leu Gln Gly
  35          40          45
Pro Ala Ala Trp Leu Pro Leu Leu Asp Thr His Gly Arg Arg Pro Leu
  50          55          60
Arg Val Ala Val Thr Glu Ala Cys Thr Pro Thr Thr Ala Ile Ser Arg
  65          70          75          80
Ser Arg Ser Met Leu Gly Thr Ser His His Ser Ala Leu Pro Ala Arg
  85          90          95
His Gln Ile Trp Val Val Cys Gly Val Ile Glu Arg Asp Ser Ala Arg
  100         105         110
Gly Leu Ser Val Phe Ala Gln Trp Ser Pro Ser Met Pro Lys Ala Arg
  115         120         125
Ser Ala Val Cys Thr Ala Ser Cys Arg Pro Thr Lys Asn Ala Trp Cys
  130         135         140
Gly Arg Pro Ala Thr Arg Thr Asp Cys Ala Ala Ile Arg Ser Ala Ser
  145         150         155         160

```

Ser Ala Ser Ala Ala Gln Leu Leu Gly Glu Leu Asp Ala Ala Gly Ala
 165 170 175
 Arg Arg Pro Val Arg Pro Gly Arg Val Phe Ala Cys Cys Ile Leu Ala
 180 185 190
 Arg Gln Ser Pro Gln His Arg Asp His Tyr Ser Leu His Arg Pro Arg
 195 200 205
 Arg Pro Gln Leu Arg Ala Ser Ala Ser Ser Val Leu His Arg Asp Asp
 210 215 220
 Leu Pro Asp Ser Val Pro Ala Leu Ser Val Leu Arg Asp Cys Leu Arg
 225 230 235 240
 Thr Trp Pro Thr Ala Ala Pro Ala Ser Pro Ala Pro Thr Asp Ile Ser
 245 250 255
 Ser Ser Arg Ser Ser Pro Gly Arg Ala Ala Arg Ala Asp Arg Ser
 260 265 270
 Cys Pro Gly Thr Arg Gly Thr Ser Glu Leu Arg Pro Leu Gly His Tyr
 275 280 285
 Ser Arg Pro Glu Leu Leu Ser Leu Val Val Asp Thr Arg Arg Ala Ser
 290 295 300
 Gly Val Gln Ile Val Asn Ala Asp His Gly Phe Lys Pro
 305 310 315

<210> 369

<211> 1074

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 369

atgtccgaag	agaacaccac	caccgaatca	agctcggacg	cgatctggac	cgttgcgggc	60
gtccaggcgg	cgccggtgtt	cttgaatcgg	gatgcgacgg	tgcgtaaggc	cgtctcgctg	120
attgccgagg	ccgcggcgca	cggcgcgcg	ctcattgttt	ttcccagggc	gttcattcca	180
tcgtacccgg	attgggcgtg	ggcgggtccc	cccggacagg	gcggaaccaa	ctcgagactg	240
tatgccaaac	tgctcgacaa	ttcggttacg	gtgcccagcc	cagccaccga	tgccctggcc	300
agggcggtc	gcgacgcggg	cgctacgtc	gtcatgggca	taaacgagcg	gaacacggcg	360
gcgagcgggc	gaagtctcta	caacagcttg	ctctatatg	gtccggacgg	tcgcatcctg	420
ggcattcatc	ggaagtgtgt	gccgacctcg	gcggagcggc	tgatctgggc	acaaggcgat	480
ggaagcacgc	ttggcgtgtt	cgatacgccg	ggcgccggcg	ttggcggcct	gatctgctgg	540
gaaaactata	tgccgctggc	ccgataattc	atgtacgcgc	gcggcggtgca	aatatatgtt	600
gcggcgacct	gggacagggg	cgagccatgg	ctttcgacgc	tgcgacacat	agccaaggaa	660
ggccagacct	acgtgatagg	ctgttgcatc	gccatgcgga	cggccgacat	cgacgacgcc	720
gagctcgtcg	agaagtatta	cgcggacgcc	ggtgagtggg	tcaatgaagg	cgacagcgcg	780
attgtcgatc	cgagcggaac	aatcattgcc	ggtccggccc	atcagaccac	tgaaatcctc	840
tacgccgcga	tcgatcgcca	gaagggtgctg	gaatcaaaat	ggatgttgga	cgtggccggg	900
cactacgcgc	gtccggacgt	gttttcattt	ggcgttcgaa	ccgatgccaa	cccgataatg	960
accatgaacg	aaccaagcgc	gacggccgag	ccgaggcaca	atagcgcggg	agccgagggt	1020
cgcgacggcc	tacgcggggc	tcgtgaccct	cgctcgagaa	ttcggcagat	gtag	1074

<210> 370

<211> 346

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 370

Met	Ser	Glu	Glu	Asn	Thr	Thr	Thr	Glu	Ser	Ser	Ser	Asp	Ala	Ile	Trp
1				5				10					15		
Thr	Val	Ala	Ala	Val	Gln	Ala	Ala	Gly	Val	Leu	Glu	Ser	Gly	Cys	Asp

20 25 30
 Gly Ala Gly Arg Leu Ala Asp Cys Arg Gly Arg Gly Ala Arg Ala Arg
 35 40 45
 Leu Ile Val Phe Pro Glu Ala Phe Ile Pro Ser Tyr Pro Asp Trp Ala
 50 55 60
 Trp Ala Val Pro Pro Gly Gln Ala Glu Pro Thr Arg Asp Cys Met Pro
 65 70 75 80
 Asn Cys Ser Thr Ile Arg Leu Arg Cys Pro Ala Gln Pro Pro Met Pro
 85 90 95
 Gly Gln Gly Gly Ser Arg Arg Gly Arg Leu Arg Arg His Gly His Lys
 100 105 110
 Arg Ala Glu His Gly Gly Ser Gly Gly Ser Leu Tyr Asn Ser Leu Leu
 115 120 125
 Tyr Ile Gly Pro Asp Gly Arg Ile Leu Gly Ile His Arg Lys Leu Cys
 130 135 140
 Arg Pro Arg Arg Ser Gly Ser Gly His Lys Ala Met Glu Ala Arg Leu
 145 150 155 160
 Ala Cys Ser Ile Arg Arg Ala Ala Gly Leu Ala Ala Ser Ala Gly Lys
 165 170 175
 Thr Ile Cys Arg Trp Pro Asp Ile Arg Cys Thr Arg Ala Val Gln Ile
 180 185 190
 Tyr Val Ala Ala Thr Trp Asp Arg Gly Glu Pro Trp Leu Ser Thr Leu
 195 200 205
 Arg His Ile Ala Lys Lys Ala Arg Pro Thr Ala Val Ala Ser Pro Cys
 210 215 220
 Gly Arg Pro Thr Ser Thr Thr Pro Ser Ser Ser Arg Ser Ile Thr Arg
 225 230 235 240
 Thr Pro Val Ser Gly Ser Met Lys Ala Thr Ala Arg Leu Ser Ile Arg
 245 250 255
 Ala Glu Ile Ile Ala Gly Pro Ala His Gln Thr Asn Glu Ile Leu Tyr
 260 265 270
 Ala Ala Ile Asp Arg Gln Lys Val Leu Glu Lys Met Asp Val Gly Arg
 275 280 285
 Gly Arg Ala Leu Arg Ala Ser Gly Arg Val Phe Ile Trp Arg Ser Asn
 290 295 300
 Arg Cys Gln Pro Asp Asn Asp His Glu Arg Thr Lys Arg Asp Gly Arg
 305 310 315 320
 Ala Glu Ala Gln Arg Gly Ser Arg Val Ala Thr Ala Tyr Ala Gly Val
 325 330 335
 Val Thr Leu Ala Arg Glu Phe Gly Arg Cys
 340 345

<210> 371

<211> 1014

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 371

atgggtatcg	aacatccgaa	gtacaagggt	gcggtggtac	aggcggcgcc	ggcctggctc	60
gatctcgacg	catcgatcgc	caagaccatc	gcgctgatcg	aggaggcggc	cgccaagggc	120
gccaaagctga	tcgcattccc	tgaggccttc	attcccggct	atccttgcca	tatctggatg	180
gactcgccgg	cctgggcgat	cgggcgcgga	ttgtgcagc	gctatttcga	caattcgctt	240
tcctacgaca	gcccgcaggc	cgaacggctg	cggtcgcgg	tgaagaaggc	cggcatacacc	300
gccgtgctcg	gcctgtccga	gcgggaaggc	ggcagccttt	atctcgcgca	atggctgatc	360
ggtcccgcag	gcgagaccat	cgccaagcgg	cgcaagctgc	ggccgacgca	tgccgagcgc	420
accgtctacg	gcgaaggcga	cggcagtgac	cttgcggtcc	atgaccgcgc	tgacattggc	480
cgctcggcg	cgctgtgctg	ctgggaacat	ctgcagccgc	tgtcgaaata	cgccatgtat	540
gcccagaacg	agcaggtgca	tgtcgcggcc	tgcccgagtt	tttcgctgta	cgacccgttc	600

```

gcgccggcgc tgggctggga ggtcaacaac gcggcatccc gcgtctatgc ggtcgaaggc 660
tcctgcttcg tgctggcgcc gtgtgccacc gtctcgagg cgatgggtga cgaactctgc 720
gaccgcgacg acaagcatgc gctgctgcat gtcggcggcg gccacgcgc gatctacgga 780
ccggacggca gctcgatggc gaacaagctc gatcccgagc aggagggcct gctgttcgcc 840
gacatcgatc tcggggcgat cgggggtggca aagaacgccg ccgatccggc cgggcactat 900
tcgcgccggg atgtgaccgc tctgctcttg aacagaaaac cctcaaagcg cgtcgagcac 960
tttgcgctgc cgctcgacca tctcgcgac gagggcggtg ctccggtgac ctga 1014

```

<210> 372

<211> 327

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 372

```

Met Gly Ile Glu His Pro Lys Tyr Lys Val Ala Val Val Gln Ala Ala
 1          5          10          15
Pro Ala Trp Leu Asp Leu Asp Ala Arg Ser Pro Arg Pro Ser Arg Ser
 20          25          30
Arg Arg Arg Pro Pro Arg Ala Pro Ser Ser His Ser Leu Ala Phe Ile
 35          40          45
Pro Gly Tyr Pro Trp His Ile Trp Met Asp Ser Pro Ala Trp Ala Ile
 50          55          60
Gly Arg Gly Phe Val Gln Ala Ile Ser Thr Ile Arg Phe Pro Thr Thr
 65          70          75          80
Ala Arg Arg Pro Asn Gly Cys Gly Ser Arg Arg Arg Pro His His Arg
 85          90          95
Arg Ala Arg Pro Val Arg Ala Gly Arg Gln Pro Leu Ser Arg Ala
100          105          110
Met Ala Asp Arg Ser Thr Ala Arg Pro Ser Pro Ser Gly Ala Ser Cys
115          120          125
Gly Arg Arg Met Pro Ser Ala Pro Ser Thr Ala Lys Ala Thr Ala Val
130          135          140
Thr Leu Arg Ser Met Thr Ala Leu Thr Leu Ala Val Ser Ala Arg Cys
145          150          155          160
Ala Ala Gly Asn Leu Gln Pro Leu Ser Lys Tyr Ala Met Tyr Ala Gln
165          170          175
Asn Glu Gln Val His Val Ala Ala Trp Pro Ser Phe Ala Val Arg Pro
180          185          190
Val Arg Ala Gly Ala Gly Leu Gly Gly Gln Gln Arg Gly Ile Pro Arg
195          200          205
Leu Cys Gly Arg Gly Ser Cys Phe Val Leu Ala Pro Cys Ala Thr Val
210          215          220
Ser Gln Ala Met Val Asp Glu Leu Cys Asp Arg Asp Gln Ala Cys Ala
225          230          235          240
Ala Ala Cys Arg Arg Arg Pro Arg Arg Asp Leu Arg Thr Gly Arg Gln
245          250          255
Leu Asp Gly Thr Ser Ser Ile Pro Ser Arg Arg Ala Cys Cys Ser Pro
260          265          270
Thr Ser Ile Ser Gly Arg Ser Gly Trp Gln Arg Thr Pro Pro Ile Arg
275          280          285
Pro Gly Thr Ile Arg Gly Arg Met Pro Val Cys Ser Thr Glu Asn Pro
290          295          300
Gln Ala Arg Arg Ala Leu Cys Ala Ala Ala Arg Pro Ser Arg Gly Arg
305          310          315          320
Gly Arg Cys Ser Gly Asp Leu
325

```

<210> 373

<211> 1056

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 373

```

atgacgaatt ttctggacgt gacggtggca gcggttcagg cggctcccgt ctatttcgat      60
cgggaggcat cgacggagaa agcgtgccgg ttgatccacg aagcggcagg gctcggcgcg      120
acgctcgag cgttcggcga aacctggttg ccagggtatc cgttcttcgt ctgggggttc      180
gcgcacaacc ggagcctgtt ctggcaggcc gccgccgagt acatcgccaa tgcggtggag      240
attccgagtc ccacaacgga ccgtctctgt gcggcggcga aggctgccgg ggctcgacgtc      300
gtcattggcg tcgttgaact ggatgaacga acacgagctt cggtttacag tacgctgctt      360
ttcatcggtc gcgacgggac gatcctgggc cgccaccgca agctgaagcc aacacacatg      420
gagcggacga tctggggcga aggggacgca tatggactcc gcgtctacga acgttcgtac      480
ggcgcggtga gcgcctgaa ttgctgggaa cacaatatga tgctgcccg ctacgtgctt      540
gccgcacagg gcacgcagtt tcacgtcgcc gcatggcccg gaaaggagag gctcaccgtc      600
ccgccgaacg aagcggctta tacgcgccag cttctcctct ctcgcgcgta tgcatcccag      660
gccggcgcgat acgtgatcag cgtcgccggg ctgctcgcac cagactccat gcccgagcgt      720
tatcgcgagt tagggcggtc atatgagttg accggcgaca gcgtcatcgt cgaccgcgc      780
ggcgaggtca ttgcggggcc tgcaaaaggc gagaccatcc tgctcgcgca gtgcagtcag      840
gaagctctcc tcgcggccaa gtccgccatc gacctcggcg gccattactc acgcccggat      900
atctttcagc tcggtgtcaa cgtcaactg cagcatcggg tccggagagt tgagccacac      960
ttcacggcgg cgtcgggaca tatcggagcc gagcgccgat cccaggagga tgggtactggt     1020
cccttcgacc tggcgggaatc tctcacgaac tcctag                                1056

```

<210> 374

<211> 351

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 374

```

Met Thr Asn Phe Leu Asp Val Thr Val Ala Ala Val Gln Ala Ala Pro
 1          5          10          15
Val Tyr Phe Asp Arg Glu Ala Ser Thr Glu Lys Ala Cys Arg Leu Ile
      20          25          30
His Glu Ala Ala Gly Leu Gly Ala Thr Leu Ala Ala Phe Gly Glu Thr
      35          40          45
Trp Leu Pro Gly Tyr Pro Phe Val Trp Gly Phe Ala His Asn Arg
      50          55          60
Ser Leu Phe Trp Gln Ala Ala Ala Glu Tyr Ile Ala Asn Ala Val Glu
      65          70          75          80
Ile Pro Ser Pro Thr Thr Asp Arg Leu Cys Ala Ala Ala Lys Ala Ala
      85          90          95
Gly Val Asp Val Val Ile Gly Val Val Glu Leu Asp Glu Arg Thr Arg
      100         105         110
Ala Ser Val Tyr Ser Thr Leu Leu Phe Ile Gly Arg Asp Gly Thr Ile
      115         120         125
Leu Gly Arg His Arg Lys Leu Lys Pro Thr His Met Glu Arg Thr Ile
      130         135         140
Trp Gly Glu Gly Asp Ala Tyr Gly Leu Arg Val Tyr Glu Arg Ser Tyr
      145         150         155         160
Gly Arg Leu Ser Gly Leu Asn Cys Trp Glu His Asn Met Met Leu Pro
      165         170         175
Gly Tyr Val Leu Ala Ala Gln Gly Thr Gln Phe His Val Ala Ala Trp
      180         185         190
Pro Gly Lys Glu Arg Leu Thr Val Pro Pro Asn Glu Ala Ala Tyr Thr

```

```

      195              200              205
Arg  Gln  Leu  Leu  Leu  Ser  Arg  Ala  Tyr  Ala  Ser  Gln  Ala  Gly  Ala  Tyr
210              215              220
Val  Ile  Ser  Val  Ala  Gly  Leu  Leu  Ala  Pro  Asp  Ser  Met  Pro  Glu  Arg
225              230              235              240
Tyr  Arg  Glu  Leu  Gly  Arg  Ser  Tyr  Glu  Leu  Thr  Gly  Asp  Ser  Val  Ile
      245              250              255
Val  Asp  Pro  Arg  Gly  Glu  Val  Ile  Ala  Gly  Pro  Ala  Lys  Gly  Glu  Thr
      260              265              270
Ile  Leu  Leu  Ala  Gln  Cys  Ser  Gln  Glu  Ala  Leu  Leu  Ala  Ala  Lys  Ser
      275              280              285
Ala  Ile  Asp  Leu  Gly  Gly  His  Tyr  Ser  Arg  Pro  Asp  Ile  Phe  Gln  Leu
      290              295              300
Arg  Val  Asn  Asp  Gln  Leu  Gln  His  Arg  Val  Arg  Arg  Val  Glu  Pro  His
305              310              315              320
Phe  Thr  Ala  Ala  Ile  Gly  His  Ile  Gly  Ala  Glu  Arg  Arg  Ser  Gln  Glu
      325              330              335
Asp  Gly  Thr  Gly  Pro  Phe  Asp  Leu  Ala  Glu  Ser  Leu  Thr  Asn  Ser
      340              345              350

```

<210> 375

<211> 939

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 375

```

atgaccaaaa tcgctgtcat tcaagaaccc ccggtctatc tgaatctgag caaatcgatg      60
gaccgagcgg tcgacttgat tgccgatgcc gcgagccagg ggtgtcagtt gattgtgttt      120
cccgaagcct ggcttgagg ttaccccacc ttcgtctggc gtcttgccgc gggcagcgga      180
atgggaaaaa ccgatgagct ttacgcgcgt ttgctcgcca actcggtcga ccgcagcaaa      240
gaggggcttc ggcctttgca ggaggctgca aaagagcatg gcgttgtcat tgttctgggt      300
tatcaagagg tggacggctc gggcagcagc agcacaatct tcaacagctg cgcgattatt      360
gatgccgacg ggcgactggc caacaacat cgcaagttga tgcccaccaa tgcggagcgg      420
atggtgtggg ggtttggcga cggttcgggc ctgaacgttg ttgacaccgc ggtgggcagg      480
atcggcacgc tgatttgctg ggaactac atgcccttgg cgcgctacgc gctgtatgcc      540
caaacatcg aaatctatgt ggcgcgac tgggacagcg gtgccatgtg gcaagccacc      600
ctgcaacata tcgcacgtga agtggtgc tggtcatcg gatgtgcaac ctcgctgcaa      660
gcctctgaca tcccggacga ccttcccat cgggatgagt tattcccga caaagacgaa      720
tgggtgaacc ctggcgatgc ggtggtttac aaacctttg gcggccttgt ggccggcccc      780
atgcatcagg aaaaggggct tctcatcgca gattggacg tcgccgctgt tcaggtctca      840
cgtcggaagt tcgatgcgac cgggcattac gctcgcccc atgtcttcca actgcacgtg      900
aatcgacgcg cgatgcggcc ggttgagttc acgaattag      939

```

<210> 376

<211> 312

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 376

```

Met  Thr  Lys  Ile  Ala  Val  Ile  Gln  Glu  Pro  Val  Tyr  Leu  Asn  Leu
 1              5              10              15
Ser  Lys  Ser  Met  Asp  Arg  Ala  Val  Asp  Leu  Ile  Ala  Asp  Ala  Ser
      20              25              30
Gln  Gly  Cys  Gln  Leu  Ile  Val  Phe  Pro  Glu  Ala  Trp  Leu  Ala  Gly  Tyr
      35              40              45

```

Pro Thr Phe Val Trp Arg Leu Ala Pro Gly Ser Gly Met Gly Lys Thr
 50 55 60
 Asp Glu Leu Tyr Ala Arg Leu Leu Ala Asn Ser Val Asp Arg Ser Lys
 65 70 75 80
 Glu Gly Leu Arg Pro Leu Gln Glu Ala Ala Lys Glu His Gly Val Val
 85 90 95
 Ile Val Leu Gly Tyr Gln Glu Val Asp Gly Ser Gly Ser Ser Thr
 100 105 110
 Ile Phe Asn Ser Cys Ala Ile Ile Asp Ala Asp Gly Arg Leu Ala Asn
 115 120 125
 Asn His Arg Lys Leu Met Pro Thr Asn Ala Glu Arg Met Val Trp Gly
 130 135 140
 Phe Gly Asp Gly Ser Gly Leu Asn Val Val Asp Thr Ala Val Gly Arg
 145 150 155 160
 Ile Gly Thr Leu Ile Cys Trp Glu Asn Tyr Met Pro Leu Ala Arg Tyr
 165 170 175
 Ala Leu Tyr Ala Gln Asn Ile Glu Ile Tyr Val Ala Pro Thr Trp Asp
 180 185 190
 Ser Gly Ala Met Trp Gln Ala Thr Leu Gln His Ile Ala Arg Glu Gly
 195 200 205
 Gly Cys Trp Val Ile Gly Cys Ala Thr Ser Leu Gln Ala Ser Asp Ile
 210 215 220
 Pro Asp Asp Leu Pro His Arg Asp Glu Leu Phe Pro Asn Lys Asp Glu
 225 230 235 240
 Trp Val Asn Pro Gly Asp Ala Val Val Tyr Lys Pro Phe Gly Gly Leu
 245 250 255
 Val Ala Gly Pro Met His Gln Glu Lys Gly Leu Leu Ile Ala Glu Leu
 260 265 270
 Asp Val Ala Ala Val Gln Val Ser Arg Arg Lys Phe Asp Ala Thr Gly
 275 280 285
 His Tyr Ala Arg Pro Asp Val Phe Gln Leu His Val Asn Arg Ser Ala
 290 295 300
 Met Arg Pro Val Glu Phe Thr Asn
 305 310

<210> 377

<211> 1050

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 377

atgtccagca	ccacccatcc	ccgcctgcgc	gtcgccgcgc	tgcaagccgc	ccccgtcttc	60
ctcgacctcg	acggcaccat	cgacaagacc	atcgacctga	tgccccgggc	ggccggccag	120
ggcgtgcagc	tgatcgccct	tcccagagacc	tggggtgccc	gctatccgtg	gtggatctgg	180
ctcgattcgc	cggcctgggg	catgcagttc	gtgcagcgct	accacgacaa	cggcctgggc	240
gtcggctcgc	ccgagttcga	ccgcattcgc	gaggccgcgc	gcaagcaccg	catctgggtc	300
tcgctcggct	acagcgagaa	ggccgcccgc	agcctctaca	tcgcccaggc	gctgatcgac	360
gaccagggca	acacgctgca	gactcggcgc	aagctcaagc	cgacgcacgt	ggagcgcacc	420
gtgttcggcg	agggcgacgg	atcggacctg	agcgtggctg	agacggctat	cggcaacatc	480
ggctcgctgt	cgtgctggga	gcacctgcag	ccgctcagca	agtacgcgat	gtactcgcag	540
aacgagcaga	tccattgcgg	cgcctggccc	agcttctcgc	tctaccgcgg	cggcgcctac	600
gcgctcggcg	ccgaagtga	caacgccgcc	agccaggtgt	acgcggccga	gggccagtgc	660
ttcgtgatcg	cgccctgcgc	cacggtctcg	aaggcgatgc	acgaactgct	gtgcaccgac	720
cctggcaagc	agcagatgct	gctggctcgc	ggcggcttcg	cgcgcatcta	cggacccgac	780
ggatcgccgc	tcggcaagaa	cctggcagag	gacgaggaag	ggctgggtgt	ggccgacatc	840
gacctcggca	tgatctccct	ggccaaggcg	gccggcgacc	cggccggcca	ctattcgcgg	900
cccgcagtg	cgagttgct	gttcaacagg	aagcggcgcg	agccgggtgt	gctgcaaggc	960
ccggccgagc	ccgagaaggc	ggtcgccgag	ccggtgtcca	cgccgagcga	agcggcgcg	1020

gcccgcgccc gccagccggt cgtggcctga

1050

<210> 378

<211> 349

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 378

```

Met Ser Ser Thr Thr His Pro Arg Leu Arg Val Ala Ala Val Gln Ala
 1          5          10          15
Ala Pro Val Phe Leu Asp Leu Asp Gly Thr Ile Asp Lys Thr Ile Asp
          20          25          30
Leu Met Ala Arg Ala Ala Gly Gln Gly Val Gln Leu Ile Ala Phe Pro
          35          40          45
Glu Thr Trp Val Pro Gly Tyr Pro Trp Trp Ile Trp Leu Asp Ser Pro
          50          55          60
Ala Trp Gly Met Gln Phe Val Gln Arg Tyr His Asp Asn Ala Leu Val
          65          70          75          80
Val Gly Ser Pro Glu Phe Asp Arg Ile Arg Glu Ala Ala Arg Lys His
          85          90          95
Arg Ile Trp Val Ser Leu Gly Tyr Ser Glu Lys Ala Ala Gly Ser Leu
          100          105          110
Tyr Ile Ala Gln Ala Leu Ile Asp Asp Gln Gly Asn Thr Leu Gln Thr
          115          120          125
Arg Arg Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu
          130          135          140
Gly Asp Gly Ser Asp Leu Ser Val Val Glu Thr Ala Ile Gly Asn Ile
          145          150          155          160
Gly Ser Leu Ser Cys Trp Glu His Leu Gln Pro Leu Ser Lys Tyr Ala
          165          170          175
Met Tyr Ser Gln Asn Glu Gln Ile His Cys Gly Ala Trp Pro Ser Phe
          180          185          190
Ser Leu Tyr Arg Gly Gly Ala Tyr Ala Leu Gly Ala Glu Val Asn Asn
          195          200          205
Ala Ala Ser Gln Val Tyr Ala Ala Glu Gly Gln Cys Phe Val Ile Ala
          210          215          220
Pro Cys Ala Thr Val Ser Lys Ala Met His Glu Leu Leu Cys Thr Asp
          225          230          235          240
Pro Gly Lys Gln Gln Met Leu Leu Val Gly Gly Gly Phe Ala Arg Ile
          245          250          255
Tyr Gly Pro Asp Gly Ser Pro Leu Gly Lys Asn Leu Ala Glu Asp Glu
          260          265          270
Glu Gly Leu Val Val Ala Asp Ile Asp Leu Gly Met Ile Ser Leu Ala
          275          280          285
Lys Ala Ala Gly Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val Thr
          290          295          300
Gln Leu Leu Phe Asn Arg Lys Arg Arg Glu Pro Val Val Leu Gln Gly
          305          310          315          320
Pro Ala Glu Pro Glu Lys Ala Val Ala Glu Pro Val Ser Thr Pro Ser
          325          330          335
Glu Ala Ala Ala Ala Ala Ala Arg Gln Pro Val Val Ala
          340          345

```

<210> 379

<211> 936

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 379

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atggctaaaa tagcgattgt acaaaaggcg tctgttacct tgaataaaca agaaactgtc      60
gccagtgtctg taagagaggt agagctggca gcggcggaag gtgccgagct ggtagtgttt      120
actgagggcat ttattgctgg gtatccggcc tggatctggc gtttgcggcc aggtgggtgac      180
tggggggctat ctgaagatct tcattcccggt ttgttgacaa gcgccgtaga cctgggtggt      240
gatgacctgg atccacttta tgccgcagct aaagaaaata acgtgacgat agtggtgcggt      300
attaatgaac gtgataaccg gctcagtaag gcaacgctat ataattctat cgttattatt      360
ggttccgatg gttcattggt aaatcgacat cgtaagtga tgccgacgaa tccggagaga      420
atggtatggg gctttggtga tgcctctggt ctgaaggctg ttgatacccc cgttggctcg      480
gttggttacgc ttgtctggtg ggaaaactat atgcccttgg ccagatatgc gttgtattcg      540
cagggggttag aggtttatat tgcgccgacc tacgatagcg gtgatgactg gatttctaca      600
ttacagcata ttgccaggga gggctcgtgt tgggttggtg gctgtggcaa tctattgcgt      660
ggcagcgata taccggatga cttccctgag aagttggcgt tatacccaga tgaggatgag      720
tgataaatc ctggggattc cgttgtgatt gcacctgggg gtaaaatcat ggccggggcca      780
ttgcgccagg aggcggggat tgtctattgt gatattgcgt ctgaaagtgc cagtcaggca      840
aaacgtgcgc tggatgtggc tggacattat tcccggcctg atatctttga gttgcatgtg      900
aatacgaagg tgcagacccc ggttgatat gattag                                936

```

<210> 380

<211> 311

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 380

```

Met Ala Lys Ile Ala Ile Val Gln Lys Ala Ser Val Thr Leu Asn Lys
 1          5          10          15
Gln Glu Thr Val Ala Ser Ala Val Arg Glu Val Glu Leu Ala Ala Ala
 20          25          30
Glu Gly Ala Glu Leu Val Val Phe Thr Glu Ala Phe Ile Ala Gly Tyr
 35          40          45
Pro Ala Trp Ile Trp Arg Leu Arg Pro Gly Gly Asp Trp Gly Leu Ser
 50          55          60
Glu Asp Leu His Ser Arg Leu Leu Thr Ser Ala Val Asp Leu Gly Gly
 65          70          75          80
Asp Asp Leu Asp Pro Leu Tyr Ala Ala Ala Lys Glu Asn Asn Val Thr
 85          90          95
Ile Val Cys Gly Ile Asn Glu Arg Asp Asn Arg Leu Ser Lys Ala Thr
100          105          110
Leu Tyr Asn Ser Ile Val Ile Ile Gly Ser Asp Gly Ser Leu Leu Asn
115          120          125
Arg His Arg Lys Leu Met Pro Thr Asn Pro Glu Arg Met Val Trp Gly
130          135          140
Phe Gly Asp Ala Ser Gly Leu Lys Val Val Asp Thr Pro Val Gly Arg
145          150          155          160
Val Gly Thr Leu Val Cys Trp Glu Asn Tyr Met Pro Leu Ala Arg Tyr
165          170          175
Ala Leu Tyr Ser Gln Gly Val Glu Val Tyr Ile Ala Pro Thr Tyr Asp
180          185          190
Ser Gly Asp Asp Trp Ile Ser Thr Leu Gln His Ile Ala Arg Glu Gly
195          200          205
Arg Cys Trp Val Val Gly Cys Gly Asn Leu Leu Arg Gly Ser Asp Ile
210          215          220
Pro Asp Asp Phe Pro Glu Lys Leu Ala Leu Tyr Pro Asp Glu Asp Glu
225          230          235          240
Trp Ile Asn Pro Gly Asp Ser Val Val Ile Ala Pro Gly Gly Lys Ile

```

```

                245                250                255
Met Ala Gly Pro Leu Arg Gln Glu Ala Gly Ile Val Tyr Cys Asp Ile
                260                265                270
Ala Ser Glu Ser Ala Ser Gln Ala Lys Arg Ala Leu Asp Val Ala Gly
                275                280                285
His Tyr Ser Arg Pro Asp Ile Phe Glu Leu His Val Asn Thr Lys Val
                290                295                300
Gln Thr Pro Val Val Tyr Asp
305                310

```

<210> 381

<211> 945

<212> DNA

<213> Clostridium acetobutylicum ATCC 3625

<400> 381

```

atgggcgaat tccgtgaagt taccctgggc gtggctcagg ctgctcccgt gtactttgac      60
cgcgaggcct cgaccgagaa agcctgtggc ctgatccgcg aggcgggcga aaagggtgta      120
gatcttctgg cgttcgggtga aacgtgggta accggctatc catactggaa agatgcgcct      180
tggtctcgcg aatacaacga cttgcgtgca cgttatgttg cgaacgggtg gatgattcct      240
ggtccggaaa cggacgctct gtgccaagca gccgcggaag caggtgtgga tgtggcgatc      300
ggagtagtag aactggagcc gggctctctt tcctcggttt attgactct gttatttata      360
agccgcgagg gcgagatcct gggctgtcac cgcaaaactga aaccgaccga tagcgaacgt      420
cgttactggg ctgaaggcga cgcgactggg ctgcgcgttt atgagcgccc atatggtcgg      480
cttagcggcc tgaattgctg ggagcacact atgatgctgc cggggtacgc cctggcgggc      540
cagggcaccc agttccatgt ggccgcttgg ccaaacatgg catcctcgaa ttctgaactt      600
ctgtctcgtg cctacgctat gcaggcgggc tgctacgttt tatgcgcggg tggcctgggc      660
ccggcccccag gtgaactgcc ggatggtatc gcggcggaaa gtttagatca cttgactgga      720
gagtcagtga tcatcgaccc gtgggggaaa gtaattgctg gtccggtgtc ttgcgaggaa      780
acccttatca cggctcgcgt tagcaccgca tctatttata gccgcaaaag tttgacggac      840
gtgggcggtc attatagccg cccggatgtt ttccgttttg aagtcgatcg ctctgagcgt      900
ccccgtgtcg tgtttcgcga tggtagcgtg gatgaccgag gtttaa      945

```

<210> 382

<211> 314

<212> PRT

<213> Clostridium acetobutylicum ATCC 3625

<400> 382

```

Met Gly Glu Phe Gly Glu Val Thr Leu Gly Val Ala Gln Ala Ala Pro
 1          5          10          15
Val Tyr Phe Asp Arg Glu Ala Ser Thr Glu Lys Ala Cys Gly Leu Ile
          20          25          30
Arg Glu Ala Gly Glu Lys Gly Val Asp Leu Leu Ala Phe Gly Glu Thr
          35          40          45
Trp Leu Thr Gly Tyr Pro Tyr Trp Lys Asp Ala Pro Trp Ser Arg Glu
          50          55          60
Tyr Asn Asp Leu Arg Ala Arg Tyr Val Ala Asn Gly Val Met Ile Pro
          65          70          75          80
Gly Pro Glu Thr Asp Ala Leu Cys Gln Ala Ala Ala Glu Ala Gly Val
          85          90          95
Asp Val Ala Ile Gly Val Val Glu Leu Glu Pro Gly Ser Leu Ser Ser
          100          105          110
Val Tyr Cys Thr Leu Leu Phe Ile Ser Arg Glu Gly Glu Ile Leu Gly
          115          120          125
Arg His Arg Lys Leu Lys Pro Thr Asp Ser Glu Arg Arg Tyr Trp Ser
          130          135          140
Glu Gly Asp Ala Thr Gly Leu Arg Val Tyr Glu Arg Pro Tyr Gly Arg
          145          150          155          160
Leu Ser Gly Leu Asn Cys Trp Glu His Thr Met Met Leu Pro Gly Tyr
          165          170          175

```


Ala Leu Ala Ala Gln Gly Thr Gln Phe His Val Ala Ala Trp Pro Asn
 180 185 190
 Met Ala Ser Ser Asn Ser Glu Leu Leu Ser Arg Ala Tyr Ala Met Gln
 195 200 205
 Ala Gly Cys Tyr Val Leu Cys Ala Gly Gly Leu Gly Pro Ala Pro Gly
 210 215 220
 Glu Leu Pro Asp Gly Ile Ala Ala Glu Ser Leu Asp His Leu Thr Gly
 225 230 235 240
 Glu Ser Cys Ile Ile Asp Pro Trp Gly Lys Val Ile Ala Gly Pro Val
 245 250 255
 Ser Cys Glu Glu Thr Leu Ile Thr Ala Arg Val Ser Thr Ala Ser Ile
 260 265 270
 Tyr Arg Arg Lys Ser Leu Thr Asp Val Gly Gly His Tyr Ser Arg Pro
 275 280 285
 Asp Val Phe Arg Phe Glu Val Asp Arg Ser Glu Arg Pro Arg Val Val
 290 295 300
 Phe Arg Asp Gly Asp Val Asp Arg Gly
 305 310

<210> 383
 <211> 1041
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 383
 atgtcggagc ccatgacgaa gtatcgcggc gcggcgggtgc aggccgcgcc ggtgttcctc 60
 gatctcgacc gcacagtcga gaaagcgatc ggcctgatcg agcaggcggc caagcaggac 120
 gtgcgcctga tcgcattccc agagacttgg attcccggt atcccttttg gatatggctg 180
 ggcgcgcggg cttggggcat gcgcttcgtc cagcgctatt tcgagaattc gctcgtgcgc 240
 ggcagcaagc agtggcaggc cctggcggat gcggcccgcc gccacggcat gcatgtcgtg 300
 gccggctata gcgagcgcgc gggcggcagc ctctatatgg gccaggcgat cttcggcccc 360
 gatggcgatc tgatcgccgc gcgccgcaag ctcaagccta cccatgcgga gcgcaccgtg 420
 ttcggcgagg gagacggcag ccatctcgcg gtgcacgata ccgccatcgg gcgcctcggc 480
 gcgctctgtt gctgggagca catccagcca ttgtcgaaat acgccatgta cgccgcccgc 540
 gaacaggtcc acgtcgcgtc gtggccgagc ttcagcctct atcgcgcat ggcctatgcg 600
 ctcggaaccg aggtcaatac cgccgcaagc cagatctacg cggtcgaggg cggctgctac 660
 gtgctggcgt cgtgcgcgac cgtttcgccg gagatgatca aggtattggt ggatacgccc 720
 gacaaggaga tgttcctcaa ggccggcggc ggttttgcca tgattttcgg gcccgacggc 780
 cgcgcctcgg ccgagccgct cccggagacc gaagagggac tgctggtcgc cgatatcgac 840
 ctcggcctga tcgctgtgac caaggcggcg gccgatccgg cgggccacta ttcacggccc 900
 gacgtaacgc ggtgctgct ggatcgacgt ccggcccaac gcgtcgctac gcttgatgcc 960
 gcattcgaac cgcaaaacga ggacaagggc gacgcgccc cgctgcgct ggtggcgga 1020
 agcgccgccc ccgcgcagta g 1041

<210> 384
 <211> 346
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 384
 Met Ser Glu Pro Met Thr Lys Tyr Arg Gly Ala Ala Val Gln Ala Ala
 1 5 10 15
 Pro Val Phe Leu Asp Leu Asp Arg Thr Val Glu Lys Ala Ile Gly Leu
 20 25 30
 Ile Glu Gln Ala Ala Lys Gln Asp Val Arg Leu Ile Ala Phe Pro Glu

```

      35      40      45
Thr Trp Ile Pro Gly Tyr Pro Phe Trp Ile Trp Leu Gly Ala Pro Ala
  50      55      60
Trp Gly Met Arg Phe Val Gln Arg Tyr Phe Glu Asn Ser Leu Val Arg
  65      70      75      80
Gly Ser Lys Gln Trp Gln Ala Leu Ala Asp Ala Ala Arg Arg His Gly
      85      90      95
Met His Val Val Ala Gly Tyr Ser Glu Arg Ala Gly Gly Ser Leu Tyr
      100      105      110
Met Gly Gln Ala Ile Phe Gly Pro Asp Gly Asp Leu Ile Ala Ala Arg
      115      120      125
Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly Glu Gly
      130      135      140
Asp Gly Ser His Leu Ala Val His Asp Thr Ala Ile Gly Arg Leu Gly
  145      150      155      160
Ala Leu Cys Cys Trp Glu His Ile Gln Pro Leu Ser Lys Tyr Ala Met
      165      170      175
Tyr Ala Ala Asp Glu Gln Val His Val Ala Ser Trp Pro Ser Phe Ser
      180      185      190
Leu Tyr Arg Gly Met Ala Tyr Ala Leu Gly Pro Glu Val Asn Thr Ala
      195      200      205
Ala Ser Gln Ile Tyr Ala Val Glu Gly Gly Cys Tyr Val Leu Ala Ser
      210      215      220
Cys Ala Thr Val Ser Pro Glu Met Ile Lys Val Leu Val Asp Thr Pro
  225      230      235      240
Asp Lys Glu Met Phe Leu Lys Ala Gly Gly Phe Ala Met Ile Phe
      245      250      255
Gly Pro Asp Gly Arg Ala Leu Ala Glu Pro Leu Pro Glu Thr Glu Glu
      260      265      270
Gly Leu Leu Val Ala Asp Ile Asp Leu Gly Met Ile Ala Leu Ala Lys
      275      280      285
Ala Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val Thr Arg
      290      295      300
Leu Leu Leu Asp Arg Arg Pro Ala Gln Arg Val Val Thr Leu Asp Ala
  305      310      315      320
Ala Phe Glu Pro Gln Asn Glu Asp Lys Gly Asp Ala Pro Ala Leu Arg
      325      330      335
Val Val Ala Glu Ser Ala Ala Ala Ala Gln
      340      345

```

<210> 385

<211> 1014

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 385

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atgaaagaag ctatcaaggt cgcctgcgtg caagccgccc cgatctacat ggatttgaag      60
gcgacgggtg acaaaacccat tgagttgatg gaagaagcag cacgtaataa tgctcgtctg      120
atcgccctttc cggaacttg gattccaggc taccatgggt ttctttggct tgactcacca      180
gcatgggcaa tgcaatttgt acgccaatac catgagaact cattggagtt ggatggccct      240
caagctaagc gcatttcaga tgcagccaag cggttgggaa tcatggtcac cctggggatg      300
agtgaacggg tcggtggcac cctttacatc agtcagtggt tcataggcga taatgggtgac      360
accattgggg cccggcgaaa gttgaaacct acttttgttg aacgtacttt gttcggcgaa      420
ggggatgggt catcgctagc gggtttcgag acgtctgttg gaaggctggg tggttatgc      480
tggtgggagc accttcaacc gctaacaaaa tacgctttgt atgcacaaaa tgaagagatt      540
cattgtgagg cttggccgag ctttagcctt tatocctaat cggcgaaaag cctggggcct      600
gatgtcaatg tagcggcctc tcgaatctat gccgttgaag ggcaatgctt cgtactagcg      660
tcgtgtgcgc tcgtttcaca atccatgatc gatatgcttt gtacagatga cgaaaagcat      720

```

```

gcgttgcttc tggctggtgg tggacactca cgtatcatag ggcctgatgg tggtgacttg      780
gtcgcgcctc ttgccgaaaa tgaagagggt attctctacg caaaccttga tcctggagta      840
cgcatccttg ctaaaatggc ggcagaccct gctggtcatt attcccgtcc cgacattact      900
cgcttgctaa tagatcgag ccctaaatta cggtagttg aaattgaagg tgatcttcgt      960
ccttacgctt tgggtaaagc gtctgagacg ggtgcgcaac tcgaagaaat ttga      1014

```

<210> 386

<211> 337

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 386

```

Met Lys Glu Ala Ile Lys Val Ala Cys Val Gln Ala Ala Pro Ile Tyr
 1          5          10          15
Met Asp Leu Lys Ala Thr Val Asp Lys Thr Ile Glu Leu Met Glu Glu
 20          25          30
Ala Ala Arg Asn Asn Ala Arg Leu Ile Ala Phe Pro Glu Thr Trp Ile
 35          40          45
Pro Gly Tyr Pro Trp Phe Leu Trp Leu Asp Ser Pro Ala Trp Ala Met
 50          55          60
Gln Phe Val Arg Gln Tyr His Glu Asn Ser Leu Glu Leu Asp Gly Pro
 65          70          75          80
Gln Ala Lys Arg Ile Ser Asp Ala Ala Lys Arg Leu Gly Ile Met Val
 85          90          95
Thr Leu Gly Met Ser Glu Arg Val Gly Gly Thr Leu Tyr Ile Ser Gln
100          105          110
Trp Phe Ile Gly Asp Asn Gly Asp Thr Ile Gly Ala Arg Arg Lys Leu
115          120          125
Lys Pro Thr Phe Val Glu Arg Thr Leu Phe Gly Glu Gly Asp Gly Ser
130          135          140
Ser Leu Ala Val Phe Glu Thr Ser Val Gly Arg Leu Gly Gly Leu Cys
145          150          155          160
Cys Trp Glu His Leu Gln Pro Leu Thr Lys Tyr Ala Leu Tyr Ala Gln
165          170          175
Asn Glu Glu Ile His Cys Ala Ala Trp Pro Ser Phe Ser Leu Tyr Pro
180          185          190
Asn Ala Ala Lys Ala Leu Gly Pro Asp Val Asn Val Ala Ala Ser Arg
195          200          205
Ile Tyr Ala Val Glu Gly Gln Cys Phe Val Leu Ala Ser Cys Ala Leu
210          215          220
Val Ser Gln Ser Met Ile Asp Met Leu Cys Thr Asp Asp Glu Lys His
225          230          235          240
Ala Leu Leu Leu Ala Gly Gly Gly His Ser Arg Ile Ile Gly Pro Asp
245          250          255
Gly Gly Asp Leu Val Ala Pro Leu Ala Glu Asn Glu Glu Gly Ile Leu
260          265          270
Tyr Ala Asn Leu Asp Pro Gly Val Arg Ile Leu Ala Lys Met Ala Ala
275          280          285
Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Ile Thr Arg Leu Leu Ile
290          295          300
Asp Arg Ser Pro Lys Leu Pro Val Val Glu Ile Glu Gly Asp Leu Arg
305          310          315          320
Pro Tyr Ala Leu Gly Lys Ala Ser Glu Thr Gly Ala Gln Leu Glu Glu
325          330          335
Ile

```